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(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING STRESS, RESISTANCE AND TOLERANCE PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated SRT nucleic acid molecules, which encode novel SRT proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SRT nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SRT proteins, mutated SRT proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SRT genes in this organism.

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS, RESISTANCE AND TOLERANCE PROTEINS

Related Applications

This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/142692, filed July 1, 1999, and also to U.S. Provisional Patent Application Serial No. 60/151214, filed August 27, 1999. This application also claims priority to German Patent Application No. 19930429.7, filed July 1, 1999, German Patent Application No. 19931413.6, filed July 8, 1999, German Patent Application No. 19931457.8, filed July 8, 1999, German Patent Application No. 19931541.8, filed July 8, 1999, German Patent Application No. 19932209.0, filed July 9, 1999, German Patent Application No. 19932230.9, filed July 9, 1999, German Patent Application No. 19932914.1, filed July 14, 1999, German Patent Application No. 19940764.9, filed August 27, 1999, and German Patent Application No. 19941382.7, filed August 31, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein in their entirety by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through large-scale culture of bacteria developed to produce and secrete large quantities of a particular desired molecule. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as stress, resistance and tolerance (SRT) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The SRT nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the SRT nucleic acids of the invention, or modification of the sequence of the SRT nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a Corynebacterium or Brevibacterium species).

The SRT nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The SRT nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms.

Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered Corynebacterium or Brevibacterium species.

The SRT proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, permitting *C. glutamicum* to survive in a setting which is either chemically or environmentally hazardous to this microorganism. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama et al, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals, through the ability of these proteins to permit growth and multiplication of *C. glutamicum* (and also continuous production of one or more fine chemicals) under circumstances which would normally impede growth of the organism, such as those conditions frequently encountered during large-scale fermentative growth. For example, by overexpressing or engineering a heat-shock induced protease molecule such that it is optimized in activity, one may increase the ability of the bacterium to degrade incorrectly folded proteins when the bacterium is challenged with high temperatures. By having fewer misfolded (and possibly misregulated or nonfunctional) proteins to interfere with normal reaction mechanisms in the cell, the cell is increased in its ability to function normally in such a culture, which should in turn provide increased viability. This overall increase in number of cells having greater viability and activity in the culture should also result in an increase in yield, production, and/or efficiency of production of one or more desired fine chemicals, due at least to the relatively greater number of cells producing these chemicals in the culture.

This invention provides novel SRT nucleic acid molecules which encode SRT proteins which are capable of, for example, permitting *C. glutamicum* to survive in a setting which is either chemically or environmentally hazardous to this microorganism. Nucleic acid molecules encoding an SRT protein are referred to herein as SRT nucleic acid molecules. In a preferred embodiment, the SRT protein participates in metabolic pathways permitting *C. glutamicum* to survive in a setting which is either chemically or

environmentally hazardous to this microorganism. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an SRT protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of SRT-encoding nucleic acid (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth as the odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth as an odd-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....), or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth as an even-numbered SEQ ID NO in the Sequence Listing (*e.g.*, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8....).. The preferred SRT proteins of the present invention also preferably possess at least one of the SRT activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence having an even-numbered SEQ ID NO: in the Sequence Listing), *e.g.*, sufficiently homologous to an amino acid sequence of the invention such that the protein or portion thereof maintains an SRT activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or

more homologous to an amino acid sequence of the invention (*e.g.*, an entire amino acid sequence selected from those having an even-numbered SEQ ID NO in the Sequence Listing). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention (encoded by an open reading frame shown the corresponding odd-numbered SEQ ID NOs in the Sequence Listing (*e.g.*, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7....).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an SRT fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of one of the even-numbered SEQ ID NOs in the Sequence Listing) and has the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism, or possesses one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO in the Sequence Listing). Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* SRT protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an SRT protein by culturing the host cell in a suitable medium. The SRT protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an SRT gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by the introduction of a nucleic acid molecule of the invention encoding wild-type or mutated SRT sequence as

a transgene. In another embodiment, an endogenous SRT gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered SRT gene. In another embodiment, an endogenous or introduced SRT gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SRT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of a SRT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SRT gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in the Sequence Listing as SEQ ID NOs 1 through 304)) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated SRT protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated SRT protein or portion thereof possesses the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism. In another preferred embodiment, the isolated SRT protein or portion thereof is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: in the Sequence Listing) such that the protein or portion thereof maintains the ability to increase the survival of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism.

The invention also provides an isolated preparation of an SRT protein. In preferred embodiments, the SRT protein comprises an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In another preferred embodiment, the invention pertains to an isolated full length protein

which is substantially homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) (encoded by an open reading frame set forth in a corresponding odd-numbered SEQ ID NO: of the Sequence Listing).). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing). In other embodiments, the isolated SRT protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and is able to improve the survival rate of *C. glutamicum* in a setting which is either chemically or environmentally hazardous to this microorganism, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated SRT protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologousto a nucleotide sequence of one of the even-numbered SEQ ID NOs set forth in the Sequence Listing. It is also preferred that the preferred forms of SRT proteins also have one or more of the SRT bioactivities described herein.

The SRT polypeptide, or a biologically active portion thereof, can be operatively linked to a non-SRT polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the SRT protein alone. In other preferred embodiments, this fusion protein results in increased yields, production, and/or efficiency of production of a desired fine chemical from *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates the production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an SRT protein, either by interacting with the protein itself or a substrate or binding partner of the SRT protein, or by modulating the transcription or translation of an SRT nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an SRT nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an SRT nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates SRT protein activity or SRT nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated in resistance to one or more toxic chemicals or in resistance to one or more environmental stresses, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates SRT protein activity can be an agent which stimulates SRT protein activity or SRT nucleic acid expression. Examples of agents which stimulate SRT protein activity or SRT nucleic acid expression include small molecules, active SRT proteins, and nucleic acids encoding SRT proteins that have been introduced into the cell. Examples of agents which inhibit SRT activity or expression include small molecules, and antisense SRT nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant SRT gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides SRT nucleic acid and protein molecules which are involved in the survival of *C. glutamicum* upon exposure of this microorganism to chemical or environmental hazards. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, since these SRT proteins provide a means for continued growth and multiplication of *C. glutamicum* in the presence of toxic chemicals or hazardous environmental conditions, such as may be encountered during large-scale fermentative growth. By increasing the growth rate or at least maintaining normal growth in the face of poor, if not toxic, conditions, one may increase the yield, production, and/or efficiency of production of one or more fine chemicals from such a culture, at least due to the relatively greater number of cells producing the fine chemical in the culture. Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in

Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in

both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino aids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α-ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β-carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of

the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms, such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B_1) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B_2) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B_6' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B_5), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives

of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B_{12}) and porphyrines belong to a group of chemicals characterized by a tetrapyrole ring system. The biosynthesis of vitamin B_{12} is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B_6, pantothenate, and biotin. Only Vitamin B_{12} is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are

nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell.

Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α-1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) J. Japan 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Resistance to Damage from Chemicals, Environmental Stress, and Antibiotics

Production of fine chemicals is typically performed by large-scale culture of bacteria developed to produce and secrete large quantities of these molecules. However, this type of large-scale fermentation results in the subjection of the microorganisms to stresses of various kinds. These stresses include environmental stress and chemical stress.

A. Resistance to Environmental Stress

Examples of environmental stresses typically encountered in large-scale fermentative culture include mechanical stress, heat stress, stress due to limited oxygen, stress due to oxygen radicals, pH stress, and osmotic stress. The stirring mechanism used in most large-scale fermentors to ensure aeration of the culture produces heat, thus increasing the temperature of the culture. Increases in temperature induce the well-characterized heat shock response, in which a set of proteins are expressed which not

only aid in the survival of the bacterium in the face of high temperatures, but also increase survival in response to a number of other environmental stresses (see Neidhardt, F.C., *et al.*, eds. (1996) *E. coli* and *Salmonella.* ASM Press: Washington, D.C., p. 1382-1399; Wosten, M. M. (1998) *FEMS Microbiology Reviews* 22(3): 127-50; Bahl, H. *et al.* (1995) *FEMS Microbiology Reviews* 17(3): 341-348; Zimmerman, J.L., Cohill, P.R. (1991) *New Biologist* 3(7): 641-650; Samali, A., and Orrenius, S. (1998) *Cell. Stress Chaperones* 3(4): 228-236, and references contained therein from each of these citations). Regulation of the heat shock response in bacteria is facilitated by specific sigma factors and other cellular regulators of gene expression (Hecker, M., Volker, U (1998). *Molecular Microbiology* 29(5): 1129-1136). One of the largest problems that the cell encounters when exposed to high temperature is that protein folding is impaired; nascent proteins have sufficient kinetic energy in high temperature circumstances that it is difficult for the growing polypeptide chain to remain in a stable conformation long enough to fold properly. Thus, two of the key types of proteins expressed during the heat shock response consist of chaperones (proteins which assist in the folding or unfolding of other proteins – see, *e.g.*, Fink, A.L. (1999) *Physiol. Rev.* 79(2): 425-449), and proteases, which can destroy any improperly folded proteins. Examples of chaperones expressed during the heat shock response include GroEL and DNAK; proteases known to be expressed during this cellular reaction to heat shock include Lon, FtsH, and ClpB.

Other environmental stresses besides heat may also provoke a stress response. Though the fermentor stirring process is meant to introduce oxygen into the culture, oxygen may remain in limited supply, particularly when the culture is advanced in growth and the oxygen needs of the culture are thereby increased; an insufficient supply of oxygen is another stress for the microorganism. Cells in fermentor cultures are also subjected to a number of osmotic stresses, particularly when nutrients are added to the culture, resulting in a high extracellular and low intracellular concentration of these molecules. Further, the large quantities of the desired molecules produced by these organisms in culture may contribute to osmotic stress of the bacteria. Lastly, aerobic metabolism such as that used by *C. glutamicum* results in carbon dioxide as a waste product; secretion of this molecule may acidify the culture medium due to conversion of this molecule to carboxylic acid. Thus, bacteria in culture are also frequently subjected

to acidic pH stress. The converse may also be true – when high levels of basic waste molecules such as ammonium are present in the culture medium, the bacteria in culture may be subjected to basic pH stress as well.

To combat such environmental stresses, bacteria have elegant gene systems which are expressed upon exposure to one or more stresses, such as the aforementioned heat shock system. Genes expressed in response to osmotic stress, for example, encode proteins capable of transporting or synthesizing compatible solutes such that osmotic intake or export of a particular molecule is slowed to manageable levels. Other examples of stress-induced bacterial proteins are those involved in trehalose biosynthesis, those encoding enzymes involved in ppGpp metabolism, those involved in signal transduction, particularly those encoding two-component systems which are sensitive to osmotic pressure, and those encoding transcription factors which are responsive to a variety of stress factors (*e.g.*, RssB analogues and/or sigma factors). Many other such genes and their protein products are known in the art.

B. Resistance to Chemical Stress

Aside from environmental stresses, cells may also experience a number of chemical stresses. These may fall into two categories. The first are natural waste products of metabolism and other cellular processes which are secreted by the cell to the surrounding medium. The second are chemicals present in the extracellular medium which do not originate from the cell. Generally, when cells excrete toxic waste products from the concentrated intracellular cytoplasm into the relatively much more dilute extracellular medium, these products dissipate such that extracellular levels of the possibly toxic compound are quite low. However, in large-scale fermentative culture of the bacterium, this may not be the case: so many bacteria are grown in a relatively small environment and at such a high metabolic rate that waste products may accumulate in the medium to nearly toxic levels. Examples of such wastes are carbon dioxide, metal ions, and reactive oxygen species such as hydrogen peroxide. These compounds may interfere with the activity or structure of cell surface molecules, or may re-enter the cell, where they can seriously damage proteins and nucleic acids alike. Certain other chemicals hazardous to the normal functioning of cells may be naturally found in the extracellular medium. For example, metal ions such as mercury, cadmium, nickel or

copper are frequently found in water sources, and may form tight complexes with cellular enzymes which prevent the normal functioning of these proteins.

C. Resistance to Antibiotics

Bacteriocidal proteins or antibiotics, may also be found in the extracellular milieu, either through the intervention of the researcher, or as a natural product from another organism, utilized to gain a competitive advantage. Microorganisms have several art-known mechanisms to protect themselves against antimicrobial chemicals. Degradation, modification, and export of compounds toxic to the cell are common methods by which microorganisms eliminate or detoxify antibiotics. Cytoplasmic 'efflux-pumps' are known in several prokaryotes and show similarities to the so-called 'multidrug resistance' proteins from higher eukaryotes (Neyfakh, A. A. , *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88: 4781-4785). Examples of such proteins include emrAB from *E. coli* (Lomovskaya, O. and K. Lewis (1992) *Proc. Natl. Acad. Sci. USA* 89: 8938-8942), lmrB from *B. subtilis* (Kumano, M. *et al.* (1997) *Microbiology* 143: 2775-2782), smr from *S. aureus* (Grinius, L.G. *et al.* (1992) *Plasmid* 27: 119-129) or cmr from *C. glutamicum* (Kaidoh, K. *et al.* (1997) *Micro. Drug Resist.* 3: 345-350). *C. glutamicum* itself is non-pathogenic, in contrast to several other members of the genus Corynebacterium , such as *C. diphtheriae* or *C. pseudotuberculosis*. Several pathogenic Corynebacteria are known to have multiple resistances against a variety of antibiotics, such as *C. jeikeium* and *C. urealyticum* (Soriano, F. *et al.* (1995) *Antimicrob. Agents Chemother.* 39: 208-214).

Lincosamides are recognized as effective antibiotics against Corynebacterium species (Soriano, F. *et al.* (1995) *Antimicrob. Agents Chemother.* 39: 208-214). An unexpected result of the present invention was the identification of a gene encoding a lincosamide-resistance protein (in particular, a lincomycin-resistance protein). The LMRB protein from *C. glutamicum* shows 40% homology to the product of the lmrB gene from *B. subtilis* (see Genbank accession no. AL009126), as calculated using version 1.7 of the program CLUSTALW (Thompson, J.D., Higgins, D.G., Gibson, T. J. (1994) *Nucl. Acids Res.* 22: 4673-4680) using standard parameters (PAIRWISE ALIGNMENT PARAMETERS: slow/accurate alignments: Gap Open Penalty = 10.00, Gap Extension Penalty = 0.10, Protein weight matrix = BLOSUM 30, DNA weight

matrix = IUB, Fast/Approximate alignments: Gap penalty = 3, K-tuple (word) size = 1, No. of top diagonals = 5, Window size = 5, Toggle Slow/Fast pairwise alignments = slow. Multiple alignment parameters: Gap Opening Penalty = 10.00, Gap Extension Penalty = 0.05, Delay divergent sequences = 40%, DNA transitions weight = 0.50, Protein weight matrix = BLOSUM series, DNA weight matrix = IUB, Use negative matrix = OFF).

Environmental stress, chemical stress, and antibiotic or other antimicrobial stress may influence the behavior of the microorganisms during fermentor culture, and may have an impact on the production of the desired compound from these organisms. For example, osmotic stress of a microorganism may cause inappropriate or inappropriately rapid uptake of one or more compounds which can ultimately lead to cellular damage or death due to osmotic shock. Similarly, chemicals present in the culture, either exogenously added (*e.g.*, antimicrobial compounds intended to eliminate unwanted microbes) or generated by the bacteria themselves (*e.g.*, waste compounds such as heavy metals or oxygen radicals, or even antimicrobial compounds) may result in inhibition of fine chemical production or even death of the organism. The genes of the invention encode C. glutamicum proteins which act to prevent cell damage or death, by specifically counteracting the source or effect of the environmental or chemical stress.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as SRT nucleic acid and protein molecules, which increase the ability of *C. glutamicum* to survive in chemically or environmentally hazardous settings. In one embodiment, the SRT molecules function to confer resistance to one or more environmental or chemical stresses to *C. glutamicum*. In a preferred embodiment, the activity of the SRT molecules of the present invention has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the SRT molecules of the invention are modulated in activity, such that the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum* is also modulated.

The language, "SRT protein" or "SRT polypeptide" includes proteins which participate in the resistance of *C. glutamicum* to one or more environmental or chemical stresses. Examples of SRT proteins include those encoded by the SRT genes set forth in Table 1 and by the odd-numbered SEQ ID NOs. The terms "SRT gene" or "SRT nucleic acid sequence" include nucleic acid sequences encoding an SRT protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of SRT genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The terms "resistance" and "tolerance" are art-known and include the ability of a cell to not be affected by exposure to a chemical or an environment which would otherwise be detrimental to the normal functioning of these organisms. The terms "stress" or "hazard" include factors which are detrimental to the normal functioning of

cells such as *C. glutamicum*. Examples of stresses include "chemical stress", in which a cell is exposed to one or more chemicals which are detrimental to the cell, and "environmental stress" where a cell is exposed to an environmental condition outside of those to which it is adapted. Chemical stresses may be either natural metabolic waste products such as, but not limited to reactive oxygen species or carbon dioxide, or chemicals otherwise present in the environment, including, but not limited to heavy metal ions or bacteriocidal proteins such as antibiotics. Environmental stresses may be, but are not limited to temperatures outside of the normal range, suboptimal oxygen availability, osmotic pressures, or extremes of pH, for example.

In another embodiment, the SRT molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum.* Using recombinant genetic techniques, one or more of the SRT proteins of the invention may be manipulated such that its function is modulated. The alteration of activity of stress response, resistance or tolerance genes such that the cell is increased in tolerance to one or more stresses may improve the ability of that cell to grow and multiply in the relatively stressful conditions of large-scale fermentor culture. For example, by overexpressing or engineering a heat-shock induced chaperone molecule such that it is optimized in activity, one may increase the ability of the bacterium to correctly fold proteins in the face of nonoptimal temperature conditions. By having fewer misfolded (and possibly misregulated or nonfunctional) proteins, the cell is increased in its ability to function normally in such a culture, which should in turn provide increased viability. This overall increase in number of cells having greater viability and activity in the culture should also result in an increase in the yield, production, and/or efficiency of production of one or more desired fine chemicals, due at least to the relatively greater number of cells producing these chemicals in the culture.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* SRT DNAs and the predicted amino acid sequences of the *C. glutamicum* SRT proteins are shown the Sequence Listing as odd-numbered SEQ ID NOs and even-numbered SEQ ID NOs, respectively.,.

Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode chemical and environmental stress, resistance, and tolerance proteins.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of the invention (*e.g.*, the sequence of an even-numbered SEQ ID NO of the Sequence Listing). As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 75%-80% identical, 85-87% identical, 91-92% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included.

The SRT proteins or biologically active portions or fragments thereof of the invention can confer resistance or tolerance to one or more chemical or environmental stresses, or may have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode SRT polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of SRT-encoding nucleic acid (*e.g.*, SRT DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides

of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3'end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated SRT nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g,* a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of an odd-numbered SEQ ID NO of the Sequence Listing, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* SRT DNA can be isolated from a *C. glutamicum* library using all or portion of one of the odd-numbered SEQ ID NO sequences of the Sequence Listing as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.,* an odd-numbered SEQ ID NO:) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the nucleic acid sequences of the invention (*e.g.*, an odd-numbered SEQ ID NO of the Sequence Listing) can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate

extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in the Sequence Listing. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an SRT nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in the Sequence Listing. The nucleic acid sequences of the invention, as set forth in the Sequence Listing, correspond to the *Corynebacterium glutamicum* SRT DNAs of the invention. This DNA comprises sequences encoding SRT proteins (*i.e.*, the "coding region", indicated in each odd-numbered SEQ ID NO: sequence in the Sequence Listing), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in each odd-numbered SEQ ID NO: in the Sequence Listing. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the nucleic acid sequences of the Sequence Listing.

For the purposes of this application, it will be understood that each of the nucleic acid and amino acid sequences set forth in the Sequence Listing has an identifying RXA, RXN, or RXS number having the designation “RXA”, “RXN”, or “RXS” followed by 5 digits (*i.e.*, RXA01524, RXN00493, or RXS01027). Each of the nucleic acid sequences comprises up to three parts: a 5’ upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation “one of the odd-numbered sequences of the Sequence Listing”, then, refers to any of the nucleic acid sequences in the Sequence Listing, , which may be also be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is also et forth in the Sequence Listing, as an

even-numbered SEQ ID NO: immediately following the corresponding nucleic acid sequence. For example, the coding region for RXA01524 is set forth in SEQ ID NO:1, while the amino acid sequence which it encodes is set forth as SEQ ID NO:2. The sequences of the nucleic acid molecules of the invention are identified by the same RXA, RXN, or RXS designations as the amino acid molecules which they encode, such that they can be readily correlated. For example, the amino acid sequence designated RXA01524 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXA01524, the amino acid sequence designated RXN00034 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXN00034, and the amino acid sequence in designated RXS00568 is a translation of the coding region of the nucleotide sequence of nucleic acid molecule RXS00568. The correspondence between the RXA, RXN, and RXS nucleotide and amino acid sequences of the invention and their assigned SEQ ID NOs is set forth in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, or RXS designation. For example, SEQ ID NO:7, designated, as indicated on Table 1, as "F RXA00498", is an F-designated gene, as are SEQ ID NOs: 25, 33, and 37 (designated on Table 1 as "F RXA01345", "F RXA02543", and "F RXA02282", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences of the invention is one which is sufficiently complementary to one of the nucleotide sequences shown in the Sequence

Listing (*e.g.*, the sequence of an odd-numbered SEQ ID NO:) such that it can hybridize to one of the nucleotide sequences of the invention, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing), or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences of the invention,, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of the sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an SRT protein. The nucleotide sequences determined from the cloning of the SRT genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning SRT homologues in other cell types and organisms, as well as SRT homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the nucleotide sequences of the invention (*e.g.*, a sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing),, an anti-sense sequence of one of these sequences, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of the invention can be used in PCR reactions to clone SRT homologues.

Probes based on the SRT nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an SRT protein, such as by measuring a level of an SRT-encoding nucleic acid in a sample of cells, *e.g.*, detecting SRT mRNA levels or determining whether a genomic SRT gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO of the Sequence Listing) such that the protein or portion thereof maintains the ability to confer resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in a sequence of one of the even-numbered SEQ ID NOs of the Sequence Listing) amino acid residues to an amino acid sequence of the invention such that the protein or portion thereof is capable of participating in the resistance of *C. glutamicum* to one or more chemical or environmental stresses. Protein members of such metabolic pathways, as described herein, function to increase the resistance or tolerance of *C. glutamicum* to one or more environmental or chemical hazards or stresses. Examples of such activities are also described herein. Thus, “the function of an SRT protein" contributes to the overall resistance of *C. glutamicum* to elements of its surroundings which may impede its normal growth or functioning, and/or contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of SRT protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of

the Sequence Listing). Ranges and identity values intermediate to the above-recited values, (*e.g.*, 75%-80% identical, 85-87% identical, or 91-92% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included.

Portions of proteins encoded by the SRT nucleic acid molecules of the invention are preferably biologically active portions of one of the SRT proteins. As used herein, the term "biologically active portion of an SRT protein" is intended to include a portion, *e.g.*, a domain/motif, of an SRT protein that is capable of imparting resistance or tolerance to one or more environmental or chemical stresses or hazards, or has an activity as set forth in Table 1. To determine whether an SRT protein or a biologically active portion thereof can increase the resistance or tolerance of C. glutamicum to one or more chemical or environmental stresses or hazards, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an SRT protein can be prepared by isolating a portion of one of the amino acid sequences of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing), expressing the encoded portion of the SRT protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the SRT protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing) (and portions thereof) due to degeneracy of the genetic code and thus encode the same SRT protein as that encoded by the nucleotide sequences of the invention. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in the Sequence Listing (*e.g.*, an even-numbered SEQ ID NO:).. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of the invention (encoded by an open reading frame shown in an odd-numbered SEQ ID NO: of the Sequence Listing).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 39% identical to the nucleotide sequence designated RXA00084 (SEQ ID NO:189), a nucleotide sequence which is greater than and/or at least 56% identical to the nucleotide sequence designated RXA00605 (SEQ ID NO:11), and a nucleotide sequence which is greater than and/or at least 50% identical to the nucleotide sequence designated RXA00886 (SEQ ID NO:39). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* SRT nucleotide sequences set forth in the Sequence Listing as odd-numbered SEQ ID NOs, it will be appreciated by one of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of SRT proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the SRT gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an SRT protein, preferably a *C. glutamicum* SRT protein. Such

natural variations can typically result in 1-5% variance in the nucleotide sequence of the SRT gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in SRT that are the result of natural variation and that do not alter the functional activity of SRT proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* SRT DNA of the invention can be isolated based on their homology to the *C. glutamicum* SRT nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of an odd-numbered SEQ ID NO: of the Sequence Listing. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art in the art and can be found in Ausubel *et al.*, *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a nucleotide sequence of the invention corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* SRT protein.

In addition to naturally-occurring variants of the SRT sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be

introduced by mutation into a nucleotide sequence of the invention, thereby leading to changes in the amino acid sequence of the encoded SRT protein, without altering the functional ability of the SRT protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a nucleotide sequence of the invention. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the SRT proteins (*e.g.*, an even-numbered SEQ ID NO: of the Sequence Listing) without altering the activity of said SRT protein, whereas an "essential" amino acid residue is required for SRT protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having SRT activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SRT activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding SRT proteins that contain changes in amino acid residues that are not essential for SRT activity. Such SRT proteins differ in amino acid sequence from a sequence of an even-numbered SEQ ID NO: of the Sequence Listing yet retain at least one of the SRT activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of the invention and is capable of increasing the resistance or tolerance of C. glutamicum to one or more environmental or chemical stresses, or has one or more of the activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to the amino acid sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, more preferably at least about 60-70% homologous to one of these sequences, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of these sequences in, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the amino acid sequences of the invention.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the amino acid sequences of the invention and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one

sequence (*e.g.*, one of the amino acid sequences of the invention) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the amino acid sequence), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an SRT protein homologous to a protein sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing)can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of the invention such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the nucleotide sequences of the invention by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an SRT protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an SRT coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an SRT activity described herein to identify mutants that retain SRT activity. Following mutagenesis of one the nucleotide sequence of one of the odd-numbered SEQ ID NOs of the Sequence Listing, the encoded protein can be expressed recombinantly and the activity of the protein can

be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding SRT proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire SRT coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an SRT protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO.: 120 (RXA00600) comprises nucleotides 1 to1098). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding SRT. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding SRT disclosed herein (*e.g.*, the sequences set forth as odd-numbered SEQ ID NOs in the Sequence Listing), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of SRT mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of SRT mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of SRT mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to

increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5- oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an SRT protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in

which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave SRT mRNA transcripts to thereby inhibit translation of SRT mRNA. A ribozyme having specificity for an SRT-encoding nucleic acid can be designed based upon the nucleotide sequence of an SRT cDNA disclosed herein (*i.e.*, SEQ ID NO:119 (RXA00600)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an SRT-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, SRT mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, SRT gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an SRT nucleotide sequence (*e.g.*, an SRT promoter and/or enhancers) to form triple helical structures that prevent transcription of an SRT gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an SRT protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185,

Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, $lacI^q$-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, arny, SPO2, λ-P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MFα, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, SRT proteins, mutant forms of SRT proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of SRT proteins in prokaryotic or eukaryotic cells. For example, SRT genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the SRT protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant SRT protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λgt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7

gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the SRT protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ, pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the SRT proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the SRT proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and

European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to SRT mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an SRT protein can be expressed in bacterial cells such as *C. glutamicum,* insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related

to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA)) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an SRT protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an SRT gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the SRT gene. Preferably, this SRT gene is a *Corynebacterium glutamicum* SRT gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous SRT gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively,

the vector can be designed such that, upon homologous recombination, the endogenous SRT gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous SRT protein). In the homologous recombination vector, the altered portion of the SRT gene is flanked at its 5' and 3' ends by additional nucleic acid of the SRT gene to allow for homologous recombination to occur between the exogenous SRT gene carried by the vector and an endogenous SRT gene in a microorganism. The additional flanking SRT nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced SRT gene has homologously recombined with the endogenous SRT gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an SRT gene on a vector placing it under control of the lac operon permits expression of the SRT gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous SRT gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous or introduced SRT gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional SRT protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an SRT gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the SRT gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described SRT gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an SRT protein. Accordingly, the invention further provides methods for producing SRT proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an SRT protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SRT protein) in a suitable medium until SRT protein is produced. In another embodiment, the method further comprises isolating SRT proteins from the medium or the host cell.

C. Isolated SRT Proteins

Another aspect of the invention pertains to isolated SRT proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of SRT protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of SRT protein having less than about 30% (by dry weight) of non-SRT protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-SRT protein, still more preferably less than about 10% of non-SRT protein, and most preferably less than about 5% non-SRT protein. When the SRT protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SRT protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of SRT protein having less than about 30% (by dry weight) of chemical precursors or non-SRT chemicals, more preferably less than

about 20% chemical precursors or non-SRT chemicals, still more preferably less than about 10% chemical precursors or non-SRT chemicals, and most preferably less than about 5% chemical precursors or non-SRT chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the SRT protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* SRT protein in a microorganism such as *C. glutamicum*.

An isolated SRT protein or a portion thereof of the invention can contribute to the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) such that the protein or portion thereof maintains the ability to mediate the resistance or tolerance of *C. glutamicum* to one or more chemical or environmental stresses or hazards. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an SRT protein of the invention has an amino acid sequence set forth as an even-numbered SEQ ID NO: of the Sequence Listing. In yet another preferred embodiment, the SRT protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention (*e.g.*, a sequence of an odd-numbered SEQ ID NO: of the Sequence Listing). In still another preferred embodiment, the SRT protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of the invention , or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper

and/or lower limits are intended to be included. The preferred SRT proteins of the present invention also preferably possess at least one of the SRT activities described herein. For example, a preferred SRT protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of the invention, and which can increase the resistance or tolerance of C. glutamicum to one or more environmental or chemical stresses, or which has one or more of the activities set forth in Table 1.

In other embodiments, the SRT protein is substantially homologous to an amino acid sequence of the invention (*e.g.*, a sequence of an even-numbered SEQ ID NO: of the Sequence Listing) and retains the functional activity of the protein of one of the amino acid sequences of the invention yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the SRT protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of the invention and which has at least one of the SRT activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of the invention .

Biologically active portions of an SRT protein include peptides comprising amino acid sequences derived from the amino acid sequence of an SRT protein, *e.g.*, an amino acid sequence of an even-numbered SEQ ID NO: of the Sequence Listing or the amino acid sequence of a protein homologous to an SRT protein, which include fewer amino acids than a full length SRT protein or the full length protein which is homologous to an SRT protein, and exhibit at least one activity of an SRT protein.

Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an SRT protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an SRT protein include one or more selected domains/motifs or portions thereof having biological activity.

SRT proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the SRT protein is expressed in the host cell. The SRT protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an SRT protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native SRT protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-SRT antibody, which can be produced by standard techniques utilizing an SRT protein or fragment thereof of this invention.

The invention also provides SRT chimeric or fusion proteins. As used herein, an SRT "chimeric protein" or "fusion protein" comprises an SRT polypeptide operatively linked to a non-SRT polypeptide. An "SRT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to SRT, whereas a "non-SRT polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the SRT protein, *e.g.*, a protein which is different from the SRT protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the SRT polypeptide and the non-SRT polypeptide are fused in-frame to each other. The non-SRT polypeptide can be fused to the N-terminus or C-terminus of the SRT polypeptide. For example, in one embodiment the fusion protein is a GST-SRT fusion protein in which the SRT sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant SRT proteins. In another embodiment, the fusion protein is an SRT protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression

and/or secretion of an SRT protein can be increased through use of a heterologous signal sequence.

Preferably, an SRT chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An SRT-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the SRT protein.

Homologues of the SRT protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the SRT protein. As used herein, the term "homologue" refers to a variant form of the SRT protein which acts as an agonist or antagonist of the activity of the SRT protein. An agonist of the SRT protein can retain substantially the same, or a subset, of the biological activities of the SRT protein. An antagonist of the SRT protein can inhibit one or more of the activities of the naturally occurring form of the SRT protein, by, for example, competitively binding to a downstream or upstream member of the SRT system which includes the SRT protein. Thus, the *C. glutamicum* SRT protein and homologues thereof of the present invention may increase the tolerance or resistance of *C. glutamicum* to one or more chemical or environmental stresses.

In an alternative embodiment, homologues of the SRT protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the SRT protein for SRT protein agonist or antagonist activity. In one embodiment, a variegated library of SRT variants is generated by combinatorial mutagenesis at the nucleic acid

level and is encoded by a variegated gene library. A variegated library of SRT variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SRT sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of SRT sequences therein. There are a variety of methods which can be used to produce libraries of potential SRT homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SRT sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the SRT protein coding can be used to generate a variegated population of SRT fragments for screening and subsequent selection of homologues of an SRT protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an SRT coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the SRT protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SRT homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of

vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SRT homologues (Arkin and Yourvan (1992) *PNAS* *89*:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated SRT library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of SRT protein regions required for function; modulation of an SRT protein activity; modulation of the activity of an SRT pathway; and modulation of cellular production of a desired compound, such as a fine chemical.

The SRT nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the

body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth as odd-numbered or even-numbered SEQ ID NOs, respectively, in the Sequence Listing) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The SRT nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The resistance processes in which the molecules of the invention participate are utilized by a wide variety of cells; by comparing the sequences

of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

The genes of the invention, *e.g.*, the gene encoding LMRB (SEQ ID NO:1) or other gene of the invention encoding a chemical or environmental resistance or tolerance protein (*e.g.*, resistance against one or more antibiotics), may be used as genetic markers for the genetic transformation of (*e.g.*, the transfer of additional genes into or disruption of preexisting genes of) organisms such as *C. glutamicum* or other bacterial species. Use of these nucleic acid molecules permits efficient selection of organisms which have incorporated a given transgene cassette (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon, or other nucleic acid element), based on a trait which permits the survival of the organism in an otherwise hostile or toxic environment (*e.g.*, in the presence of an antimicrobial compound). By employing one or more of the genes of the invention as genetic markers, the speed and ease with which organisms having desirable transformed traits (*e.g.*, modulated fine chemical production) are engineered and isolated are improved. While it is advantageous to use the genes of the invention for selection of transformed *C. glutamicum* and related bacteria, it is possible, as described herein, to use homologs (*e.g.*, homologs from other organisms), allelic variants or fragments of the gene retaining desired activity. Furthermore, 5' and 3' regulatory elements of the genes of the invention may be modified as described herein (*e.g.*, by nucleotide substitution, insertion, deletion, or replacement with a more desirable genetic element) to modulate the transcription of the gene. For example, an LMRB variant in which the nucleotide sequence in the region from –1 to –200 5' to the start codon has been altered to modulate (preferably increase) the transcription and/or translation of LMRB may be employed, as can constructs in which a gene of the invention (*e.g.*, the LMRB gene (SEQ ID NO:1)) is functionally coupled to one or more regulatory signals (*e.g.*, inducer or repressor binding sequences) which can be used for modulating gene expression.

Similarly, more than one copy of a gene (functional or inactivated) of the invention may be employed.

An additional application of the genes of the invention (*e.g.*, the gene encoding LMRB (SEQ ID NO:1) or other drug- or antibiotic-resistance gene) is in the discovery of new antibiotics which are active against Corynebacteria and/or other bacteria. For example, a gene of the invention may be expressed (or overexpressed) in a suitable host to generate an organism with increased resistance to one or more drugs or antibiotics (in the case of LMRB, lincosamides in particular, especially lincomycin). This type of resistant host can subsequently be used to screen for chemicals with bacteriostatic and/or bacteriocidal activity, such as novel antibiotic compounds. It is possible, in particular, to use the genes of the invention (*e.g.*, the LMRB gene) to identify new antibiotics which are active against those microorganisms which are already resistant to standard antibiotic compounds.

The invention provides methods for screening molecules which modulate the activity of an SRT protein, either by interacting with the protein itself or a substrate or binding partner of the SRT protein, or by modulating the transcription or translation of an SRT nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more SRT proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the SRT protein is assessed.

Manipulation of the SRT nucleic acid molecules of the invention may result in the production of SRT proteins having functional differences from the wild-type SRT proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity. The goal of such manipulations is to increase the viability and activity of the cell when the cell is exposed to the environmental and chemical stresses and hazards which frequently accompany large-scale fermentative culture. Thus, by increasing the activity or copy number of a heat-shock-regulated protease, one may increase the ability of the cell to destroy incorrectly folded proteins, which may otherwise interfere with normal cellular functioning (for example, by continuing to bind substrates or cofactors although the protein lacks the activity to act on these molecules appropriately). The same is true for the overexpression or optimization of activity of one or more chaperone molecules

induced by heat or cold shock. These proteins aid in the correct folding of nascent polypeptide chains, and thus their increased activity or presence should increase the percentage of correctly folded proteins in the cell, which in turn should increase the overall metabolic efficiency and viability of the cells in culture. The overexpression or optimization of the transporter molecules activated by osmotic shock should result in an increased ability on the part of the cell to maintain intracellular homeostasis, thereby increasing the viability of these cells in culture. Similarly, the overproduction or increase in activity by mutagenesis of proteins involved in the development of cellular resistance to chemical stresses of various kinds (either by transport of the offending chemical out of the cell or by modification of the chemical to a less hazardous substance) should increase the fitness of the organism in the environment containing the hazardous substance (*i.e.*, large-scale fermentative culture), and thereby may permit relatively larger numbers of cells to survive in such a culture. The net effect of all of these mutagenesis strategies is to increase the quantity of fine-chemical-producing compounds in the culture, thereby increasing the yield, production, and/or efficiency of production of one or more desired fine chemicals from the culture.

This aforementioned list of mutagenesis strategies for SRT proteins to result in increased yields of a desired compound is not meant to be limiting; variations on these mutagenesis strategies will be readily apparent to one of ordinary skill in the art. By these mechanisms, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated SRT nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, and the sequence listing cited throughout this application are hereby incorporated by reference.

TABLE 1: Genes Included in the Application

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXA01524	GR00424	29041	30483	Lincomycine RESISTANCE PROTEIN
3	4	RXA00497	GR00124	52	348	10 KD CHAPERONIN
5	6	RXN00493	VV0086	14389	16002	60 KD CHAPERONIN
7	8	F RXA00498	GR00124	363	1601	60 KD CHAPERONIN
9	10	RXA01217	GR00353	802	203	GENERAL STRESS PROTEIN CTC
11	12	RXA00605	GR00159	7412	5865	CATALASE (EC 1.11.1.6)
13	14	RXA00404	GR00089	2909	594	CARBON STARVATION PROTEIN A
15	16	RXN03119	VV0098	86877	87008	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1)
17	18	RXN03120	VV0098	87351	87476	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1)
19	20	RXN00575	VV0323	14716	15252	PHOSPHINOTHRICIN-RESISTANCE PROTEIN
21	22	F RXA00575	GR00156	2130	1648	PHOSPHINOTHRICIN-RESISTANCE PROTEIN

Chaperones

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
23	24	RXN01345	VV0123	4883	3432	Moleculares chaperon (HSP70/DnaK family)
25	26	F RXA01345	GR00391	1172	6	Molecular chaperones (HSP70/DnaK family)
27	28	RXA02541	GR00726	13657	12473	DNAJ PROTEIN
29	30	RXA02542	GR00726	14518	13865	GRPE PROTEIN
31	32	RXN02543	VV0057	22031	20178	DNAK PROTEIN
33	34	F RXA02543	GR00726	16375	14522	DNAK PROTEIN
35	36	RXN02280	VV0152	1849	26	TRAP1
37	38	F RXA02282	GR00659	1145	1480	Molecular chaperone, HSP90 family
39	40	RXA00886	GR00242	12396	13541	DNAJ PROTEIN
41	42	RXS00568	VV0251	2928	1582	TRIGGER FACTOR
43	44	RXN03038	VV0017	42941	43666	PS1 PROTEIN VORLÄUFER
45	46	RXN03039	VV0018	2	631	PS1 PROTEIN VORLÄUFER
47	48	RXN03040	VV0018	761	1069	PS1 PROTEIN VORLÄUFER
49	50	RXN03051	VV0022	2832	3566	PS1 PROTEIN VORLÄUFER
51	52	RXN03054	VV0026	1906	3486	PS1 PROTEIN VORLÄUFER
53	54	RXN02949	VV0025	31243	31575	PREPROTEIN TRANSLOKASE SECE UNTEREINHEIT
55	56	RXN02462	VV0124	11932	13749	PREPROTEIN TRANSLOKASE SECA UNTEREINHEIT
57	58	RXN01559	VV0171	7795	5954	PROTEIN-EXPORT MEMBRANE PROTEIN SECD
59	60	RXN00046	VV0119	5363	6058	Signal Erkennung particle GTPase
61	62	RXN01863	VV0206	1172	24	/O/C Thioredoxin-ähnliche oxidoreductase
63	64	RXN00833	VV0180	8039	8533	THIOL PEROXIDASE (EC 1.11.1.-)

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
65	66	RXN01676	VV0179	12059	11304	THIOL:DISULFIDE AUSTAUSCH PROTEIN DSBD
67	68	RXN00380	VV0223	836	216	THIOL:DISULFIDE AUSTAUSCH PROTEIN TLPA
69	70	RXN00937	VV0079	42335	42706	THIOREDOXIN
71	72	RXN02325	VV0047	5527	6393	THIOREDOXIN
73	74	RXN01837	VV0320	7103	7879	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8)
75	76	RXN01926	VV0284	1	741	PEPTID KETTE RELEASE FACTOR 3
77	78	RXN02002	VV0111	141	518	PEPTID KETTE RELEASE FACTOR 3
79	80	RXN02736	VV0074	13600	14556	PUTATIVES OXPPCYCLE PROTEIN OPCA
81	82	RXS03217				SMALL COLD-SHOCK PROTEIN
83	84	F RXA01917	GR00549	3465	3665	SMALL COLD-SHOCK PROTEIN

Proteins involved in stress responses

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
85	86	RXA02184	GR00641	19628	19248	COLD SHOCK-LIKE PROTEIN CSPC
87	88	RXA00810	GR00218	792	992	SMALL COLD-SHOCK PROTEIN
89	90	RXA01674	GR00467	1878	2771	PROBABLE HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR
91	92	RXA02431	GR00708	2	1192	damage-inducible protein P
93	94	RXA02446	GR00709	11640	11206	OSMOTICALLY INDUCIBLE PROTEIN C
95	96	RXA02861	GR10006	551	1633	probable metallothionein u0308aa - Mycobacterium leprae
97	98	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
99	100	RXN00786	VV0321	1680	706	LYTB PROTEIN
101	102	RXS01027	VV0143	5761	6768	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
103	104	RXS01528	VV0050	17276	16749	DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
105	106	RXS01716	VV0319	3259	2774	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
107	108	RXS01835	VV0143	10575	10045	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
109	110	RXS02497	VV0007	15609	16535	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
111	112	RXS02972	VV0319	2763	2353	EXOPOLYPHOSPHATASE (EC 3.6.1.11)

Resistance and tolerance

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
113	114	RXA02159	GR00640	6231	6743	ARGININE HYDROXIMATE RESISTANCE PROTEIN
115	116	RXA02201	GR00646	5837	6199	ARSENATE REDUCTASE
117	118	RXA00599	GR00159	1843	1457	ARSENICAL-RESISTANCE PROTEIN ACR3
119	120	RXA00600	GR00159	2940	1843	ARSENICAL-RESISTANCE PROTEIN ACR3
121	122	RXA02200	GR00646	4651	5760	ARSENICAL-RESISTANCE PROTEIN ACR3
123	124	RXA02202	GR00646	6278	6916	ARSENICAL-RESISTANCE PROTEIN ACR3
125	126	RXA02205	GR00646	9871	8993	BACITRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) (EC 2.7.1.66)
127	128	RXA00900	GR00245	4052	3201	BICYCLOMYCIN RESISTANCE PROTEIN

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
129	130	RXN00901	VV0140	8581	8168	BICYCLOMYCIN RESISTANCE PROTEIN
131	132	F RXA00901	GR00245	4357	3980	BICYCLOMYCIN RESISTANCE PROTEIN
133	134	RXA00289	GR00046	3263	4438	CHLORAMPHENICOL RESISTANCE PROTEIN
135	136	RXN01984	VV0056	1515	1811	CHLORAMPHENICOL RESISTANCE PROTEIN
137	138	F RXA01984	GR00574	282	4	CHLORAMPHENICOL RESISTANCE PROTEIN
139	140	RXA00109	GR00015	1176	565	COPPER RESISTANCE PROTEIN C PRECURSOR
141	142	RXA00109	GR00015	1176	565	COPPER RESISTANCE PROTEIN C PRECURSOR
143	144	RXA00996	GR00283	1763	1023	DAUNORUBICIN RESISTANCE ATP-BINDING PROTEIN DRRA
145	146	RXN00829	VV0180	7950	5611	DAUNORUBICIN RESISTANCE PROTEIN
147	148	F RXA00829	GR00224	2	256	DAUNORUBICIN RESISTANCE PROTEIN
149	150	F RXA00834	GR00225	463	2025	DAUNORUBICIN RESISTANCE PROTEIN
151	152	RXA00995	GR00283	1023	283	DAUNORUBICIN RESISTANCE TRANSMEMBRANE PROTEIN
153	154	RXN00803	VV0009	53858	52629	METHYLENOMYCIN A RESISTANCE PROTEIN
155	156	F RXA00803	GR00214	4560	5162	METHYLENOMYCIN A RESISTANCE PROTEIN
157	158	RXA01407	GR00410	3918	3028	METHYLENOMYCIN A RESISTANCE PROTEIN
159	160	RXA01408	GR00410	4384	4184	METHYLENOMYCIN A RESISTANCE PROTEIN
161	162	RXN01922	VV0020	2031	3182	METHYLENOMYCIN A RESISTANCE PROTEIN
163	164	F RXA01922	GR00552	3	1109	METHYLENOMYCIN A RESISTANCE PROTEIN
165	166	RXA02060	GR00626	1	339	MYCINAMICIN-RESISTANCE PROTEIN MYRA
167	168	RXN01936	VV0127	40116	41387	MACROLIDE-EFFLUX PROTEIN
169	170	F RXA01936	GR00555	9796	8975	NICKEL RESISTANCE PROTEIN
171	172	F RXA01937	GR00555	10246	9821	NICKEL RESISTANCE PROTEIN
173	174	RXN01010	VV0209	3776	4894	QUINOLONE RESISTANCE NORA PROTEIN
175	176	F RXA01010	GR00288	774	4	QUINOLONE RESISTANCE NORA PROTEIN
177	178	RXN03142	VV0136	5754	4612	QUINOLONE RESISTANCE NORA PROTEIN
179	180	F RXA01150	GR00323	3807	2917	QUINOLONE RESISTANCE NORA PROTEIN
181	182	RXN02964	VV0102	7931	6714	QUINOLONE RESISTANCE NORA PROTEIN
183	184	F RXA02116	GR00636	911	6	QUINOLONE RESISTANCE NORA PROTEIN
185	186	RXA00858	GR00233	1680	2147	TELLURIUM RESISTANCE PROTEIN TERC
187	188	RXA02305	GR00663	2921	2070	DAUNOMYCIN C-14 HYDROXYLASE
189	190	RXA00084	GR00013	2367	1543	VIBRIOBACTIN UTILIZATION PROTEIN VIUB
191	192	RXA00843	GR00228	3236	3580	ARSENATE REDUCTASE
193	194	RXA01052	GR00296	3398	3706	MERCURIC REDUCTASE (EC 1.16.1.1)
195	196	RXA01053	GR00296	3772	4191	MERCURIC REDUCTASE (EC 1.16.1.1)
197	198	RXA01054	GR00296	4229	4717	MERCURIC REDUCTASE (EC 1.16.1.1)
199	200	RXN03123	VV0106	808	1245	HEAVY METAL TOLERANCE PROTEIN PRECURSOR
201	202	F RXA00993	GR00282	641	6	HEAVY METAL TOLERANCE PROTEIN PRECURSOR
203	204	RXA01051	GR00296	3298	2690	VANZ PROTEIN , teicoplanin resistance protein
205	206	RXN01873	VV0248	2054	819	Hypothetical Drug Resistance Protein
207	208	F RXA01873	GR00535	855	1946	Hypothetical Drug Resistance Protein
209	210	RXN00034	VV0020	16933	18381	MULTIDRUG RESISTANCE PROTEIN B
211	212	F RXA02273	GR00655	8058	9002	Hypothetical Drug Resistance Protein
213	214	RXN03075	VV0042	2491	3216	Hypothetical Drug Transporter
215	216	F RXA02907	GR10044	1395	2120	Hypothetical Drug Transporter
217	218	RXA00479	GR00119	16290	14101	Hypothetical Drug Transporter
219	220	RXN03124	VV0108	4	963	Hypothetical Drug Transporter
221	222	F RXA01180	GR00336	4	765	Hypothetical Drug Transporter

Table 1 (continued)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
223	224	RXA02586	GR00741	10296	10027	Hypothetical Drug Transporter
225	226	RXA02587	GR00741	12343	10253	Hypothetical Drug Transporter
227	228	RXN03042	VV0018	2440	1835	Hypothetical Drug Transporter
229	230	F RXA02893	GR10035	1841	1236	Hypothetical Drug Transporter
231	232	RXA01616	GR00450	1684	203	MULTIDRUG EFFLUX PROTEIN QACB
233	234	RXA01666	GR00463	2307	3683	MULTIDRUG RESISTANCE PROTEIN
235	236	RXA00062	GR00009	13252	11855	MULTIDRUG RESISTANCE PROTEIN B
237	238	RXA00215	GR00032	13834	15294	MULTIDRUG RESISTANCE PROTEIN B
239	240	RXN03064	VV0038	4892	6223	MULTIDRUG RESISTANCE PROTEIN B
241	242	F RXA00565	GR00151	4892	5884	MULTIDRUG RESISTANCE PROTEIN B
243	244	F RXA02878	GR10016	1837	1481	MULTIDRUG RESISTANCE PROTEIN B
245	246	RXA00648	GR00169	2713	1304	MULTIDRUG RESISTANCE PROTEIN B
247	248	RXN01320	VV0082	13146	11500	MULTIDRUG RESISTANCE PROTEIN B
249	250	F RXA01314	GR00382	744	4	MULTIDRUG RESISTANCE PROTEIN B
251	252	F RXA01320	GR00383	1979	1200	MULTIDRUG RESISTANCE PROTEIN B
253	254	RXN02926	VV0082	11497	9866	MULTIDRUG RESISTANCE PROTEIN B
255	256	F RXA01319	GR00383	1197	4	MULTIDRUG RESISTANCE PROTEIN B
257	258	RXA01578	GR00439	1423	29	MULTIDRUG RESISTANCE PROTEIN B
259	260	RXA02087	GR00629	7076	5730	MULTIDRUG RESISTANCE PROTEIN B
261	262	RXA02088	GR00629	8294	7080	MULTIDRUG RESISTANCE PROTEIN B
263	264	RXA00764	GR00204	3284	2169	BMRU PROTEIN Bacillus subtilis bmrU, multidrug efflux transporter
265	266	RXN03125	VV0108	972	1142	Hypothetical Drug Transporter
267	268	RXN01553	VV0135	25201	26520	Hypothetical Drug Permease
269	270	RXN00535	VV0219	5155	5871	Hypothetical Drug Resistance Protein
271	272	RXN00453	VV0076	1173	3521	Hypothetical Drug Transporter
273	274	RXN00932	VV0171	13120	13593	Hypothetical Drug Transporter
275	276	RXN03022	VV0002	65	511	MULTIDRUG RESISTANCE PROTEIN B
277	278	RXN03151	VV0163	489	4	MYCINAMICIN-RESISTANCE PROTEIN MYRA
279	280	RXN02832	VV0358	547	5	LYSOSTAPHIN IMMUNITY FACTOR
281	282	RXN00165	VV0232	3275	1860	MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL
283	284	RXN01190	VV0169	8992	10338	MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL
285	286	RXN01102	VV0059	6128	4884	QUINOLONE RESISTANCE NORA PROTEIN
287	288	RXN00788	VV0321	3424	3648	CHLORAMPHENICOL RESISTANCE PROTEIN
289	290	RXN02119	VV0102	11242	9602	A201A-RESISTANCE ATP-BINDING PROTEIN
291	292	RXN01605	VV0137	7124	5610	DAUNORUBICIN RESISTANCE TRANSMEMBRANE PROTEIN
293	294	RXN01091	VV0326	567	4	MAZG PROTEIN
295	296	RXS02979	VV0149	2150	2383	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
297	298	RXS02987	VV0234	527	294	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
299	300	RXS03095	VV0057	4056	4424	CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG

TABLE 2 – Excluded Genes

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat corboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," *Biochem. Biophys. Res. Commun.*, 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," *Appl. Microbiol. Biotechnol.*, 51(2):223-228 (1999)
AB018530	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, which rescues the detergent sensitivity of a mutant derived from *Brevibacterium lactofermentum*," *Biosci. Biotechnol. Biochem.*, 60(10):1565-1570 (1996)
AB018531	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	
AF038548	pyc	Pyruvate carboxylase	

Table 2 (continued)

AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," *Microbiology*, 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," *Mol. Cells.*, 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," *Appl. Environ. Microbiol.*, 65(4)1530-1539 (1999)
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		

Table 2 (continued)

AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete[i])	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," *J. Bacteriol.*, 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzmye); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," *FEMS Microbiol.*, 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol aceteyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," *Eur. J. Biochem.*, 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," *Biochemistry*, 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes et al."Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," *Mol. Microbiol.*, 11(4):739-746 (1994)
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," *Microbiology*, 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87

Table 2 (continued)

E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94

Table 2 (continued)

E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97

Table 2 (continued)

E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," *J. Bacteriol.*, 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," *FEMS Microbiol. Lett.*, 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," *J. Bacteriol.*, 175(17):5595-5603 (1993)
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," *PNAS USA*, 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," *FEMS Microbiol. Lett.*, 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," *J. Microbiol. Biotechnol.*, 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," *Appl. Environ. Microbiol.*, 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," *J. Bacteriol.*, 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," *J. Bacteriol.*, 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," *J. Bacteriol.*, 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene*, 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3'end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene*, 52:191-200 (1987)

Table 2 (continued)

M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," *Gene,* 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.,* 138:1167-1175 (1992)
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.,* 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," *J. Bacteriol.,* 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," *Arch. Microbiol.,* 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," *Appl. Environ. Microbiol.,* 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; clgIIR	Putative type II 5-cytosoine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," *J. Bacteriol.,* 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," *Gene,* 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.,* 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.,* 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.,* 178(15):4412-4419 (1996)

Table 2 (continued)

U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of Methylobacillus flagellatum and Corynebacterium glutamicum," *Gene,* 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A Corynebacterium glutamicum gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," *Arch. Microbiol.,* 166(2);76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli," *J. Bacteriol.,* 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon," *Nucleic Acids Res.,* 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of Corynebacterium glutamicum and possible mechanisms for modulation of its expression," *Mol. Gen. Genet.,* 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: Molecular cloning, nucleotide sequence, and expression," *Mol. Gen. Genet.,* 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," *Plant. Mol. Biol.,* 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the Corynebacterium glutamicum fda gene: structural comparison of C. glutamicum fructose-1, 6-biphosphate aldolase to class I and class II aldolases," *Mol. Microbiol.,*
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 18(21):6421 (1990)
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," *Mol. Microbiol.,* 4(11):1819-1830 (1990)

Table 2 (continued)

X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," *Nucleic Acids Res.*, 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," *Mol. Microbiol.*, 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.*, 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," *Mol. Microbiol.*, 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspertate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," *Mol. Gen. Genet.*, 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," *J. Bacteriol.*, 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," *Mol. Microbiol.*, 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," *Mol. Microbiol.*, 5(12):2995-3005 (1991)
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," *Mol. Microbiol.*, 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," *Microbiol.*, 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," *Mol. Microbiol.*, 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," *Mol. Microbiol.*, 14(3):571-581 (1994)

Table 2 (continued)

X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," *Appl. Environ. Microbiol.*, 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," *J. Bacteriol.*, 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," *Biochem. Biophys. Res. Commun.*, 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," *Appl. Microbiol. Biotechnol.*, 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," *J. Bacteriol.*, 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek*, 64:285-305 (1993)
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek*, 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," *DNA Seq.*, 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," *Microbiology*, 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," *Microbiol.*, 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," *J. Bacteriol.*, 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," *Microbiology*, 40:3349-56 (1994)

Table 2 (continued)

X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus Corynebacterium deduced from analyses of small-subunit ribosomal DNA sequences," *Int. J. Syst. Bacteriol.*, 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.*, 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.*, 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus Corynebacterium based on 16S rRNA gene sequences," *Int. J. Syst. Bacteriol.*, 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann et al. "Functional analysis of sequences adjacent to dapE of C. glutamicum proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," *J. Bacteriol.*, 177(20):5991-5993 (1995)
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," *Microbiology*, 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," *Microbiology*, 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," *J. Bacteriol.*, 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)

Table 2 (continued)

X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from C. glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," *J. Biol. Chem.*, 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," *J. Bacteriol.*, 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," *Biotechnol. Lett.*, 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," *Mol. Microbiol.*, 22(5):815-826 (1996)

Table 2 (continued)

X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," *Appl. Environ. Microbiol.*, 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," *Gene*, 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," *Nucleic Acids Res.*, 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," *Mol. Microbiol.*, 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," *Mol. Gen. Genet.*, 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," *Arch. Microbiol.*, 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," *Microbiology*, 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," *Appl. Microbiol. Biotechnol.*, 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," *Microbiol.*, 145:539-548 (1999)
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)

Table 2 (continued)

Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," *FEMS Microbiol. Lett.*, 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," *Virology*, 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," *J. Bacteriol.*, 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," *J. Bacteriol.*, 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," *Appl. Environ. Microbiol.*, 60(7)2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," *Gene*, 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.*, 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," *Gene*, 170(1):91-94 (1996)

[1] A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							
Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							
Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							
Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							
Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4^{th} edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

TABLE 4: ALIGNMENT RESULTS

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rxa00062	1521	GB_HTG2:AC007366	185001	AC007366	Homo sapiens clone NH0501G22, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	39,080	5-Jun-99
rxa00084	948	GB_PR3:HSU80741	912	U80741	Homo sapiens CAGH44 mRNA, partial cds.	Homo sapiens	39,264	18-DEC-1997
		GB_PL1:BNDNATRNA	1732	X89901	B.nigra DNA for tRNA like gene.	Brassica nigra	36,725	6-Feb-97
		GB_PR3:HSU80741	912	U80741	Homo sapiens CAGH44 mRNA, partial cds.	Homo sapiens	38,957	18-DEC-1997
rxa00109	735	GB_GSS9:AQ163721	388	AQ163721	HS_2245_A1_F07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2245 Col=13 Row=K, genomic survey sequence.	Homo sapiens	45,066	16-OCT-1998
		GB_HTG4:AC007054	171979	AC007054	Drosophila melanogaster chromosome 2 clone BACR45O18 (D527) RPCI-98 45.O.18 map 41E-41E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 13 unordered pieces.	Drosophila melanogaster	36,589	13-OCT-1999
		GB_HTG4:AC007054	171979	AC007054	Drosophila melanogaster chromosome 2 clone BACR45O18 (D527) RPCI-98 45.O.18 map 41E-41E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 13 unordered pieces.	Drosophila melanogaster	36,589	13-OCT-1999
rxa00215	1449	GB_BA1:SC9C7	31360	AL035161	Streptomyces coelicolor cosmid 9C7.	Streptomyces coelicolor	44,444	12-Jan-99
		GB_BA1:SCE94	38532	AL049628	Streptomyces coelicolor cosmid E94.	Streptomyces coelicolor	36,313	12-Apr-99
		GB_BA2:AF110185	20302	AF110185	Burkholderia pseudomallei strain 1026b DbhB (dbhB), general secretory pathway protein D (gspD), general secretory pathway protein E (gspE), general secretory pathway protein F (gspF), GspC (gspC), general secretory pathway protein G (gspG), general secretory pathway protein H (gspH), general secretory pathway protein I (gspI), general secretory pathway protein J (gspJ), general secretory pathway protein K (gspK), general secretory pathway protein L (gspL), general secretory pathway protein M (gspM), and general secretory pathway protein N (gspN) genes, complete cds; and unknown genes.	Burkholderia pseudomallei	44,159	2-Aug-99
rxa00289	1299	GB_EST6:N80167	384	N80167	za65g02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:297458 3', mRNA sequence.	Homo sapiens	40,420	29-MAR-1996
		GB_STS:G37084	384	G37084	SHGC-56832 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	40,420	30-MAR-1998
		GB_STS:G37084	384	G37084	SHGC-56832 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	40,420	30-MAR-1998
rxa00404	2439	GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	60,271	17-Jun-98
		GB_BA1:ECU82598	136742	U82598	Escherichia coli genomic sequence of minutes 9 to 12.	Escherichia coli	54,256	15-Jan-97
		GB_BA2:AE000165	12003	AE000165	Escherichia coli K-12 MG1655 section 55 of 400 of the complete genome.	Escherichia coli	54,256	12-Nov-98
rxa00479	2313	GB_BA1:SCF43A	35437	AL096837	Streptomyces coelicolor cosmid F43A.	Streptomyces coelicolor A3(2)	36,245	13-Jul-99
		GB_GSS2:CNS015U4	1036	AL105910	Drosophila melanogaster genome survey sequence SP6 end of BAC BACN14G08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	37,573	26-Jul-99

Table 4 (continued)

		GB_PR3:HSA494O16	50502	AL117328	Human DNA sequence from clone 494O16 on chromosome 22, complete sequence.	Homo sapiens	36,475	23-Nov-99
rxa00497	420	GB_BA1:MTCY78	33818	Z77165	Mycobacterium tuberculosis H37Rv complete genome; segment 145/162.	Mycobacterium tuberculosis	40,250	17-Jun-98
		GB_BA2:AF079544	817	AF079544	Mycobacterium avium GroESL operon, partial sequence.	Mycobacterium avium	64,439	16-Aug-98
		GB_BA1:MTGROEOP	2987	X60350	M.tuberculosis groE gene for KCS and 10-kDa products.	Mycobacterium tuberculosis	62,857	23-Apr-92
rxa00575								
rxa00599	510	GB_GSS10:AQ199703	439	AQ199703	RPCI11-46O13.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-46O13, genomic survey sequence.	Homo sapiens	42,657	20-Apr-99
		GB_PR2:AC002127	144165	AC002127	Human BAC clone RG305H12 from 7q21, complete sequence.	Homo sapiens	37,052	27-MAY-1997
		GB_STS:G51234	439	G51234	SHGC-80708 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens	42,657	25-Jun-99
rxa00600	1221	GB_BA1:MTCY441	35187	Z80225	Mycobacterium tuberculosis H37Rv complete genome; segment 118/162.	Mycobacterium tuberculosis	56,183	18-Jun-98
		GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis	37,217	10-DEC-1996
		GB_BA1:BSUB0014	213420	Z99117	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.	Bacillus subtilis	36,553	26-Nov-97
rxa00605	1603	GB_BA2:AF069070	2776	AF069070	Endosymbiont of Onchocerca volvulus catalase gene, complete cds.	endosymbiont of Onchocerca volvulus	55,396	25-Nov-98
		GB_BA1:OVCAT	1845	X82176	Onchocerca volvulus endobacterial mRNA for catalase.	endosymbiont of Onchocerca volvulus	55,396	26-Nov-98
		GB_BA1:SC2G5	38404	AL035478	Streptomyces coelicolor cosmid 2G5.	Streptomyces coelicolor	39,530	11-Jun-99
rxa00648	1533	GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,327	27-Aug-99
		GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,327	27-Aug-99
		GB_HTG1:HS74O16	169401	AL110119	Homo sapiens chromosome 21 clone RPCIP704O1674 map 21q21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	35,119	27-Aug-99
rxa00764	1239	GB_EST36:AI898007	609	AI898007	EST267450 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED31K22, mRNA sequence.	Lycopersicon esculentum	34,323	27-Jul-99
		GB_BA2:PAU93274	8008	U93274	Pseudomonas aeruginosa YafE (yafE), LeuB (leuB), Asd (asd), FimV (fimV), and HisT (hisT) genes, complete cds; TrpF (trpF) gene, partial cds; and unknown	Pseudomonas aeruginosa	35,895	23-Jun-98
		GB_BA2:PAU93274	8008	U93274	Pseudomonas aeruginosa YafE (yafE), LeuB (leuB), Asd (asd), FimV (fimV), and HisT (hisT) genes, complete cds; TrpF (trpF) gene, partial cds; and unknown	Pseudomonas aeruginosa	41,417	23-Jun-98
rxa00803	1353	GB_IN2:CELH34C03	27748	AF100662	Caenorhabditis elegans cosmid H34C03.	Caenorhabditis elegans	34,152	28-OCT-1998
		GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	37,472	24-Jun-99
		GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	37,472	24-Jun-99

Table 4 (continued)

rxa00810	324	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	34,615	17-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	34,615	27-Aug-99
		GB_BA1:ECOUW76	225419	U00039	E. coli chromosomal region from 76.0 to 81.5 minutes.	Escherichia coli	52,997	7-Nov-96
rxa00829	2463	GB_BA1:SC5C7	41906	AL031515	Streptomyces coelicolor cosmid 5C7.	Streptomyces coelicolor	65,269	7-Sep-98
		GB_BA1:SC5F2A	40105	AL049587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor	37,490	24-MAY-1999
		GB_BA1:STMDRRC	3374	L76359	Streptomyces peucetius daunorubicin resistance protein (drrC) gene, complete	Streptomyces peucetius	55,279	24-DEC-1996
rxa00843	468	GB_BA1:MTCY9C4	15916	Z77250	Mycobacterium tuberculosis H37Rv complete genome; segment 113/162.	Mycobacterium tuberculosis	40,000	17-Jun-98
		GB_BA1:MTCY9C4	15916	Z77250	Mycobacterium tuberculosis H37Rv complete genome; segment 113/162.	Mycobacterium tuberculosis	37,773	17-Jun-98
rxa00858	568	GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	39,602	11-Jun-99
		GB_EST18:N96610	547	N96610	21285 Lambda-PRL1 Arabidopsis thaliana cDNA clone F10G3T7, mRNA	Arabidopsis thaliana	37,801	5-Jan-98
		GB_EST18:T45493	436	T45493	8756 Lambda-PRL2 Arabidopsis thaliana cDNA clone 133C14T7, mRNA	Arabidopsis thaliana	34,194	4-Aug-98
rxa00886	1269	GB_BA1:SYCSLLLH	132106	D64006	Synechocystis sp. PCC6803 complete genome, 25/27, 3138604-3270709.	Synechocystis sp.	37,459	13-Feb-99
		GB_BA1:SCDNAJ	5611	X77458	S.coelicolor dnaK, grpE and dnaJ genes.	Streptomyces coelicolor	49,744	21-Nov-96
		GB_BA1:STMDNAK	4648	L46700	Streptomyces coelicolor (strain A3(2)) dnaK operon encoding molecular chaperones (dnaK, dnaJ), grpE and hspR genes, complete cds's.	Streptomyces coelicolor	49,583	22-Nov-96
rxa00900	975	GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	38,314	U18997
		GB_BA2:ECOUW67_0	110000	U18997	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	Escherichia coli	37,759	U18997
		GB_BA2:AE000393	10516	AE000393	Escherichia coli K-12 MG1655 section 283 of 400 of the complete genome.	Escherichia coli	38,314	12-Nov-98
rxa00901	537	GB_HTG3:AC010757	175571	AC010757	Homo sapiens chromosome 18 clone 128_C_18 map 18, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	34,857	22-Sep-99
		GB_HTG3:AC010757	175571	AC010757	Homo sapiens chromosome 18 clone 128_C_18 map 18, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	34,857	22-Sep-99
		GB_HTG3:AC011283	87295	AC011283	Homo sapiens clone MS2016A09, *** SEQUENCING IN PROGRESS ***, 1 unordered pieces.	Homo sapiens	35,448	07-OCT-1999
rxa00981	753	GB_OV:GGA245664	512	AJ245664	Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	Gallus gallus	37,538	28-Sep-99
		GB_PL2:AC007887	159434	AC007887	Genomic sequence for Arabidopsis thaliana BAC F15O4 from chromosome I, complete sequence.	Arabidopsis thaliana	37,600	04-OCT-1999
		GB_GSS1:CNS00RNW	542	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	41,264	28-Jun-99
rxa00995	864	GB_EST29:AI553951	450	AI553951	te54d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090497 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN);, mRNA sequence.	Homo sapiens	42,627	13-Apr-99
		GB_PR3:AC003029	139166	AC003029	Homo sapiens Chromosome 12q24 PAC RPCI3-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.	Homo sapiens	38,915	17-Sep-98
		GB_BA1:EAY14603	4479	Y14603	Erwinia amylovora srlA, srlE, srlB, srlD, srlM and srlR genes.	Erwinia amylovora	37,694	6-Jan-98
rxa00996	864	GB_BA2:AE001001	10730	AE001001	Archaeoglobus fulgidus section 106 of 172 of the complete genome.	Archaeoglobus fulgidus	41,078	15-DEC-1997
		GB_EST30:AV018764	242	AV018764	AV018764 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190006M16, mRNA sequence.	Mus musculus	39,669	28-Aug-99

Table 4 (continued)

		GB_GSS3:B24189	377	B24189	F19E16TF IGF Arabidopsis thaliana genomic clone F19E16, genomic survey sequence.	Arabidopsis thaliana	44,385	10-OCT-1997
rxa01010	1242	GB_OV:AF007068	356	AF007068	Coturnix coturnix arylalkylamine N-acetyltransferase mRNA, partial cds.	Coturnix coturnix	46,629	12-Jul-97
		GB_EST10:AA166324	514	AA166324	ms50c09.r1 Life Tech mouse embryo 13 5dpc 10666014 Mus musculus cDNA clone IMAGE:614992 5' similar to SW:NEST_RAT P21263 NESTIN. ;, mRNA sequence.	Mus musculus	38,677	19-DEC-1996
		GB_EST7:W89968	46	W89968	mf64g11.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:419108 5' similar to SW:NEST_RAT P21263 NESTIN. [1] ;, mRNA sequence.	Mus musculus	58,696	12-Sep-96
rxa01051	732	GB_GSS12:AQ381423	579	AQ381423	RPCI11-135F10.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-135F10, genomic survey sequence.	Homo sapiens	37,651	21-MAY-1999
		GB_HTG6:AC010901	206121	AC010901	Homo sapiens clone RP11-544J22, WORKING DRAFT SEQUENCE, 1 unordered pieces.	Homo sapiens	36,011	04-DEC-1999
		GB_GSS5:AQ746932	837	AQ746932	HS_5538_A1_A11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1114 Col=21 Row=A, genomic survey sequence.	Homo sapiens	38,640	19-Jul-99
rxa01052	432	GB_IN1:CELC13D9	43487	AF016420	Caenorhabditis elegans cosmid C13D9.	Caenorhabditis elegans	39,344	2-Aug-97
		GB_IN1:CELC13D9	43487	AF016420	Caenorhabditis elegans cosmid C13D9.	Caenorhabditis elegans	38,780	2-Aug-97
rxa01053	543	GB_OV:CHKMAFG1	1316	D28601	Chicken novel maf-related gene mafG encoding bZip nuclear protein MafG, promoter region and exon 1.	Gallus gallus	39,205	7-Feb-99
		GB_HTG6:AC010765	146468	AC010765	Homo sapiens clone RP11-115N6, *** SEQUENCING IN PROGRESS ***, 26 unordered pieces.	Homo sapiens	32,961	07-DEC-1999
		GB_HTG6:AC010765	146468	AC010765	Homo sapiens clone RP11-115N6, *** SEQUENCING IN PROGRESS ***, 26 unordered pieces.	Homo sapiens	38,476	07-DEC-1999
rxa01054	612	GB_PL1:PHNPNGLP	962	D45425	Pharbitis nil mRNA for Pharbitis nil Germin-like protein precursor, complete cds.	Ipomoea nil	42,925	10-Feb-99
		GB_HTG2:HSJ402N21	170302	AL049553	Homo sapiens chromosome 6 clone RP3-402N21 map p21.1-21.31, ***SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,825	03-DEC-1999
		GB_HTG2:HSJ402N21	170302	AL049553	Homo sapiens chromosome 6 clone RP3-402N21 map p21.1-21.31, ***SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,825	03-DEC-1999
rxa01217	723	GB_IN2:CELF18A12	29784	AF016688	Caenorhabditis elegans cosmid F18A12.	Caenorhabditis elegans	35,794	08-OCT-1999
		GB_IN2:CELF18A12	29784	AF016688	Caenorhabditis elegans cosmid F18A12.	Caenorhabditis elegans	40,625	08-OCT-1999
		GB_RO:MUSMCFTR	6304	M60493	Mouse cystic fibrosis transmembrane conductance regulator (CFTR) mRNA, complete cds.	Mus musculus	37,793	10-Jun-94
rxa01320	1770	GB_BA2:AF031037	1472	AF031037	Neisseria meningitidis chloramphenicol acetyltransferase gene, complete cds.	Neisseria meningitidis	35,014	21-Apr-98
		GB_HTG1:PFMAL13PA80518		AL109815	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	17,697	19-Aug-99
		GB_HTG1:PFMAL13PA80518		AL109815	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	17,697	19-Aug-99
rxa01345	1575	GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	38,195	14-Aug-98
		GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	36,611	14-Aug-98
		GB_HTG3:AC011500_1300851		AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	36,446	AC011500
rxa01407	1014	GB_HTG3:AC010831	70233	AC010831	Homo sapiens clone 6_L_24, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,764	23-Sep-99

Table 4 (continued)

		GB_HTG3:AC010831	70233	AC010831	Homo sapiens clone 6_L_24, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,764	23-Sep-99
		GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	40,778	30-Sep-98
rxa01408	324	GB_PR4:AF152365	246546	AF152365	Homo sapiens constitutive fragile region FRA3B sequence.	Homo sapiens	41,234	1-Aug-99
		GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPCI-98 02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.	Drosophila melanogaster	39,432	3-Sep-99
		GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPCI-98 02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.	Drosophila melanogaster	39,432	3-Sep-99
rxa01524	1566	GB_BA1:BSUB0015	218410	Z99118	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.	Bacillus subtilis	38,201	26-Nov-97
		GB_HTG2:AC008260	107439	AC008260	Drosophila melanogaster chromosome 2 clone BACR13J10 (D924) RPCI-98 13.J.10 map 47B-47C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 82 unordered pieces.	Drosophila melanogaster	38,302	2-Aug-99
		GB_HTG2:AC008260	107439	AC008260	Drosophila melanogaster chromosome 2 clone BACR13J10 (D924) RPCI-98 13.J.10 map 47B-47C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 82 unordered pieces.	Drosophila melanogaster	38,302	2-Aug-99
rxa01578	1510	GB_PR4:AF111170	148083	AF111170	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene.	Homo sapiens	37,873	14-Jul-99
		GB_PR4:AF111170	148083	AF111170	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene.	Homo sapiens	40,220	14-Jul-99
		GB_BA1:AEY13732	6740	Y13732	Alcaligenes eutrophus genes for ureases, ureD1, ureD2, ureA, ureB, and ORF1, ORF2.	Ralstonia eutropha	42,960	23-Sep-97
rxa01616	1605	GB_BA2:AF088857	2908	AF088857	Vogesella indigofera indigoidine biosynthesis regulatory locus, complete	Vogesella indigofera	37,626	10-Sep-99
		GB_IN1:CEM04D8	21552	Z32682	Caenorhabditis elegans cosmid M04D8, complete sequence.	Caenorhabditis elegans	37,237	23-Nov-98
		GB_EST25:AI281910	276	AI281910	qt82d04.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:1961767 3', mRNA sequence.	Homo sapiens	38,406	21-DEC-1998
rxa01666	1500	GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	99,933	9-Apr-97
		GB_HTG3:AC009213	114735	AC009213	Drosophila melanogaster chromosome 3 clone BACR09F18 (D812) RPCI-98 09.F.18 map 98D-98D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 109 unordered pieces.	Drosophila melanogaster	36,111	23-Aug-99
		GB_HTG3:AC009213	114735	AC009213	Drosophila melanogaster chromosome 3 clone BACR09F18 (D812) RPCI-98 09.F.18 map 98D-98D strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 109 unordered pieces.	Drosophila melanogaster	36,111	23-Aug-99
rxa01674	1017	GB_PL1:AB017159	1859	AB017159	Daucus carota mRNA for citrate synthase, complete cds.	Daucus carota	39,537	01-MAY-1999
		GB_PR1:HUMGNOS48	23142	D26607	Homo sapiens endothelial nitric oxide synthase gene, complete cds.	Homo sapiens	36,419	13-Jul-99
		GB_HTG3:AC011234	154754	AC011234	Homo sapiens clone NH0166D23, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	36,317	04-OCT-1999
rxa01873	1359	GB_HTG3:AC009450	124337	AC009450	Homo sapiens chromosome 9 clone 30_C_23 map 9, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	35,303	22-Aug-99
		GB_HTG3:AC009450	124337	AC009450	Homo sapiens chromosome 9 clone 30_C_23 map 9, *** SEQUENCING IN PROGRESS ***, 20 unordered pieces.	Homo sapiens	35,303	22-Aug-99
		GB_HTG3:AC009919	134724	AC009919	Homo sapiens clone 115_I_23, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,409	8-Sep-99
rxa01922	1275	GB_BA1:ECONEUC	1676	M84026	E.coli protein p7 (neu C) gene, complete cds.	Escherichia coli	35,189	26-Apr-93

Table 4 (continued)

		GB_HTG2:AC007853	116280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03L02 (D766) RPCI-98 03.L.2 map 96B-96C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 80 unordered pieces.	Drosophila melanogaster	34,365	2-Aug-99
		GB_HTG2:AC007853	116280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03L02 (D766) RPCI-98 03.L.2 map 96B-96C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 80 unordered pieces.	Drosophila melanogaster	34,365	2-Aug-99
rxa01936	1395	GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3L/66B6 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS ***, 52 unordered pieces.	Drosophila melanogaster	38,534	16-OCT-1999
		GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3L/66B6 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS ***, 52 unordered pieces.	Drosophila melanogaster	38,534	16-OCT-1999
		GB_PR4:AC005552	167228	AC005552	Homo sapiens chromosome 17, clone hRPK.212_E_8, complete sequence.	Homo sapiens	36,249	26-Nov-98
rxa01984	420	GB_PR1:HS169C8F	245	Z57239	H.sapiens CpG island DNA genomic Mse1 fragment, clone 169c8, forward read cpg169c8.ft1a.	Homo sapiens	45,679	18-OCT-1995
		GB_BA1:SERATTBXIS	3255	L11597	Saccharopolyspora erythraea excisionase (xis) gene, integrase (int) gene, complete cds's and attB site.	Saccharopolyspora erythraea	36,232	6-Jul-94
		GB_EST7:W97557	267	W97557	mf98a09.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:422296 5', mRNA sequence.	Mus musculus	42,969	16-Jul-96
rxa02060								
rxa02087	1470	GB_PR3:AC005544	169045	AC005544	Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence.	Homo sapiens	35,724	25-Sep-98
		GB_PL1:ATF20B18	104738	AL049483	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project).	Arabidopsis thaliana	35,890	24-MAR-1999
		GB_PL2:ATT25K17	89904	AL049171	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project).	Arabidopsis thaliana	38,128	27-Aug-99
rxa02088	1338	GB_HTG3:AC008697	167932	AC008697	Homo sapiens chromosome 5 clone CIT978SKB_70D3, *** SEQUENCING IN PROGRESS ***, 54 unordered pieces.	Homo sapiens	36,662	3-Aug-99
		GB_HTG3:AC008697	167932	AC008697	Homo sapiens chromosome 5 clone CIT978SKB_70D3, *** SEQUENCING IN PROGRESS ***, 54 unordered pieces.	Homo sapiens	36,662	3-Aug-99
		GB_HTG3:AC008703	213971	AC008703	Homo sapiens chromosome 5 clone CIT978SKB_76P12, *** SEQUENCING IN PROGRESS ***, 54 unordered pieces.	Homo sapiens	34,768	3-Aug-99
rxa02159	636	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
		GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamolytransferase (argF) gene, complete cds.	Corynebacterium glutamicum	88,679	5-Jan-99
		GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
rxa02184	504	GB_BA1:BSZ92953	8164	Z92953	B.subtilis yws[A,B,C] genes and rbs[A,C,D,K,R] genes.	Bacillus subtilis	38,951	24-Jun-98
		GB_EST36:AI878071	593	AI878071	fc57a12.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR:Q13151 Q13151 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A0 ;, mRNA sequence.	Danio rerio	36,774	21-Jul-99

Table 4 (continued)

		GB_EST37:AI958166	641	AI958166	fc91f01.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to TR:Q13151 Q13151 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A0 ;, mRNA sequence.	Danio rerio	36,774	20-Aug-99
rxa02200	1233	GB_PR3:HSA494O16	50502	AL117328	Human DNA sequence from clone 494O16 on chromosome 22, complete sequence.	Homo sapiens	38,648	23-Nov-99
		GB_HTG2:AC008161	158440	AC008161	Mus musculus clone 182_H_5, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces.	Mus musculus	35,938	28-Jul-99
		GB_HTG2:AC008161	158440	AC008161	Mus musculus clone 182_H_5, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces.	Mus musculus	35,938	28-Jul-99
rxa02201	486	GB_EST4:H16949	465	H16949	ym34a11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:50010 5', mRNA sequence.	Homo sapiens	38,267	29-Jun-95
		GB_EST4:H16949	465	H16949	ym34a11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:50010 5', mRNA sequence.	Homo sapiens	36,552	29-Jun-95
rxa02202	762	GB_IN1:CELC41A3	37149	U41541	Caenorhabditis elegans cosmid C41A3.	Caenorhabditis elegans	41,678	08-DEC-1995
		GB_EST33:AV080151	236	AV080151	AV080151 Mus musculus stomach C57BL/6J adult Mus musculus cDNA clone 2210413B04, mRNA sequence.	Mus musculus	43,348	25-Jun-99
		GB_GSS5:AQ766877	545	AQ766877	HS_2017_B2_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2017 Col=16 Row=D, genomic survey sequence.	Homo sapiens	35,568	28-Jul-99
rxa02205	1002	GB_HTG2:AC005959	127587	AC005959	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	40,310	11-Nov-98
		GB_HTG2:AC005959	127587	AC005959	Homo sapiens, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	40,310	11-Nov-98
		GB_IN1:BRPTUBBA	4571	M36380	B.pahangi beta-tubulin gene, complete cds.	Brugia pahangi	37,703	26-Apr-93
rxa02305	975	GB_RO:MUSPAFR	1140	D50872	Mouse gene for platelet activating factor receptor, complete cds.	Mus musculus	38,420	10-Feb-99
		GB_PR3:HUMARL1A	1008	L28997	Homo sapiens ARL1 mRNA, complete cds.	Homo sapiens	42,188	13-Jan-95
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	42,000	27-Aug-99
rxa02431	899	GB_EST4:H35255	407	H35255	EST111890 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNCO03, mRNA sequence.	Rattus sp.	39,098	2-Apr-98
		GB_HTG1:HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	39,456	23-Nov-99
		GB_HTG1:HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	39,456	23-Nov-99
rxa02446	558	GB_BA2:AF036166	895	AF036166	Xanthomonas campestris organic hydroperoxide resistance protein (ohr) gene, complete cds.	Xanthomonas campestris	49,369	19-MAY-1998
		GB_EST5:N25122	620	N25122	yx19d10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262195 5', mRNA sequence.	Homo sapiens	35,417	28-DEC-1995
		GB_EST5:N25122	620	N25122	yx19d10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262195 5', mRNA sequence.	Homo sapiens	37,172	28-DEC-1995
rxa02541	1308	GB_BA2:DPU93358	1267	U93358	Deinococcus proteolyticus 40 kDa heat shock chaperone protein (dnaJ) gene, complete cds.	Deinococcus proteolyticus	42,115	17-Jan-98
		GB_EST30:AI658096	343	AI658096	fc14c09.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:DNJ2_HUMAN P31689 DNAJ PROTEIN HOMOLOG 2. ;, mRNA sequence.	Danio rerio	52,059	06-MAY-1999
		GB_EST37:AI959242	545	AI959242	fd25h11.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:DNJ2_HUMAN P31689 DNAJ PROTEIN HOMOLOG 2. ;, mRNA sequence.	Danio rerio	45,438	20-Aug-99

Table 4 (continued)

rxa02542	777	EM_PAT:E10832	1856	E10832	DNA encoding Dnak protein which is one of heat shock protein from	Corynebacterium glutamicum	99,000	08-OCT-1997 (Rel. 52, Created)
		GB_EST24:Z82017	396	Z82017	SSZ82017 Porcine small intestine cDNA library Sus scrofa cDNA clone c12c06 5' similar to eukaryotic initiation factor 4 gamma, mRNA sequence.	Sus scrofa	37,067	30-Apr-99
		GB_OM:CATERYTHRO	681	L10606	Cat erythropoietin mRNA, 3' end.	Felis catus	39,409	14-OCT-1993
rxa02543	1977	EM_PAT:E10832	1856	E10832	DNA encoding Dnak protein which is one of heat shock protein from	Corynebacterium glutamicum	97,306	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:MPHSP70	2179	X59437	M.paratuberculosis gene for 70 kD heat shock protein.	Mycobacterium avium subsp. paratuberculosis	73,404	23-Apr-92
		GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	72,028	17-Jun-98
rxa02586	393	GB_IN2:AC006472	156362	AC006472	Drosophila melanogaster, chromosome 2R, region 45E1-46A2, BAC clone BACR48G21, complete sequence.	Drosophila melanogaster	37,958	30-Jan-99
		GB_HTG4:AC010020	106541	AC010020	Drosophila melanogaster chromosome 3L/66D10 clone RPCI98-26I3, *** SEQUENCING IN PROGRESS ***, 55 unordered pieces.	Drosophila melanogaster	37,333	16-OCT-1999
		GB_HTG4:AC010020	106541	AC010020	Drosophila melanogaster chromosome 3L/66D10 clone RPCI98-26I3, *** SEQUENCING IN PROGRESS ***, 55 unordered pieces.	Drosophila melanogaster	37,333	16-OCT-1999
rxa02587	2214	GB_BA1:MLCL622	42498	Z95398	Mycobacterium leprae cosmid L622.	Mycobacterium leprae	39,848	24-Jun-97
		GB_RO:AF074879	3316	AF074879	Rattus norvegicus testis-specific protein TSPY gene, complete cds.	Rattus norvegicus	35,830	6-Jul-99
		GB_RO:RNJ001380	2641	AJ001380	Rattus norvegicus Tspy partial genomic sequence, exons 1-6.	Rattus norvegicus	37,702	29-Jun-98
rxs03217	331	GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	37,888	27-Aug-99
		GB_HTG2:HSJ662M14	174772	AL079336	Homo sapiens chromosome 20 clone RP4-662M14, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Homo sapiens	36,420	4-Feb-00
		GB_HTG2:HSJ662M14	174772	AL079336	Homo sapiens chromosome 20 clone RP4-662M14, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Homo sapiens	35,962	4-Feb-00

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l $MgSO_4 \times 7H_2O$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(NH_4)_2SO_4$, 1 g/l NaCl, 2 g/l $MgSO_4 \times 7H_2O$, 0.2 g/l $CaCl_2$, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $FeSO_4 \times H_2O$, 10 mg/l $ZnSO_4 \times 7\ H_2O$, 3 mg/l $MnCl_2 \times 4\ H_2O$, 30 mg/l H_3BO_3 20 mg/l $CoCl_2 \times 6\ H_2O$, 1 mg/l $NiCl_2 \times 6\ H_2O$, 3 mg/l $Na_2MoO_4 \times 2\ H_2O$, 500 mg/l complexing agent (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30

min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.*, Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g. Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain

the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*, Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli and C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vector into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.*

(1990) J. Bacteriol. 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other Corynebacterium or Brevibacterium species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) From Genes to Clones – Introduction to Gene Technology. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.*

(1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for Corynebacteria are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be

advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(NH_4)_2SO_4$, NH_4OH, nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It

is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD_{600} of O.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be

found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example,

Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall yield, production, and/or efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*

cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. *et al.* (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

EXAMPLE 11: Cloning of a *Corynebacterium glutamicum* Gene Involved in Lincomycin Resistance Using a Reporter Gene Approach

A. Identification of the Gene Encoding the LMRB Protein

Plasmid pSL130 was constructed by ligation of the aceB promoter region (paceB) of *C. glutamicum* (Kim, H.J. *et al.* (1997) *J. Microbiol. Biotechnol.* 7: 287-292) into the polylinker of the lac operon fusion vector pRS415, which lacks a promoter (Simon, R.W. *et al.* (1987) *Gene* 53: 85-96). Plasmid pSL145 was constructed by ligating the resulting paceB-lac region into the *E. coli* cloning vector pACYC184. *E. coli* DH5αF' was transformed with pSL145 and the resulting strain was used as a host for screening of a genomic *C. glutamicum* library (in pSL109).

Transformants were screened by growth on agar medium containing 5-bromo-4-chloro-3-indolyl-beta-D-glalactopyranoside (X-Gal). A white colony, containing DNA influencing lacZ expression, was selected for further analysis. This clone was found to contain a 4 kB fragment from the gene library. Subclones were constructed in pSL109 and a subclone which retained the white phenotype on X-Gal plates was identified. This subclone was found to contain a 2.6 kB BamH1-XhoI fragment (plasmid pSL149-5). The fragment was sequenced and identified as a membrane protein-encoding gene (LMRB gene).

The 1442 nucleotides of the coding sequence of the LMRB gene encode a polypeptide of 481 amino acid residues with a high percentage of hydrophobic amino acids. A Genbank search determined that the LMRB protein is 40% identical to the protein product of the lmrB gene from *Bacillus subtilis* (Genbank Accession AL009126, TREMBL Accession P94422), as determined using a CLUSTAL W analysis (using standard parameters).

The LMRN protein contains a sequence pattern: 158-A-P-A-L-G-P-T-L-S-G-167 (SEQ ID NO:301), which resembles the known multi-drug-resistance-protein consensus motif G-X-X-X-G-P-X-X-G-G (SEQ ID NO:302) (Paulsen, I.T., and Skurray, R.A. (1993) *Gene* 124: 1-11). Therefore, the LMRB protein was classified as a drug resistance protein.

B. In vivo Analysis of lmrB Function

The lmrB gene was overexpressed in *C. glutamicum* ASO19E12 (Kim, H.J. *et al.* (1997) *J. Microbiol. Biotechnol.* 7: 287-292) using the plasmid pSL149-5, described above.

Disruption of the LMRB gene was accomplished by use of the vector pSL18-lmrB. This vector was constructed as follows: an internal fragment of the LMRB gene was amplified by PCR under standard conditions using primers 5'-CTCCAGGATTGCTCCGAAGG-3' (SEQ ID NO:303) and 5'-CACAGTGGTTGACCACTGGC-3' (SEQ ID NO:304). The resulting PCR product was treated with T7 DNA polymerase and T7 polynucleotide kinase, and was cloned into the SmaI site of plasmid pSL18 (Kim, Y.H. and H.-S. Lee (1996) *J. Microbiol. Biotechnol.* 6: 315-320). The disruption of the LMRB gene in *C. glutamicum* ASO19E12 was performed by conjugation, as previously described (Schwarzer and Puhler (1991) *Bio/Technology* 9:84-87).

C. glutamicum cells transformed with pSL149-5 displayed similar resistances as untransformed cells against erythromycin, penicillin G, tetracycline, chloramphenicol, spectinomycin, nalidixic acid, gentamycin, streptomycin, ethidium bromide, carbonyl cyanide m-chlorophenylhydrazone (CCCP), and sodium dodecyl sulfate. Significant differences were observed, however, in the resistance of transformed and untransformed cells to lincomycin.

LMRB-overexpressing *C. glutamicum* cells were found to be able to grow in the presence of 20 μg/ml lincomycin. In contrast, cells which do not overexpress LMRB (or cells carrying a LMRB disruption) were not able to grow on agar media containing 5 μg/ml lincomycin. This effect was clearly visible in liquid culture. LMRB overexpression led to a 9-fold increased resistance (compared to wild-type) against lincomycin and LMRB disruption resulted in a decreased resistance (28% of wild-type) to this antibiotic.

Example 12: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.* USA 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100,

wordlength = 12 to obtain nucleotide sequences homologous to SRT nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to SRT protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the

top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 13: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic

acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C.*

glutamicum or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 14: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and

include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S-methionine, ^{35}S-cysteine, ^{14}C-labelled amino acids, ^{15}N-amino acids, $^{15}NO_3$ or $^{15}NH_4^+$ or ^{13}C-labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

<u>What is claimed:</u>

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a stress, resistance, or tolerance gene, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

2. The isolated nucleic acid molecule of claim 1, wherein said stress, resistance, or tolerance gene is selected from the group consisting of nucleic acid molecules involved in a stress response, tolerance, or resistance to temperature stresses, pH stresses, oxygen stresses, osmotic stresses, toxic chemicals, oxygen radicals, antibiotics, or to lincomycin.

3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, or

a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth as odd-numbered SEQ ID NOs of the Sequence Listing, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.

9. An isolated nucleic acid molecule comprising the nucleic acid molecule of any one of claims 1-8 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.

10. A vector comprising the nucleic acid molecule of any one of claims 1-9.

11. The vector of claim 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 11.

13. The host cell of claim 12, wherein said cell is a microorganism.

14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.

15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine

and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

18. An isolated stress, resistance, or tolerance polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The protein of claim 18, wherein said stress, resistance, or tolerance polypeptide is selected from the group consisting of proteins involved in a stress response, tolerance, or resistance to temperature stresses, pH stresses, oxygen stresses, osmotic stresses, toxic chemicals, oxygen radicals, antibiotics, or to lincomycin.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of any of claims 18-21, further comprising heterologous amino acid sequences.

23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth as odd-numbered SEQ ID

NOs of the Sequence Listing,, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth as even-numbered SEQ ID NOs of the Sequence Listing, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.

26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.

27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium, lilium, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium flavum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum,* and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides and enzymes.

32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

35. A method for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject, comprising detecting the presence of one or more SEQ ID NOs 1 through 304 of the Sequence Listing in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of Corynebacterium diphtheriae in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the nucleic acid molecule is disrupted.

37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth as odd-numbered SEQ ID NOs of the

Sequence Listing , wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth as odd-numbered SEQ ID NOs of the Sequence Listing .

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set as odd-numbered SEQ ID NOs of the Sequence Listing, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

SEQUENCE LISTING

<110> BASF Aktiengesellschaft
<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
RESISTANCE AND TOLERANCE PROTEINS
<130> BGI-124CPPC
<140>
<141>
<160> 304

<210> 1
<211> 1566
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1543)
<223> RXA01524

<400> 1

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ttgtggcact ctttagtagt tttttctcat agctcagttt cgcaacttta gagaactcta 60

gaaactgagc ttcatgctgt gaaaggcctt ttctccattc atg gat tcc caa att   115
                                           Met Asp Ser Gln Ile
                                             1               5

aat act cag acc tct ccg gca gct gcg aag ctg cct agg gag gtc gtt   163
Asn Thr Gln Thr Ser Pro Ala Ala Ala Lys Leu Pro Arg Glu Val Val
                 10                  15                  20

gtt gtt ctt tcg atc ctc gtg gtt tcc gcg atg atc atg att ctt aat   211
Val Val Leu Ser Ile Leu Val Val Ser Ala Met Ile Met Ile Leu Asn
             25                  30                  35

gaa acc att ctg tcg gtt gcg ttg cct tcc atc atg gaa gat ttc tcc   259
Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile Met Glu Asp Phe Ser
         40                  45                  50

gtg cct gaa act act gca cag tgg ttg acc act ggc ttt atg ttg acg   307
Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr Gly Phe Met Leu Thr
     55                  60                  65

atg gca gtg gtg att cca act act ggt tat ctg ctt gat cgt ttt tcc   355
Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu Leu Asp Arg Phe Ser
 70                  75                  80                  85

act aag acg atc ttt gtt act gcg ttg ttg ttc ttt acg gtt ggt acg   403
Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe Phe Thr Val Gly Thr
                 90                  95                 100

ttg act gcg gcg ttg gct cca acg ttt gcg gtg ctg ctt ggt gct cgt   451
Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val Leu Leu Gly Ala Arg
            105                 110                 115

atc gtt cag gcg gtt ggt act gcg ctg gtg atg cct ttg ctg atg acg   499
Ile Val Gln Ala Val Gly Thr Ala Leu Val Met Pro Leu Leu Met Thr
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        120                 125                 130

gtt acg ttg acg gtg gtt cct gcg gag cgt cgt ggt tcg atg atg ggc      547
Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg Gly Ser Met Met Gly
    135                 140                 145

att att tcc atc gtg att tct gtt gcg ccg gcg ctt ggt cct acg ttg      595
Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala Leu Gly Pro Thr Leu
150                 155                 160                 165

tct ggt gtc att ctt aac tct ttg acc tgg cac tgg ttg ttt tgg atg      643
Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His Trp Leu Phe Trp Met
                170                 175                 180

atg ctt ccg atc gtt gtt atc gct ttg gta att ggt ttc ttc ttg atc      691
Met Leu Pro Ile Val Val Ile Ala Leu Val Ile Gly Phe Phe Leu Ile
            185                 190                 195

aaa aat atc ggc gaa acc aag atc acc cca ctg gat gtt ctg tct gtc      739
Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu Asp Val Leu Ser Val
        200                 205                 210

atc ctt tcg gtg ttt gcc ttc ggt ggt ttg gtg tac ggc ttc agt tcc      787
Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val Tyr Gly Phe Ser Ser
    215                 220                 225

ttc gga gca atc ctg gag ggc gaa ggc acc gta ggt atc ttc gcg atc      835
Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val Gly Ile Phe Ala Ile
230                 235                 240                 245

gtc gtt ggc gcc atc gca ctc ctc atc ttt gct ttg cga cag cac caa      883
Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala Leu Arg Gln His Gln
                250                 255                 260

ctc ggc aag caa gac aaa gca ctg atg gat ctc cga gcc ttc aag gtg      931
Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu Arg Ala Phe Lys Val
            265                 270                 275

agg aac ttc agc ttc tcc ttg acc acc atc ctt ttg gcg ttc ggc gcg      979
Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu Leu Ala Phe Gly Ala
        280                 285                 290

atg ctc gga acc gtc atg gtt ttg cca atc tac ctg cag act tcc ctc      1027
Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr Leu Gln Thr Ser Leu
    295                 300                 305

gga gtt act gct ttg gtg acc ggt ttg gtt gtt atg ccc ggc ggc ctc      1075
Gly Val Thr Ala Leu Val Thr Gly Leu Val Val Met Pro Gly Gly Leu
310                 315                 320                 325

ctc cag ggt ctg atc agc cca ttc atc gga cgt ttc tac gac aag gtc      1123
Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg Phe Tyr Asp Lys Val
                330                 335                 340

ggt cca cgt ccg ctg ctg att ccc gga gca att gcg ctg gct atc gcg      1171
Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile Ala Leu Ala Ile Ala
            345                 350                 355
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gca tcc tcg atg act ttt ctc aat gag aat tca ccc gtg tgg atg gtc      1219
Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser Pro Val Trp Met Val
        360                 365                 370

gtg gtc atg cac gtt gtg ttc agc atc ggc atg tgt ttg atg atg acc      1267
Val Val Met His Val Val Phe Ser Ile Gly Met Cys Leu Met Met Thr
    375                 380                 385

cct ctc atg acc acc gct ctc ggc gcc ctt ccg aag cac ctc tat ggt      1315
Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro Lys His Leu Tyr Gly
390                 395                 400                 405

cac ggc tcc gca att ttg aac acg ttc caa cag ctc gca ggc gca gcc      1363
His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln Leu Ala Gly Ala Ala
                410                 415                 420

gga aca gcg atc atg att gca gca ctt tcc ttc ggc act tcc att gca      1411
Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe Gly Thr Ser Ile Ala
            425                 430                 435

gcg tct tcg gga tct gcg cat gct gaa gct gtt gcc gct ggt acc aag      1459
Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val Ala Ala Gly Thr Lys
        440                 445                 450

gtt gcg ttc atc gca ggc gca atc atc gcg gtg atc gct ttg gtt gtt      1507
Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val Ile Ala Leu Val Val
    455                 460                 465

tcc ctc ttc gtc act cgc gtc gag gaa gaa gct cac taaataccaa           1553
Ser Leu Phe Val Thr Arg Val Glu Glu Glu Ala His
470                 475                 480

aaaatggggc aga                                                       1566


<210> 2
<211> 481
<212> PRT
<213> Corynebacterium glutamicum

<400> 2
Met Asp Ser Gln Ile Asn Thr Gln Thr Ser Pro Ala Ala Ala Lys Leu
1               5                   10                  15

Pro Arg Glu Val Val Val Val Leu Ser Ile Leu Val Val Ser Ala Met
            20                  25                  30

Ile Met Ile Leu Asn Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile
        35                  40                  45

Met Glu Asp Phe Ser Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr
    50                  55                  60

Gly Phe Met Leu Thr Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu
65                  70                  75                  80
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Leu Asp Arg Phe Ser Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe
                85                  90                  95

Phe Thr Val Gly Thr Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val
            100                 105                 110

Leu Leu Gly Ala Arg Ile Val Gln Ala Val Gly Thr Ala Leu Val Met
        115                 120                 125

Pro Leu Leu Met Thr Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg
    130                 135                 140

Gly Ser Met Met Gly Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala
145                 150                 155                 160

Leu Gly Pro Thr Leu Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His
                165                 170                 175

Trp Leu Phe Trp Met Met Leu Pro Ile Val Val Ile Ala Leu Val Ile
            180                 185                 190

Gly Phe Phe Leu Ile Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu
        195                 200                 205

Asp Val Leu Ser Val Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val
    210                 215                 220

Tyr Gly Phe Ser Ser Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val
225                 230                 235                 240

Gly Ile Phe Ala Ile Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala
                245                 250                 255

Leu Arg Gln His Gln Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu
            260                 265                 270

Arg Ala Phe Lys Val Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu
        275                 280                 285

Leu Ala Phe Gly Ala Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr
    290                 295                 300

Leu Gln Thr Ser Leu Gly Val Thr Ala Leu Val Thr Gly Leu Val Val
305                 310                 315                 320

Met Pro Gly Gly Leu Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg
                325                 330                 335

Phe Tyr Asp Lys Val Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile
            340                 345                 350

Ala Leu Ala Ile Ala Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser
        355                 360                 365

Pro Val Trp Met Val Val Val Met His Val Val Phe Ser Ile Gly Met
    370                 375                 380
```

Cys Leu Met Met Thr Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro
385 390 395 400

Lys His Leu Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln
405 410 415

Leu Ala Gly Ala Ala Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe
420 425 430

Gly Thr Ser Ile Ala Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val
435 440 445

Ala Ala Gly Thr Lys Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val
450 455 460

Ile Ala Leu Val Val Ser Leu Phe Val Thr Arg Val Glu Glu Glu Ala
465 470 475 480

His

<210> 3
<211> 371
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (52)..(348)
<223> RXA00497

<400> 3
tggaaaccca caaccggcac acacaaaatt tttctcatgg agggattcac cgtg gca 57
Val Ala
1

aac gtc aac atc aag ccg ctt gag gac aag atc ctc gtt cag atc aac 105
Asn Val Asn Ile Lys Pro Leu Glu Asp Lys Ile Leu Val Gln Ile Asn
5 10 15

gaa gca gag acc acc acc gct tcc ggc ctg gtc att cca gat tcc gct 153
Glu Ala Glu Thr Thr Thr Ala Ser Gly Leu Val Ile Pro Asp Ser Ala
20 25 30

aag gaa aag cca caa gag gca acc gtt atc gca gtt ggc cca ggc cgc 201
Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro Gly Arg
35 40 45 50

ttc gat gac aag ggt aac cgc atc cca ctg gac atc aag gaa gat gac 249
Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu Asp Asp
55 60 65

gtt gtg atc ttc tcc cgt tac ggc ggc acc gag atc aag ttc ggt ggc 297
Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe Gly Gly
70 75 80

gtg gag tac ttg ctt ctc tcc gct cgt gac atc ctc gca atc gtc gag 345
Val Glu Tyr Leu Leu Leu Ser Ala Arg Asp Ile Leu Ala Ile Val Glu
85 90 95

aag taggggataa gttcatggca aag 371
Lys

<210> 4
<211> 99
<212> PRT
<213> Corynebacterium glutamicum

<400> 4
Val Ala Asn Val Asn Ile Lys Pro Leu Glu Asp Lys Ile Leu Val Gln
1 5 10 15

Ile Asn Glu Ala Glu Thr Thr Thr Ala Ser Gly Leu Val Ile Pro Asp
20 25 30

Ser Ala Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro
35 40 45

Gly Arg Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu
50 55 60

Asp Asp Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe
65 70 75 80

Gly Gly Val Glu Tyr Leu Leu Leu Ser Ala Arg Asp Ile Leu Ala Ile
85 90 95

Val Glu Lys

<210> 5
<211> 1737
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1714)
<223> RXN00493

<400> 5
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gtgacatcct cgcaatcgtc gagaagtagg ggataagttc atg gca aag ctc att 115
Met Ala Lys Leu Ile
1 5

gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct 163
Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala
10 15 20

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ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg    211
Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val
            25                  30                  35

gtt ctt gat aag gca ttc ggc gga cct ctg gtc acc aac gac ggt gtc    259
Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val
        40                  45                  50

acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt    307
Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly
    55                  60                  65

gcg cag ctg gtg aag tcc gtt gct gtt aag acc aac gac atc gct ggt    355
Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly
70                  75                  80                  85

gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa    403
Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu
                90                  95                  100

ggc ctg cgc aac gtt gct gct ggc gca aac cca atg gag ctc aac aag    451
Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Met Glu Leu Asn Lys
            105                 110                 115

ggt att tct gca gct gca gaa aag acc ttg gaa gag ttg aag gca cgc    499
Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg
        120                 125                 130

gca acc gag gtg tct gac acc aag gaa atc gca aac gtc gct acc gtt    547
Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val
    135                 140                 145

tca tcc cgc gat gaa gtt gtc ggc gag atc gtt gct gca gcg atg gaa    595
Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu
150                 155                 160                 165

aag gtt ggc aag gac ggt gtc gtc acc gtt gag gag tcc cag tcc atc    643
Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile
                170                 175                 180

gag act gct ctc gag gtc acc gaa ggt att tct ttc gac aag ggc tac    691
Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr
            185                 190                 195

ctt tcc cct tat ttc atc aac gac aac gac act cag cag gct gtc ctg    739
Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr Gln Gln Ala Val Leu
        200                 205                 210

gac aac cct gca gtg ctg ctt gtt cgc aac aag att tct tcc ctc cca    787
Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys Ile Ser Ser Leu Pro
    215                 220                 225

gac ttc ctc cca ttg ctg gag aag gtt gtg gag tcc aac cgt cct ttg    835
Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu Ser Asn Arg Pro Leu
230                 235                 240                 245
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ctg atc atc gca gaa gac gtc gag ggc gag cct ttg cag acc ctg gtt      883
Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro Leu Gln Thr Leu Val
                250                 255                 260

gtg aac tcc atc cgc aag acc atc aag gtc gtt gca gtg aag tcc cct      931
Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val Ala Val Lys Ser Pro
            265                 270                 275

tac ttc ggt gac cga cgc aag gcg ttc atg gat gac ctg gct att gtc      979
Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp Asp Leu Ala Ile Val
        280                 285                 290

acc aag gca act gtc gtg gat cca gaa gtg ggc atc aac ctc aac gaa     1027
Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly Ile Asn Leu Asn Glu
    295                 300                 305

gct ggc gaa gaa gtt ttc ggt acc gca cgc cgc atc acc gtt tcc aag     1075
Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg Ile Thr Val Ser Lys
310                 315                 320                 325

gac gaa acc atc atc gtt gat ggt gca ggt tcc gca gaa gac gtt gaa     1123
Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser Ala Glu Asp Val Glu
                330                 335                 340

gca cgt cgc ggc cag atc cgt cgc gaa atc gcc aac acc gat tcc acc     1171
Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala Asn Thr Asp Ser Thr
            345                 350                 355

tgg gat cgc gaa aag gca gaa gag cgt ttg gct aag ctc tcc ggt ggt     1219
Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala Lys Leu Ser Gly Gly
        360                 365                 370

att gct gtc atc cgc gtt ggt gca gca act gaa acc gaa gtc aac gac     1267
Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu Thr Glu Val Asn Asp
    375                 380                 385

cgc aag ctg cgt gtc gaa gat gcc atc aac gct gct cgc gca gca gca     1315
Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala Ala Arg Ala Ala Ala
390                 395                 400                 405

caa gaa ggc gtt atc gct ggt ggc ggt tcc gct ttg gtt cag atc gct     1363
Gln Glu Gly Val Ile Ala Gly Gly Gly Ser Ala Leu Val Gln Ile Ala
                410                 415                 420

gag act ctg aag gct tac gcc gaa gag ttc gaa ggc gac cag aag gtc     1411
Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu Gly Asp Gln Lys Val
            425                 430                 435

ggc gtt cgc gca ctg gct act gct ttg ggc aag cca gcg tac tgg atc     1459
Gly Val Arg Ala Leu Ala Thr Ala Leu Gly Lys Pro Ala Tyr Trp Ile
        440                 445                 450

gcc tcc aac gca ggt ctt gac ggc tct gtt gtt gtt gca cgc act gct     1507
Ala Ser Asn Ala Gly Leu Asp Gly Ser Val Val Val Ala Arg Thr Ala
    455                 460                 465

gct ctg cca aac ggc gag ggc ttc aac gct gca act ttg gaa tac gga     1555
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Ala Leu Pro Asn Gly Glu Gly Phe Asn Ala Ala Thr Leu Glu Tyr Gly
470                 475                 480                 485

aac ctg atc aac gac ggt gtc atc gac cca gtc aag gtc acc cat tcc      1603
Asn Leu Ile Asn Asp Gly Val Ile Asp Pro Val Lys Val Thr His Ser
                490                 495                 500

gca gta gtg aat gca acc tct gtt gca cgc atg gtt ctg acc act gag      1651
Ala Val Val Asn Ala Thr Ser Val Ala Arg Met Val Leu Thr Thr Glu
            505                 510                 515

gct tct gtt gtt gag aag cct gca gaa gaa gca gcc gat gca cat gca      1699
Ala Ser Val Val Glu Lys Pro Ala Glu Glu Ala Ala Asp Ala His Ala
        520                 525                 530

gga cat cat cac cac taaagttctg tgaaaaacac cgt                        1737
Gly His His His His
    535


<210> 6
<211> 538
<212> PRT
<213> Corynebacterium glutamicum

<400> 6
Met Ala Lys Leu Ile Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu
  1               5                  10                  15

Arg Gly Val Asp Ala Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro
             20                  25                  30

Arg Gly Arg Asn Val Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val
         35                  40                  45

Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro
     50                  55                  60

Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr
 65                  70                  75                  80

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln
                 85                  90                  95

Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
            100                 105                 110

Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu
        115                 120                 125

Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala
    130                 135                 140

Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val
145                 150                 155                 160

Ala Ala Ala Met Glu Lys Val Gly Lys Asp Gly Val Val Thr Val Glu
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165 170 175

Glu Ser Gln Ser Ile Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser
180 185 190

Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr
195 200 205

Gln Gln Ala Val Leu Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys
210 215 220

Ile Ser Ser Leu Pro Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu
225 230 235 240

Ser Asn Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro
245 250 255

Leu Gln Thr Leu Val Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val
260 265 270

Ala Val Lys Ser Pro Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp
275 280 285

Asp Leu Ala Ile Val Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly
290 295 300

Ile Asn Leu Asn Glu Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg
305 310 315 320

Ile Thr Val Ser Lys Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser
325 330 335

Ala Glu Asp Val Glu Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala
340 345 350

Asn Thr Asp Ser Thr Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala
355 360 365

Lys Leu Ser Gly Gly Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu
370 375 380

Thr Glu Val Asn Asp Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala
385 390 395 400

Ala Arg Ala Ala Ala Gln Glu Gly Val Ile Ala Gly Gly Gly Ser Ala
405 410 415

Leu Val Gln Ile Ala Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu
420 425 430

Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu Gly Lys
435 440 445

Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser Val Val
450 455 460

Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn Ala Ala

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465                 470                 475                 480

Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp Pro Val
                485                 490                 495

Lys Val Thr His Ser Ala Val Val Asn Ala Thr Ser Val Ala Arg Met
            500                 505                 510

Val Leu Thr Thr Glu Ala Ser Val Val Glu Lys Pro Ala Glu Glu Ala
        515                 520                 525

Ala Asp Ala His Ala Gly His His His His
    530                 535


<210> 7
<211> 1339
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1339)
<223> FRXA00498

<400> 7
cccgttacgg cggcaccgag atcaagttcg gtggcgtgga gtacttgctt ctctccgctc 60

gtgacatcct cgcaatcgtc gagaagtagg ggataagttc atg gca aag ctc att    115
                                          Met Ala Lys Leu Ile
                                          1               5

gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct    163
Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala
                10                  15                  20

ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg    211
Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val
            25                  30                  35

gtt ctt gat aag gca ttc ggc gga cct ctg gtc acc aac gac ggt gtc    259
Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val
        40                  45                  50

acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt    307
Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly
    55                  60                  65

gcg cag ctg gtg aag tcc gtt gct gtt aag acc aac gac atc gct ggt    355
Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly
70                  75                  80                  85

gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa    403
Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu
                90                  95                  100

ggc ctg cgc aac gtt gct gct ggc gca aac cca atg gag ctc aac aag    451
```

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Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Met Glu Leu Asn Lys
            105                 110                 115

ggt att tct gca gct gca gaa aag acc ttg gaa gag ttg aag gca cgc      499
Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg
        120                 125                 130

gca acc gag gtg tct gac acc aag gaa atc gca aac gtc gct acc gtt      547
Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val
    135                 140                 145

tca tcc cgc gat gaa gtt gtc ggc gag atc gtt gct gca gcg atg gaa      595
Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu
150                 155                 160                 165

aag gtt ggc aag gac ggt gtc gtc acc gtt gag gag tcc cag tcc atc      643
Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile
                170                 175                 180

gag act gct ctc gag gtc acc gaa ggt att tct ttc gac aag ggc tac      691
Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr
            185                 190                 195

ctt tcc cct tat ttc atc aac gac aac gac act cag cag gct gtc ctg      739
Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr Gln Gln Ala Val Leu
        200                 205                 210

gac aac cct gca gtg ctg ctt gtt cgc aac aag att tct tcc ctc cca      787
Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys Ile Ser Ser Leu Pro
    215                 220                 225

gac ttc ctc cca ttg ctg gag aag gtt gtg gag tcc aac cgt cct ttg      835
Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu Ser Asn Arg Pro Leu
230                 235                 240                 245

ctg atc atc gca gaa gac gtc gag ggc gag cct ttg cag acc ctg gtt      883
Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro Leu Gln Thr Leu Val
                250                 255                 260

gtg aac tcc atc cgc aag acc atc aag gtc gtt gca gtg aag tcc cct      931
Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val Ala Val Lys Ser Pro
            265                 270                 275

tac ttc ggt gac cga cgc aag gcg ttc atg gat gac ctg gct att gtc      979
Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp Asp Leu Ala Ile Val
        280                 285                 290

acc aag gca act gtc gtg gat cca gaa gtg ggc atc aac ctc aac gaa     1027
Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly Ile Asn Leu Asn Glu
    295                 300                 305

gct ggc gaa gaa gtt ttc ggt acc gca cgc cgc atc acc gtt tcc aag     1075
Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg Ile Thr Val Ser Lys
310                 315                 320                 325

gac gaa acc atc atc gtt gat ggt gca ggt tcc gca gaa gac gtt gaa     1123
Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser Ala Glu Asp Val Glu
```

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            330                 335                 340

gca cgt cgc ggc cag atc cgt cgc gaa atc gcc aac acc gat tcc acc     1171
Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala Asn Thr Asp Ser Thr
            345                 350                 355

tgg gat cgc gaa aag gca gaa gag cgt ttg gct aag ctc tcc ggt ggt     1219
Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala Lys Leu Ser Gly Gly
        360                 365                 370

att gct gtc atc cgc gtt ggt gca gca act gaa acc gaa gtc aac gac     1267
Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu Thr Glu Val Asn Asp
    375                 380                 385

cgc aag ctg cgt gtc gaa gat gcc atc aac gct gct cgc gca gca gca     1315
Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala Ala Arg Ala Ala Ala
390                 395                 400                 405

caa gaa ggc gtt atc gct ggt ggc                                     1339
Gln Glu Gly Val Ile Ala Gly Gly
                410
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<210> 8
<211> 413
<212> PRT
<213> Corynebacterium glutamicum

<400> 8

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Met Ala Lys Leu Ile Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu
1               5                   10                  15

Arg Gly Val Asp Ala Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro
            20                  25                  30

Arg Gly Arg Asn Val Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val
        35                  40                  45

Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro
    50                  55                  60

Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr
65                  70                  75                  80

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln
                85                  90                  95

Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
            100                 105                 110

Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu
        115                 120                 125

Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala
    130                 135                 140

Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val
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145 150 155 160

Ala Ala Ala Met Glu Lys Val Gly Lys Asp Gly Val Val Thr Val Glu
165 170 175

Glu Ser Gln Ser Ile Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser
180 185 190

Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr
195 200 205

Gln Gln Ala Val Leu Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys
210 215 220

Ile Ser Ser Leu Pro Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu
225 230 235 240

Ser Asn Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro
245 250 255

Leu Gln Thr Leu Val Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val
260 265 270

Ala Val Lys Ser Pro Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp
275 280 285

Asp Leu Ala Ile Val Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly
290 295 300

Ile Asn Leu Asn Glu Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg
305 310 315 320

Ile Thr Val Ser Lys Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser
325 330 335

Ala Glu Asp Val Glu Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala
340 345 350

Asn Thr Asp Ser Thr Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala
355 360 365

Lys Leu Ser Gly Gly Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu
370 375 380

Thr Glu Val Asn Asp Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala
385 390 395 400

Ala Arg Ala Ala Ala Gln Glu Gly Val Ile Ala Gly Gly
405 410

<210> 9
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>

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<221> CDS
<222> (101)..(700)
<223> RXA01217

<400> 9
gcgctgcctg cgaagactcg accaagacat tcgagtcggt cgcgggcatt ttttattttc 60

gcggccgagt gtccaccttc atccatgagg agaaatcact atg gca aag tac caa     115
                                            Met Ala Lys Tyr Gln
                                             1               5

acc att gag gct gct gtc cgc tct gag ttc ggc aag ggc tct gca cgt     163
Thr Ile Glu Ala Ala Val Arg Ser Glu Phe Gly Lys Gly Ser Ala Arg
                10                  15                  20

cgt gca cgc gtt gct ggc cag atc cct gct gtt gtt tac ggc gca gat     211
Arg Ala Arg Val Ala Gly Gln Ile Pro Ala Val Val Tyr Gly Ala Asp
            25                  30                  35

gtt gag tcc aac ctg cac gtc acc atc gac cac cgc acc ttc gct gcg     259
Val Glu Ser Asn Leu His Val Thr Ile Asp His Arg Thr Phe Ala Ala
        40                  45                  50

ctg gtt cgc cag gaa ggc gta aac gct gtt ctt gag ctc gac atc gag     307
Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu Glu Leu Asp Ile Glu
    55                  60                  65

ggc cag aag cag ctc acc atg atc aag cac atc gac cag aac gtg ctg     355
Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile Asp Gln Asn Val Leu
 70                  75                  80                  85

acc ttc cac atc gac cac ttg gac ctg ctt gcc att aag cgc ggc gaa     403
Thr Phe His Ile Asp His Leu Asp Leu Leu Ala Ile Lys Arg Gly Glu
                90                  95                  100

aag gtt gag gtt gac gtt cca gtt atc gtc gag ggc gag cca gct cca     451
Lys Val Glu Val Asp Val Pro Val Ile Val Glu Gly Glu Pro Ala Pro
            105                 110                 115

ggc acc atg tgg gtt cag gat gct gac acc atc aag gtt gag gct gac     499
Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile Lys Val Glu Ala Asp
        120                 125                 130

gtt ctg tcc atc cct gaa gag ttc acc gtt tcc atc gaa ggc ctt gag     547
Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser Ile Glu Gly Leu Glu
    135                 140                 145

ctc ggc gca cag atc acc gca gct gac atc aag ctc gag ggc gac acc     595
Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys Leu Glu Gly Asp Thr
150                 155                 160                 165

acc ctg gtt gag gat cct gag acc ctc atc gtc aac atc gtt ctc cca     643
Thr Leu Val Glu Asp Pro Glu Thr Leu Ile Val Asn Ile Val Leu Pro
                170                 175                 180

gct gtc gag gaa gaa gac acc gaa gag gac gaa gca gct gaa gaa gca     691
Ala Val Glu Glu Glu Asp Thr Glu Glu Asp Glu Ala Ala Glu Glu Ala
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            185                 190                 195

gct act gag taagcttttt tagatagctt tat                              723
Ala Thr Glu
        200


<210> 10
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 10
Met Ala Lys Tyr Gln Thr Ile Glu Ala Ala Val Arg Ser Glu Phe Gly
  1               5                  10                  15

Lys Gly Ser Ala Arg Arg Ala Arg Val Ala Gly Gln Ile Pro Ala Val
             20                  25                  30

Val Tyr Gly Ala Asp Val Glu Ser Asn Leu His Val Thr Ile Asp His
         35                  40                  45

Arg Thr Phe Ala Ala Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu
     50                  55                  60

Glu Leu Asp Ile Glu Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile
 65                  70                  75                  80

Asp Gln Asn Val Leu Thr Phe His Ile Asp His Leu Asp Leu Leu Ala
                 85                  90                  95

Ile Lys Arg Gly Glu Lys Val Glu Val Asp Val Pro Val Ile Val Glu
            100                 105                 110

Gly Glu Pro Ala Pro Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile
        115                 120                 125

Lys Val Glu Ala Asp Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser
    130                 135                 140

Ile Glu Gly Leu Glu Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys
145                 150                 155                 160

Leu Glu Gly Asp Thr Thr Leu Val Glu Asp Pro Glu Thr Leu Ile Val
                165                 170                 175

Asn Ile Val Leu Pro Ala Val Glu Glu Glu Asp Thr Glu Glu Asp Glu
            180                 185                 190

Ala Ala Glu Glu Ala Ala Thr Glu
        195                 200


<210> 11
<211> 1603
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (33)..(1580)
<223> RXA00605

<400> 11
ataggtaacc ctcataaaag gaaggaatgc taatg tct gag aag tca gca gca      53
                                   Met Ser Glu Lys Ser Ala Ala
                                   1               5

gac cag atc gta gat cgc gga atg cgt cca aag ctt tct gga aac act    101
Asp Gln Ile Val Asp Arg Gly Met Arg Pro Lys Leu Ser Gly Asn Thr
        10                  15                  20

acc cgc cac aac gga gca cca gtt cca tct gag aac atc tcc gca acc    149
Thr Arg His Asn Gly Ala Pro Val Pro Ser Glu Asn Ile Ser Ala Thr
    25                  30                  35

gca ggc cca cag ggt cca aac gtt ctc aat gac att cac ctc att gaa    197
Ala Gly Pro Gln Gly Pro Asn Val Leu Asn Asp Ile His Leu Ile Glu
40                  45                  50                  55

aag ctc gca cac ttt aac cgc gag aac gtt cca gag cgt atc cct cac    245
Lys Leu Ala His Phe Asn Arg Glu Asn Val Pro Glu Arg Ile Pro His
                60                  65                  70

gca aag ggc cac ggc gct ttc ggt gag ctg cac atc acc gag gac gta    293
Ala Lys Gly His Gly Ala Phe Gly Glu Leu His Ile Thr Glu Asp Val
            75                  80                  85

tcc gaa tac acc aag gca gac ctg ttc cag cct ggt aag gtc acc ccg    341
Ser Glu Tyr Thr Lys Ala Asp Leu Phe Gln Pro Gly Lys Val Thr Pro
        90                  95                  100

ctg gct gtt cgc ttc tct act gtt gct ggt gag cag ggc tcc cca gat    389
Leu Ala Val Arg Phe Ser Thr Val Ala Gly Glu Gln Gly Ser Pro Asp
    105                 110                 115

acc tgg cgc gac gtc cac ggc ttc gct ctt cgc ttc tac acc gaa gag    437
Thr Trp Arg Asp Val His Gly Phe Ala Leu Arg Phe Tyr Thr Glu Glu
120                 125                 130                 135

ggc aac tac gac atc gtg ggt aac aac acc cca acc ttc ttc ctt cgt    485
Gly Asn Tyr Asp Ile Val Gly Asn Asn Thr Pro Thr Phe Phe Leu Arg
                140                 145                 150

gac ggc atg aag ttc ccg gac ttc atc cac tca cag aag cgt ctc aac    533
Asp Gly Met Lys Phe Pro Asp Phe Ile His Ser Gln Lys Arg Leu Asn
            155                 160                 165

aag aac ggt ctg cgc gat gca gac atg cag tgg gat ttc tgg acc cgc    581
Lys Asn Gly Leu Arg Asp Ala Asp Met Gln Trp Asp Phe Trp Thr Arg
        170                 175                 180

gca cct gaa tct gca cac cag gtg acc tac ctg atg ggt gac cgc ggt    629
Ala Pro Glu Ser Ala His Gln Val Thr Tyr Leu Met Gly Asp Arg Gly
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185 190 195

acc cct aag acc tcc cgc cac cag gac ggc ttc ggc tcc cac acc ttc 677
Thr Pro Lys Thr Ser Arg His Gln Asp Gly Phe Gly Ser His Thr Phe
200 205 210 215

cag tgg atc aac gct gaa ggt aag cca gtt tgg gtt aag tac cac ttc 725
Gln Trp Ile Asn Ala Glu Gly Lys Pro Val Trp Val Lys Tyr His Phe
220 225 230

aag acc cgc cag ggc tgg gat tgc ttc acc gat gca gaa gca gca aag 773
Lys Thr Arg Gln Gly Trp Asp Cys Phe Thr Asp Ala Glu Ala Ala Lys
235 240 245

gtt gca ggc gag aac gct gac tac cag cgc gaa gac ctc tac aac gct 821
Val Ala Gly Glu Asn Ala Asp Tyr Gln Arg Glu Asp Leu Tyr Asn Ala
250 255 260

att gaa aac ggc gac ttc cca atc tgg gac gtc aag gtt cag atc atg 869
Ile Glu Asn Gly Asp Phe Pro Ile Trp Asp Val Lys Val Gln Ile Met
265 270 275

cct ttc gag gat gca gag aac tac cgc tgg aac cca ttc gac ctg acc 917
Pro Phe Glu Asp Ala Glu Asn Tyr Arg Trp Asn Pro Phe Asp Leu Thr
280 285 290 295

aag acc tgg tcc cag aag gat tac cca ctg atc cca gtc ggt tac ttc 965
Lys Thr Trp Ser Gln Lys Asp Tyr Pro Leu Ile Pro Val Gly Tyr Phe
300 305 310

atc ctg aac cgc aac cca cgc aac ttc ttc gct cag atc gag cag ctt 1013
Ile Leu Asn Arg Asn Pro Arg Asn Phe Phe Ala Gln Ile Glu Gln Leu
315 320 325

gca ctg gat cca ggc aac atc gtt cct ggc gtc ggc ctg tcc cca gac 1061
Ala Leu Asp Pro Gly Asn Ile Val Pro Gly Val Gly Leu Ser Pro Asp
330 335 340

cgc atg ctc cag gca cgt atc ttc gca tac gct gac cag cag cgt tac 1109
Arg Met Leu Gln Ala Arg Ile Phe Ala Tyr Ala Asp Gln Gln Arg Tyr
345 350 355

cgc atc ggc gct aac tac cgc gac ctg cca gtg aac cgt cca atc aac 1157
Arg Ile Gly Ala Asn Tyr Arg Asp Leu Pro Val Asn Arg Pro Ile Asn
360 365 370 375

gag gtc aac acc tac agc cgc gaa ggt tcc atg cag tac atc ttc gac 1205
Glu Val Asn Thr Tyr Ser Arg Glu Gly Ser Met Gln Tyr Ile Phe Asp
380 385 390

gct gag ggc gag cct tcc tac agc cct aac cgc tac gac aag ggc gca 1253
Ala Glu Gly Glu Pro Ser Tyr Ser Pro Asn Arg Tyr Asp Lys Gly Ala
395 400 405

ggc tac ctg gat aac ggt acg gat tcc tcc tcc aac cac acc tcc tac 1301
Gly Tyr Leu Asp Asn Gly Thr Asp Ser Ser Ser Asn His Thr Ser Tyr
410 415 420

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ggc cag gct gat gac atc tac gtc aac cca gac cca cac ggc acc gac     1349
Gly Gln Ala Asp Asp Ile Tyr Val Asn Pro Asp Pro His Gly Thr Asp
    425                 430                 435

ctg gtt cgt gct gct tac gtc aag cac cag gat gat gac gac ttc atc     1397
Leu Val Arg Ala Ala Tyr Val Lys His Gln Asp Asp Asp Asp Phe Ile
440                 445                 450                 455

cag cca ggc atc cta tac cgc gag gtc ctg gat gag ggc gag aag gag     1445
Gln Pro Gly Ile Leu Tyr Arg Glu Val Leu Asp Glu Gly Glu Lys Glu
                460                 465                 470

cga ttg gca gac aac atc tcc aac gca atg cag ggc atc tct gag gca     1493
Arg Leu Ala Asp Asn Ile Ser Asn Ala Met Gln Gly Ile Ser Glu Ala
            475                 480                 485

acc gag cca cgc gtc tac gac tac tgg aac aac gtt gat gag aac ctc     1541
Thr Glu Pro Arg Val Tyr Asp Tyr Trp Asn Asn Val Asp Glu Asn Leu
        490                 495                 500

ggc gct cgc gtc aag gag ctt tac ctc cag aag aag gct taagtccttc      1590
Gly Ala Arg Val Lys Glu Leu Tyr Leu Gln Lys Lys Ala
    505                 510                 515

tgatttaaaa tga                                                      1603


&lt;210&gt; 12
&lt;211&gt; 516
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 12
Met Ser Glu Lys Ser Ala Ala Asp Gln Ile Val Asp Arg Gly Met Arg
 1               5                  10                  15

Pro Lys Leu Ser Gly Asn Thr Thr Arg His Asn Gly Ala Pro Val Pro
            20                  25                  30

Ser Glu Asn Ile Ser Ala Thr Ala Gly Pro Gln Gly Pro Asn Val Leu
        35                  40                  45

Asn Asp Ile His Leu Ile Glu Lys Leu Ala His Phe Asn Arg Glu Asn
    50                  55                  60

Val Pro Glu Arg Ile Pro His Ala Lys Gly His Gly Ala Phe Gly Glu
65                  70                  75                  80

Leu His Ile Thr Glu Asp Val Ser Glu Tyr Thr Lys Ala Asp Leu Phe
                85                  90                  95

Gln Pro Gly Lys Val Thr Pro Leu Ala Val Arg Phe Ser Thr Val Ala
            100                 105                 110

Gly Glu Gln Gly Ser Pro Asp Thr Trp Arg Asp Val His Gly Phe Ala
        115                 120                 125
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Leu Arg Phe Tyr Thr Glu Glu Gly Asn Tyr Asp Ile Val Gly Asn Asn
130 135 140

Thr Pro Thr Phe Phe Leu Arg Asp Gly Met Lys Phe Pro Asp Phe Ile
145 150 155 160

His Ser Gln Lys Arg Leu Asn Lys Asn Gly Leu Arg Asp Ala Asp Met
165 170 175

Gln Trp Asp Phe Trp Thr Arg Ala Pro Glu Ser Ala His Gln Val Thr
180 185 190

Tyr Leu Met Gly Asp Arg Gly Thr Pro Lys Thr Ser Arg His Gln Asp
195 200 205

Gly Phe Gly Ser His Thr Phe Gln Trp Ile Asn Ala Glu Gly Lys Pro
210 215 220

Val Trp Val Lys Tyr His Phe Lys Thr Arg Gln Gly Trp Asp Cys Phe
225 230 235 240

Thr Asp Ala Glu Ala Ala Lys Val Ala Gly Glu Asn Ala Asp Tyr Gln
245 250 255

Arg Glu Asp Leu Tyr Asn Ala Ile Glu Asn Gly Asp Phe Pro Ile Trp
260 265 270

Asp Val Lys Val Gln Ile Met Pro Phe Glu Asp Ala Glu Asn Tyr Arg
275 280 285

Trp Asn Pro Phe Asp Leu Thr Lys Thr Trp Ser Gln Lys Asp Tyr Pro
290 295 300

Leu Ile Pro Val Gly Tyr Phe Ile Leu Asn Arg Asn Pro Arg Asn Phe
305 310 315 320

Phe Ala Gln Ile Glu Gln Leu Ala Leu Asp Pro Gly Asn Ile Val Pro
325 330 335

Gly Val Gly Leu Ser Pro Asp Arg Met Leu Gln Ala Arg Ile Phe Ala
340 345 350

Tyr Ala Asp Gln Gln Arg Tyr Arg Ile Gly Ala Asn Tyr Arg Asp Leu
355 360 365

Pro Val Asn Arg Pro Ile Asn Glu Val Asn Thr Tyr Ser Arg Glu Gly
370 375 380

Ser Met Gln Tyr Ile Phe Asp Ala Glu Gly Glu Pro Ser Tyr Ser Pro
385 390 395 400

Asn Arg Tyr Asp Lys Gly Ala Gly Tyr Leu Asp Asn Gly Thr Asp Ser
405 410 415

Ser Ser Asn His Thr Ser Tyr Gly Gln Ala Asp Asp Ile Tyr Val Asn
420 425 430

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Pro Asp Pro His Gly Thr Asp Leu Val Arg Ala Ala Tyr Val Lys His
        435                 440                 445

Gln Asp Asp Asp Asp Phe Ile Gln Pro Gly Ile Leu Tyr Arg Glu Val
    450                 455                 460

Leu Asp Glu Gly Glu Lys Glu Arg Leu Ala Asp Asn Ile Ser Asn Ala
465                 470                 475                 480

Met Gln Gly Ile Ser Glu Ala Thr Glu Pro Arg Val Tyr Asp Tyr Trp
                485                 490                 495

Asn Asn Val Asp Glu Asn Leu Gly Ala Arg Val Lys Glu Leu Tyr Leu
            500                 505                 510

Gln Lys Lys Ala
        515


<210> 13
<211> 2439
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2416)
<223> RXA00404

<400> 13
aagatccgat catcggcata cagaaacacc catctggccg aactttcctt tttctgcatg 60

catttctgca cacagtttct gcccgctgtt tctacgcata gtg gct ttg aaa cga   115
                                           Val Ala Leu Lys Arg
                                           1               5

ccc gaa gag aaa aca gta aag atc gtg acc ata aaa cag act gac aac   163
Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile Lys Gln Thr Asp Asn
                10                  15                  20

atc aat gac gat gat ttg gtg tac agc aac gct act gac ctt cca gta   211
Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala Thr Asp Leu Pro Val
            25                  30                  35

ggc gtg aag aag tcc cct aaa atg tca ccg acc gcc cgc gtt ggt ctc   259
Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr Ala Arg Val Gly Leu
        40                  45                  50

ctt gtc ttt ggg gtt atc gcg gcg gtg ggt tgg gga gca atc gct ttc   307
Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp Gly Ala Ile Ala Phe
    55                  60                  65

tcc cgt ggc gaa aca atc aac tct gtg tgg ctg gtt ttg gcg gca gtt   355
Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu Val Leu Ala Ala Val
70                  75                  80                  85
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ggt tcc tat atc att gcg ttt tct ttc tat gcc cga ctg att gaa tac     403
Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala Arg Leu Ile Glu Tyr
                 90                  95                 100

aaa gtt gtt aag ccg aaa gat cag cga gca acc ccg gcg gaa tac gtt     451
Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr Pro Ala Glu Tyr Val
            105                 110                 115

aat gac ggc aag gac tat gtc cca acg gat cgt cgt gtg ctt ttt ggc     499
Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg Arg Val Leu Phe Gly
        120                 125                 130

cac cac ttt gca gct att gca ggt gcc ggt cca ttg gtt gga cct gtc     547
His His Phe Ala Ala Ile Ala Gly Ala Gly Pro Leu Val Gly Pro Val
    135                 140                 145

atg gcc gcg cag atg ggc tac ctg cca ggc acc ttg tgg att atc ctc     595
Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr Leu Trp Ile Ile Leu
150                 155                 160                 165

ggt gtg att ttc gcc ggt gca gtg cag gac tac cta gtg ctg tgg gtg     643
Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr Leu Val Leu Trp Val
                170                 175                 180

tct act cgt agg cgt gga cgc tca ctt ggc cag atg gtt cgt gat gaa     691
Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln Met Val Arg Asp Glu
            185                 190                 195

atg ggc acg gtc ggt gga gct gcc ggt atc ttg gcg acc atc tcc atc     739
Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu Ala Thr Ile Ser Ile
        200                 205                 210

atg atc atc att atc gcg gtg ctc gca ttg atc gtg gtt aat gca ctg     787
Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile Val Val Asn Ala Leu
    215                 220                 225

gct gat tca cca tgg ggc gtt ttc tcc atc acc atg acc atc cca att     835
Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr Met Thr Ile Pro Ile
230                 235                 240                 245

gca ctg ttc atg ggt gtg tac ttg cgt tac ctg cgc cca ggt cgt gtt     883
Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu Arg Pro Gly Arg Val
                250                 255                 260

act gaa gtg tcc atc atc ggt gtg gca ctg ctc ctg ctg gct atc gtt     931
Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu Leu Leu Ala Ile Val
            265                 270                 275

gct ggt ggt tgg gtt gca gac acc tca tgg ggc gtg gaa tgg ttc acc     979
Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly Val Glu Trp Phe Thr
        280                 285                 290

tgg tct aag acc act ttg gcg ttg gcc ttg atc ggt tac gga atc atg    1027
Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile Gly Tyr Gly Ile Met
    295                 300                 305

gct gcg att ttg ccg gtg tgg ctg ctg ctt gca ccg cgc gat tac ctg    1075
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Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala Pro Arg Asp Tyr Leu
310 315 320 325

tct acc ttt atg aag atc ggc gtc atc ggt ctg ttg gca gtg ggt att 1123
Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu Leu Ala Val Gly Ile
330 335 340

ttg ttc gca cgt cct gag gtg cag atg cct tcc gtg acc tcc ttc gca 1171
Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser Val Thr Ser Phe Ala
345 350 355

ctt gag ggc aac ggt ccg gtg ttc tct gga agt ctg ttc cca ttc ctg 1219
Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser Leu Phe Pro Phe Leu
360 365 370

ttc atc acg att gcc tgt ggt gca ctg tct ggt ttc cac gca ctg att 1267
Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly Phe His Ala Leu Ile
375 380 385

tct tca gga acc aca cca aag ctt gtg gag aag gaa tcc cag atg cgc 1315
Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys Glu Ser Gln Met Arg
390 395 400 405

atg ctc ggc tac ggc ggc atg ttg atg gaa tct ttc gtg gcg atg atg 1363
Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser Phe Val Ala Met Met
410 415 420

gca ctg atc acc gct gtt att ctg gat cgt cac ctg tac ttc tcc atg 1411
Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His Leu Tyr Phe Ser Met
425 430 435

aac gct ccg ctg gca ctg act ggt gga gat cca gca acc gca gct gag 1459
Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro Ala Thr Ala Ala Glu
440 445 450

tgg gtt aac tcc att ggg ctg aca ggt gcg gat atc acc ccg gaa cag 1507
Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp Ile Thr Pro Glu Gln
455 460 465

ctg tcg gaa gct gct gaa agt gtc gga gaa tcc act gtt att tcc cgt 1555
Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser Thr Val Ile Ser Arg
470 475 480 485

acc ggt ggc gca cca acc ttg gcg ttc ggt atg tct gaa atc ctc tcc 1603
Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met Ser Glu Ile Leu Ser
490 495 500

gga ttc atc ggc ggc gct gga atg aag gcg ttc tgg tac cac ttc gcc 1651
Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe Trp Tyr His Phe Ala
505 510 515

atc atg ttt gag gct ctg ttc atc ctc act act gtg gat gca ggt act 1699
Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr Val Asp Ala Gly Thr
520 525 530

cgt gtg gct cgc ttt atg atg acc gat acc ttg ggc aat gtt cca ggt 1747
Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu Gly Asn Val Pro Gly

535 540 545

ctg cgc cgt ttc aag gat cct tca tgg act gtc ggt aac tgg att tct 1795
Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val Gly Asn Trp Ile Ser
550 555 560 565

acc gtg ttt gtg tgt gct cta tgg ggt gct att ttg ctc atg ggt gtt 1843
Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile Leu Leu Met Gly Val
570 575 580

acc gat cca ctg ggc ggc atc aac gtg ctt ttc cca cta ttc ggt atc 1891
Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe Pro Leu Phe Gly Ile
585 590 595

gct aac cag ctg ctc gcc gct att gca ctt gct ctc gtg ctg gtt gtt 1939
Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala Leu Val Leu Val Val
600 605 610

gtg gtg aag aag ggc ctg tac aag tgg gcg tgg att cca gct gtt cct 1987
Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp Ile Pro Ala Val Pro
615 620 625

ttg gca tgg gat ctc att gtc acg atg act gcg tca tgg cag aag att 2035
Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala Ser Trp Gln Lys Ile
630 635 640 645

ttc cac tct gat ccg gct att ggc tac tgg gct cag aac gcg aac ttc 2083
Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala Gln Asn Ala Asn Phe
650 655 660

cgc gat gca aag tct caa ggc ctt acc gaa ttt ggt gcc gct aaa tct 2131
Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe Gly Ala Ala Lys Ser
665 670 675

cct gag gca atc gat gcg gtt atc cga aac acc atg att cag ggc atc 2179
Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr Met Ile Gln Gly Ile
680 685 690

ttg tcc atc ctg ttc gcg gtg ctc gtc ctc gtt gtt gtc ggc gca gcc 2227
Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val Val Val Gly Ala Ala
695 700 705

att gcg gtg tgc atc aag tcc atc agg gct cgt gca gcc gga aca cct 2275
Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg Ala Ala Gly Thr Pro
710 715 720 725

ttg gag acc act gaa gag cct gat act gaa tct gag ttc ttc gcc cca 2323
Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser Glu Phe Phe Ala Pro
730 735 740

act gga ttc ctt gca tct tcc agg gat aag gaa gtc cag gcc atg tgg 2371
Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu Val Gln Ala Met Trp
745 750 755

gac gag cgc tac cca ggc ggt gcg ccc gtg tct tct gga ggg cac 2416
Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser Ser Gly Gly His
760 765 770

taaaacatga tggctcttac tca 2439

<210> 14
<211> 772
<212> PRT
<213> Corynebacterium glutamicum

<400> 14
Val Ala Leu Lys Arg Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile
1 5 10 15

Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala
20 25 30

Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr
35 40 45

Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp
50 55 60

Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu
65 70 75 80

Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala
85 90 95

Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr
100 105 110

Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg
115 120 125

Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro
130 135 140

Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr
145 150 155 160

Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr
165 170 175

Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln
180 185 190

Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu
195 200 205

Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile
210 215 220

Val Val Asn Ala Leu Ala Asp Ser Pro Trp Gly Val Phe Ser Ile Thr
225 230 235 240

Met Thr Ile Pro Ile Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu
245 250 255

Arg Pro Gly Arg Val Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu
260 265 270

Leu Leu Ala Ile Val Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly
275 280 285

Val Glu Trp Phe Thr Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile
290 295 300

Gly Tyr Gly Ile Met Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala
305 310 315 320

Pro Arg Asp Tyr Leu Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu
325 330 335

Leu Ala Val Gly Ile Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser
340 345 350

Val Thr Ser Phe Ala Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser
355 360 365

Leu Phe Pro Phe Leu Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly
370 375 380

Phe His Ala Leu Ile Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys
385 390 395 400

Glu Ser Gln Met Arg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser
405 410 415

Phe Val Ala Met Met Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His
420 425 430

Leu Tyr Phe Ser Met Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro
435 440 445

Ala Thr Ala Ala Glu Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp
450 455 460

Ile Thr Pro Glu Gln Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser
465 470 475 480

Thr Val Ile Ser Arg Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met
485 490 495

Ser Glu Ile Leu Ser Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe
500 505 510

Trp Tyr His Phe Ala Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr
515 520 525

Val Asp Ala Gly Thr Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu
530 535 540

Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val
545 550 555 560

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Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile
                565                 570                 575

Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe
            580                 585                 590

Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala
        595                 600                 605

Leu Val Leu Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp
    610                 615                 620

Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala
625                 630                 635                 640

Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala
                645                 650                 655

Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe
            660                 665                 670

Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr
        675                 680                 685

Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val
    690                 695                 700

Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg
705                 710                 715                 720

Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser
                725                 730                 735

Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu
            740                 745                 750

Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser
        755                 760                 765

Ser Gly Gly His
    770


<210> 15
<211> 255
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(232)
<223> RXN03119

<400> 15
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atatgctcgg tgcggaaacc tacgaaagga ttttttaccc atg gct gta tac gaa   115
                                            Met Ala Val Tyr Glu
                                            1               5

ctc cca gaa ctc gac tac gca tac gac gct ctc gag cca cac atc gtc   163
Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu Glu Pro His Ile Val
                10                  15                  20

gct gaa atc atg gag ctt gac cag tcc aag gac cac gca acc tac gtt   211
Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp His Ala Thr Tyr Val
            25                  30                  35

gcg ggc gca aat gca gca ctc taggcactag agaaggcacg cga             255
Ala Gly Ala Asn Ala Ala Leu
        40


<210> 16
<211> 44
<212> PRT
<213> Corynebacterium glutamicum

<400> 16
Met Ala Val Tyr Glu Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu
  1               5                  10                  15

Glu Pro His Ile Val Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp
            20                  25                  30

His Ala Thr Tyr Val Ala Gly Ala Asn Ala Ala Leu
        35                  40


<210> 17
<211> 249
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(226)
<223> RXN03120

<400> 17
ctgggcagtt cttgggtacg accacatatc cggtcgcctg gttatcgagc agctcaccga 60

ccaggagggc aacatctcct tcgacatcac cccagttctg atg ctc gat atg tgg   115
                                            Met Leu Asp Met Trp
                                            1               5

gag cac gct ttc tac ctg cag tac atg aac gtt aag gca gat tac gtc   163
Glu His Ala Phe Tyr Leu Gln Tyr Met Asn Val Lys Ala Asp Tyr Val
                10                  15                  20

aag gct gtt tgg aac gtc ttc aac tgg gac gac gca aga gca cgc ttc   211
Lys Ala Val Trp Asn Val Phe Asn Trp Asp Asp Ala Arg Ala Arg Phe
            25                  30                  35
```

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gca gca gct tcc aag taagcatttt tagtccgtgc aat                   249
Ala Ala Ala Ser Lys
        40


<210> 18
<211> 42
<212> PRT
<213> Corynebacterium glutamicum

<400> 18
Met Leu Asp Met Trp Glu His Ala Phe Tyr Leu Gln Tyr Met Asn Val
  1               5                  10                  15

Lys Ala Asp Tyr Val Lys Ala Val Trp Asn Val Phe Asn Trp Asp Asp
             20                  25                  30

Ala Arg Ala Arg Phe Ala Ala Ala Ser Lys
        35                  40


<210> 19
<211> 660
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(637)
<223> RXN00575

<400> 19
gaagcgtccg caggcaagaa aacgtcccgg aaaacggcga taggggtcac ccgcgcatgt 60

ccggttgccg atctatttaa ataccaggac aattgcgtgc atg gtt gaa aga gac   115
                                           Met Val Glu Arg Asp
                                             1               5

ttc act atc cga cca atc cgc gag ggt gat ttc cct cag gtg agg gac   163
Phe Thr Ile Arg Pro Ile Arg Glu Gly Asp Phe Pro Gln Val Arg Asp
                 10                  15                  20

atc tac gaa ttg ggc ctg gag acg gga cat gcg act tat gag act tct   211
Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr Glu Thr Ser
             25                  30                  35

ggt ccc acg tgg gac cag ttc tcc caa tct aaa atc atg gat acc gtc   259
Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met Asp Thr Val
         40                  45                  50

atg gtg gcg gta gaa aac aac gac ccg gac ttc atc ctc gga tgg gtg   307
Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val
     55                  60                  65

tct gct gct cca att tca agc cga cag gtt ttc cat gga gtg gtg gaa   355
Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly Val Val Glu
```

```
 70                  75                  80                  85

gat tcc atc tat atc cac ccc cag ggc caa ggc cga gga atc ggc ggc     403
Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly
                 90                  95                 100

gct ttg ctc gac gcc ctt atc acc tac tgc gaa agc aac ggc atc tgg     451
Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp
            105                 110                 115

tcg atc cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg     499
Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu
        120                 125                 130

cat gaa tcg aag ggc ttc gtg aag gtg ggc acc atg cac caa atg gca     547
His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala
    135                 140                 145

agg atg ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg     595
Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu
150                 155                 160                 165

tgg gag tgc ctc tta tcc gtt cca gag caa gct caa agt tcc             637
Trp Glu Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser Ser
                170                 175

taaagcaatt taaatctgac ttt                                           660


&lt;210&gt; 20
&lt;211&gt; 179
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 20
Met Val Glu Arg Asp Phe Thr Ile Arg Pro Ile Arg Glu Gly Asp Phe
  1               5                  10                  15

Pro Gln Val Arg Asp Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala
             20                  25                  30

Thr Tyr Glu Thr Ser Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys
         35                  40                  45

Ile Met Asp Thr Val Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe
     50                  55                  60

Ile Leu Gly Trp Val Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe
 65                  70                  75                  80

His Gly Val Val Glu Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly
                 85                  90                  95

Arg Gly Ile Gly Gly Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu
            100                 105                 110

Ser Asn Gly Ile Trp Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu
```

115 120 125

Gly Ser Ala Lys Leu His Glu Ser Lys Gly Phe Val Lys Val Gly Thr
130 135 140

Met His Gln Met Ala Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp
145 150 155 160

Arg Asp Cys Asp Leu Trp Glu Cys Leu Leu Ser Val Pro Glu Gln Ala
165 170 175

Gln Ser Ser

<210> 21
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> FRXA00575

<400> 21
gcatgtccgg ttgccgatct atttaaatac caggacaatt gcgtgcatgg ttgaaagaga 60

cttcactatc cgaccaatcc gcgagggtga tttccctcag gtg agg gac atc tac 115
Val Arg Asp Ile Tyr
1 5

gaa ttg ggc ctg gag acg gga cat gcg act tat gag act tct ggt ccc 163
Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr Glu Thr Ser Gly Pro
10 15 20

acg tgg gac cag ttc tcc caa tct aaa atc atg gat acc gtc atg gtg 211
Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met Asp Thr Val Met Val
25 30 35

gcg gta gaa aac aac gac ccg gac ttc atc ctc gga tgg gtg tct gct 259
Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val Ser Ala
40 45 50

gct cca att tca agc cga cag gtt ttc cat gga gtg gtg gaa gat tcc 307
Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly Val Val Glu Asp Ser
55 60 65

atc tat atc cac ccc cag ggc caa ggc cga gga atc ggc ggc gct ttg 355
Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly Ala Leu
70 75 80 85

ctc gac gcc ctt atc acc tac tgc gaa agc aac ggc atc tgg tcg atc 403
Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp Ser Ile
90 95 100

cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg cat gaa 451

```
His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu His Glu
        105                 110                 115

tcg aag ggc ttc gtg aag gtg ggc acc atg cac caa atg gca agg atg     499
Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala Arg Met
    120                 125                 130

ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg tgg gag     547
Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu Trp Glu
    135                 140                 145

tgc ctc tta tcc gtt cca gag caa gct caa agt tcc taaagcaatt          593
Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser Ser
150                 155                 160

taaatctgac ttt                                                      606


<210> 22
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 22
Val Arg Asp Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr
  1               5                  10                  15

Glu Thr Ser Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met
             20                  25                  30

Asp Thr Val Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu
         35                  40                  45

Gly Trp Val Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly
     50                  55                  60

Val Val Glu Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly
 65                  70                  75                  80

Ile Gly Gly Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn
                 85                  90                  95

Gly Ile Trp Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser
            100                 105                 110

Ala Lys Leu His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His
        115                 120                 125

Gln Met Ala Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp
    130                 135                 140

Cys Asp Leu Trp Glu Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser
145                 150                 155                 160

Ser
```

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<210> 23
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1552)
<223> RXN01345

<400> 23
cataacctca ttgaacatgc aaaactaatg cttttggggg gtatgcataa attcgtttcg 60

ttccactgca cagcccgaaa atgctgctag ggtcaagttc atg cgt ttt gga ctt   115
                                          Met Arg Phe Gly Leu
                                          1               5

gac ttg gga act acc cgc aca atc gcg gcc gcc gtg gac cgc gga aac   163
Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala Val Asp Arg Gly Asn
                10                  15                  20

tat ccc atc gtc act gtg gaa gat tct tta ggc gac acc cac gat ttc   211
Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly Asp Thr His Asp Phe
            25                  30                  35

att cca tct gtg gtg gcc ctc aag gca gat agg att gtc gcg ggt tgg   259
Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp
        40                  45                  50

gat gct att gag gtt ggg cag gac cac cct tcc ttc gta cgt tct ttc   307
Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser Phe Val Arg Ser Phe
    55                  60                  65

aaa cgc cta ctc tct gaa ccc aat gtc acg gaa gcc acc ccg gtc tac   355
Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu Ala Thr Pro Val Tyr
70                  75                  80                  85

ttg ggc gat cat gta cac cct ttg ggc gcc gtc ctg gag gct ttt gcg   403
Leu Gly Asp His Val His Pro Leu Gly Ala Val Leu Glu Ala Phe Ala
                90                  95                  100

gaa aac gtg gtc act gcg ctg cgt gca ttt cag acg caa ttg gga gat   451
Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln Thr Gln Leu Gly Asp
            105                 110                 115

acc tcc ccg atc gaa gta gtc att ggt gtg ccc gcc aac tcc cac agc   499
Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro Ala Asn Ser His Ser
        120                 125                 130

gcc cag cga ctg ctc acc atg tcc gcc ttc agc gcc aca ggc atc acc   547
Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser Ala Thr Gly Ile Thr
    135                 140                 145

gtt gtc ggt ttg gtc aat gag ccc agc gcc gca gct ttc gag tac acc   595
Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala Ala Phe Glu Tyr Thr
150                 155                 160                 165
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cac cgc cac gcc cgc acc tta aac tcc aag cgc caa gcc atc gtg gtt 643
His Arg His Ala Arg Thr Leu Asn Ser Lys Arg Gln Ala Ile Val Val
170 175 180

tat gat ttg gga ggc gga aca ttc gac tcc tcg ctc atc cgc atc gac 691
Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser Leu Ile Arg Ile Asp
185 190 195

ggc acc cac cac gag gtt gtg tcc tcc att ggc att tca cgc ctt ggt 739
Gly Thr His His Glu Val Val Ser Ser Ile Gly Ile Ser Arg Leu Gly
200 205 210

ggc gat gat ttc gat gaa atc ctc ctc caa tgc gcg ctc aag gcc gca 787
Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys Ala Leu Lys Ala Ala
215 220 225

ggc aga cag cac gat gcg ttt ggc aag cgt gct aaa aac acg ctt ctc 835
Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala Lys Asn Thr Leu Leu
230 235 240 245

gac gaa tcc cgc aac gcg aag gaa gct ctt gtt ccg caa tcc cgt cgc 883
Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val Pro Gln Ser Arg Arg
250 255 260

ttg gtt cta gaa att ggc gac gac gac atc acc gtt cca gtg aac aag 931
Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr Val Pro Val Asn Lys
265 270 275

ttc tac gag gct gcc act ccc ctg gtg gaa aaa tcc ttg tcc atc atg 979
Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys Ser Leu Ser Ile Met
280 285 290

gaa ccc ctc atc ggc gtc gat gat ctt aaa gat tcc gac atc gca ggc 1027
Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp Ser Asp Ile Ala Gly
295 300 305

atc tac ctt gtt ggt gga gga tcc tcg ctc cca ctc gtt tcc agg ttg 1075
Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro Leu Val Ser Arg Leu
310 315 320 325

ctc cgc gag cgt ttc ggc cgc cgt gtc cac cgc tcc cca ttc ccc tca 1123
Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg Ser Pro Phe Pro Ser
330 335 340

ggt tcc act gcg gtg ggt ctg gcc atc gcg gct gac cct tcc tct ggt 1171
Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala Asp Pro Ser Ser Gly
345 350 355

ttc cac cta agg gac cgc gtt gcg cga ggc atc ggt gtg ttc cgt gag 1219
Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile Gly Val Phe Arg Glu
360 365 370

cac gat tct ggt cgt gcc gtg agc ttt gac ccg ctg atc gcc ccg gac 1267
His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro Leu Ile Ala Pro Asp
375 380 385

acc gat tct gcg acc gtg gcg aaa cga tgc tac aag gcg gtg cac aac 1315
Thr Asp Ser Ala Thr Val Ala Lys Arg Cys Tyr Lys Ala Val His Asn
390 395 400 405

att ggt tgg ttc agg ttc gtg gaa tac tcc acc gtg tcc gag gat ggc 1363
Ile Gly Trp Phe Arg Phe Val Glu Tyr Ser Thr Val Ser Glu Asp Gly
410 415 420

agc ccc gga gat att tcc ctg ctc agt gaa atc aag att cct ttt gat 1411
Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile Lys Ile Pro Phe Asp
425 430 435

agc tcc atc acc gat gtg gat gct acc gag att tca cgt ttc gat ggc 1459
Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile Ser Arg Phe Asp Gly
440 445 450

cca gaa gta gaa gaa acc atc aca gtc aat gac aac ggc gtg gct tcc 1507
Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp Asn Gly Val Ala Ser
455 460 465

att tcc atc aag ata ctc ggc ggc gtt acc gtc gag cac aca att 1552
Ile Ser Ile Lys Ile Leu Gly Gly Val Thr Val Glu His Thr Ile
470 475 480

tagttaccat tttggtgctg gtg 1575

<210> 24
<211> 484
<212> PRT
<213> Corynebacterium glutamicum

<400> 24
Met Arg Phe Gly Leu Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala
1 5 10 15

Val Asp Arg Gly Asn Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly
20 25 30

Asp Thr His Asp Phe Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg
35 40 45

Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser
50 55 60

Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu
65 70 75 80

Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val
85 90 95

Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln
100 105 110

Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro
115 120 125

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Ala Asn Ser His Ser Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser
    130                 135                 140

Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala
145                 150                 155                 160

Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg
                165                 170                 175

Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser
            180                 185                 190

Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly
        195                 200                 205

Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys
    210                 215                 220

Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala
225                 230                 235                 240

Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val
                245                 250                 255

Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr
            260                 265                 270

Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys
        275                 280                 285

Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp
    290                 295                 300

Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro
305                 310                 315                 320

Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg
                325                 330                 335

Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala
            340                 345                 350

Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile
        355                 360                 365

Gly Val Phe Arg Glu His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro
    370                 375                 380

Leu Ile Ala Pro Asp Thr Asp Ser Ala Thr Val Ala Lys Arg Cys Tyr
385                 390                 395                 400

Lys Ala Val His Asn Ile Gly Trp Phe Arg Phe Val Glu Tyr Ser Thr
                405                 410                 415

Val Ser Glu Asp Gly Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile
            420                 425                 430
```

Lys Ile Pro Phe Asp Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile
435 440 445

Ser Arg Phe Asp Gly Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp
450 455 460

Asn Gly Val Ala Ser Ile Ser Ile Lys Ile Leu Gly Gly Val Thr Val
465 470 475 480

Glu His Thr Ile

<210> 25
<211> 1267
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1267)
<223> FRXA01345

<400> 25
cataacctca ttgaacatgc aaaactaatg cttttggggg gtatgcataa attcgtttcg 60

ttccactgca cagcccgaaa atgctgctag ggtcaagttc atg cgt ttt gga ctt 115
Met Arg Phe Gly Leu
1 5

gac ttg gga act acc cgc aca atc gcg gcc gcc gtg gac cgc gga aac 163
Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala Val Asp Arg Gly Asn
10 15 20

tat ccc atc gtc act gtg gaa gat tct tta ggc gac acc cac gat ttc 211
Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly Asp Thr His Asp Phe
25 30 35

att cca tct gtg gtg gcc ctc aag gca gat agg att gtc gcg ggt tgg 259
Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp
40 45 50

gat gct att gag gtt ggg cag gac cac cct tcc ttc gta cgt tct ttc 307
Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser Phe Val Arg Ser Phe
55 60 65

aaa cgc cta ctc tct gaa ccc aat gtc acg gaa gcc acc ccg gtc tac 355
Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu Ala Thr Pro Val Tyr
70 75 80 85

ttg ggc gat cat gta cac cct ttg ggc gcc gtc ctg gag gct ttt gcg 403
Leu Gly Asp His Val His Pro Leu Gly Ala Val Leu Glu Ala Phe Ala
90 95 100

gaa aac gtg gtc act gcg ctg cgt gca ttt cag acg caa ttg gga gat 451
Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln Thr Gln Leu Gly Asp
105 110 115

```
acc tcc ccg atc gaa gta gtc att ggt gtg ccc gcc aac tcc cac agc     499
Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro Ala Asn Ser His Ser
        120                 125                 130

gcc cag cga ctg ctc acc atg tcc gcc ttc agc gcc aca ggc atc acc     547
Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser Ala Thr Gly Ile Thr
    135                 140                 145

gtt gtc ggt ttg gtc aat gag ccc agc gcc gca gct ttc gag tac acc     595
Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala Ala Phe Glu Tyr Thr
150                 155                 160                 165

cac cgc cac gcc cgc acc tta aac tcc aag cgc caa gcc atc gtg gtt     643
His Arg His Ala Arg Thr Leu Asn Ser Lys Arg Gln Ala Ile Val Val
                170                 175                 180

tat gat ttg gga ggc gga aca ttc gac tcc tcg ctc atc cgc atc gac     691
Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser Leu Ile Arg Ile Asp
            185                 190                 195

ggc acc cac cac gag gtt gtg tcc tcc att ggc att tca cgc ctt ggt     739
Gly Thr His His Glu Val Val Ser Ser Ile Gly Ile Ser Arg Leu Gly
        200                 205                 210

ggc gat gat ttc gat gaa atc ctc ctc caa tgc gcg ctc aag gcc gca     787
Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys Ala Leu Lys Ala Ala
    215                 220                 225

ggc aga cag cac gat gcg ttt ggc aag cgt gct aaa aac acg ctt ctc     835
Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala Lys Asn Thr Leu Leu
230                 235                 240                 245

gac gaa tcc cgc aac gcg aag gaa gct ctt gtt ccg caa tcc cgt cgc     883
Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val Pro Gln Ser Arg Arg
                250                 255                 260

ttg gtt cta gaa att ggc gac gac gac atc acc gtt cca gtg aac aag     931
Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr Val Pro Val Asn Lys
            265                 270                 275

ttc tac gag gct gcc act ccc ctg gtg gaa aaa tcc ttg tcc atc atg     979
Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys Ser Leu Ser Ile Met
        280                 285                 290

gaa ccc ctc atc ggc gtc gat gat ctt aaa gat tcc gac atc gca ggc     1027
Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp Ser Asp Ile Ala Gly
    295                 300                 305

atc tac ctt gtt ggt gga gga tcc tcg ctc cca ctc gtt tcc agg ttg     1075
Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro Leu Val Ser Arg Leu
310                 315                 320                 325

ctc cgc gag cgt ttc ggc cgc cgt gtc cac cgc tcc cca ttc ccc tca     1123
Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg Ser Pro Phe Pro Ser
                330                 335                 340
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ggt tcc act gcg gtg ggt ctg gcc atc gcg gct gac cct tcc tct ggt    1171
Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala Asp Pro Ser Ser Gly
            345                     350                     355

ttc cac cta agg gac cgc gtt gcg cga ggc atc ggt gtg ttc cgt gag    1219
Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile Gly Val Phe Arg Glu
        360                     365                     370

cac gat tct ggt cgt gcc gtg agc ttt gac ccg ctg atc gcc ccg gac    1267
His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro Leu Ile Ala Pro Asp
    375                     380                     385


<210> 26
<211> 389
<212> PRT
<213> Corynebacterium glutamicum

<400> 26
Met Arg Phe Gly Leu Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala
  1               5                  10                  15

Val Asp Arg Gly Asn Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly
            20                  25                  30

Asp Thr His Asp Phe Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg
        35                  40                  45

Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser
    50                  55                  60

Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu
 65                  70                  75                  80

Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val
                85                  90                  95

Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln
            100                 105                 110

Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro
        115                 120                 125

Ala Asn Ser His Ser Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser
    130                 135                 140

Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala
145                 150                 155                 160

Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg
                165                 170                 175

Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser
            180                 185                 190

Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly
        195                 200                 205
```

Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys
    210   215   220

Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala
225   230   235   240

Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val
                245   250   255

Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr
            260   265   270

Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys
        275   280   285

Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp
    290   295   300

Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro
305   310   315   320

Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg
                325   330   335

Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala
            340   345   350

Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile
        355   360   365

Gly Val Phe Arg Glu His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro
    370   375   380

Leu Ile Ala Pro Asp
385

<210> 27
<211> 1308
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1285)
<223> RXA02541

<400> 27
atccgccggt gtccggacaa caaaacttgc aacacaagat aacttaagaa attgcataca 60

attcaccgca tataagactc atggaaggag gggatgccca gtg aac aac agc gaa 115
                                           Val Asn Asn Ser Glu
                                           1   5

tgg gca aat aag aac tat tac gca gac ctg ggg gtc tcc tcg tcc gct 163
Trp Ala Asn Lys Asn Tyr Tyr Ala Asp Leu Gly Val Ser Ser Ser Ala

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                10                  15                  20

tca gaa gat gag atc aaa aag gct tac cgc aag ctc gcc agg gaa aat     211
Ser Glu Asp Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ala Arg Glu Asn
            25                  30                  35

cac cca gat aaa aat cca ggt gac aag gcc gct gaa gat cga ttc aaa     259
His Pro Asp Lys Asn Pro Gly Asp Lys Ala Ala Glu Asp Arg Phe Lys
        40                  45                  50

aaa gcg gcc gag gca tat gac gta ctt ggt gat gac aag aaa cga aaa     307
Lys Ala Ala Glu Ala Tyr Asp Val Leu Gly Asp Asp Lys Lys Arg Lys
    55                  60                  65

gaa tac gac gag ctc aaa gca ctt cta gct tct ggt gga atc cgc gga     355
Glu Tyr Asp Glu Leu Lys Ala Leu Leu Ala Ser Gly Gly Ile Arg Gly
70                  75                  80                  85

gga ttc gga agc gga ggt gcg gga ttc ccc ggc ggg ttt cgc acg tcg     403
Gly Phe Gly Ser Gly Gly Ala Gly Phe Pro Gly Gly Phe Arg Thr Ser
                90                  95                  100

acg gga gga ttc gac acc tca gac ctc ttc gga gga gga caa ggt gga     451
Thr Gly Gly Phe Asp Thr Ser Asp Leu Phe Gly Gly Gly Gln Gly Gly
            105                 110                 115

ggg ttt tct acg gac ggc ggt ttg ggc gat atc ttc ggt ggc ctt ttc     499
Gly Phe Ser Thr Asp Gly Gly Leu Gly Asp Ile Phe Gly Gly Leu Phe
        120                 125                 130

aac cgc ggc gct ggt tct cac cag tca gct agg ccg acg cgg ggg gcg     547
Asn Arg Gly Ala Gly Ser His Gln Ser Ala Arg Pro Thr Arg Gly Ala
    135                 140                 145

gat gta caa acc gaa ata act ctc tcg ttt gtt gag gca gcg aaa ggc     595
Asp Val Gln Thr Glu Ile Thr Leu Ser Phe Val Glu Ala Ala Lys Gly
150                 155                 160                 165

acg acc atc cca gtg gaa ctc acc ggc gat gcg ccc tgc aac acc tgc     643
Thr Thr Ile Pro Val Glu Leu Thr Gly Asp Ala Pro Cys Asn Thr Cys
                170                 175                 180

cac gga tcg ggc tcc aaa tca ggc cac ccc gca aaa tgt gga acc tgt     691
His Gly Ser Gly Ser Lys Ser Gly His Pro Ala Lys Cys Gly Thr Cys
            185                 190                 195

gat gga acc gga ttc acc tct gag aac aag ggt gct ttc gga ttc tcc     739
Asp Gly Thr Gly Phe Thr Ser Glu Asn Lys Gly Ala Phe Gly Phe Ser
        200                 205                 210

gct cca tgt gca acc tgt ggt ggc act ggt gaa ata atc act gat cct     787
Ala Pro Cys Ala Thr Cys Gly Gly Thr Gly Glu Ile Ile Thr Asp Pro
    215                 220                 225

tgc gat aac tgc cac ggc cga ggc acc gtc cgg aag tct cgt tcc atc     835
Cys Asp Asn Cys His Gly Arg Gly Thr Val Arg Lys Ser Arg Ser Ile
230                 235                 240                 245
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acc gtg cgt atc cca act ggt gtg gaa gat gga cag aaa gtt cgt ctt 883
Thr Val Arg Ile Pro Thr Gly Val Glu Asp Gly Gln Lys Val Arg Leu
250 255 260

gca ggc caa ggc gaa gca gga cca aat ggc aaa cca gcg ggc gat ctc 931
Ala Gly Gln Gly Glu Ala Gly Pro Asn Gly Lys Pro Ala Gly Asp Leu
265 270 275

ttt gtg aaa gtc cac gtg aaa aag gac gat gtg ttc aca cgc gac ggc 979
Phe Val Lys Val His Val Lys Lys Asp Asp Val Phe Thr Arg Asp Gly
280 285 290

agc aac att ttg atc acc att ccc gtg agc ttc agc gag ctg gct ttg 1027
Ser Asn Ile Leu Ile Thr Ile Pro Val Ser Phe Ser Glu Leu Ala Leu
295 300 305

ggt ggc gct att tct gtg cca acg ctc aac aag cct gta aaa ctc aag 1075
Gly Gly Ala Ile Ser Val Pro Thr Leu Asn Lys Pro Val Lys Leu Lys
310 315 320 325

cta cct gcg gga acg cca gat ggt cgt act ttg cgt gta cgc ggt cgc 1123
Leu Pro Ala Gly Thr Pro Asp Gly Arg Thr Leu Arg Val Arg Gly Arg
330 335 340

ggt atc gaa gca cgt gat tcc act ggt gat ctg ctg gtt aca gtc cag 1171
Gly Ile Glu Ala Arg Asp Ser Thr Gly Asp Leu Leu Val Thr Val Gln
345 350 355

gtt tct gtc ccg aag aat ctg gat gac aac gct gcg gaa gct ctc cgc 1219
Val Ser Val Pro Lys Asn Leu Asp Asp Asn Ala Ala Glu Ala Leu Arg
360 365 370

gca tat gct gaa gca gaa act aat tca ggt ttt gat ccc cgc gct aac 1267
Ala Tyr Ala Glu Ala Glu Thr Asn Ser Gly Phe Asp Pro Arg Ala Asn
375 380 385

tgg gcg ggc cag aac cgc tagacgttct ctttgagaaa gga 1308
Trp Ala Gly Gln Asn Arg
390 395

<210> 28
<211> 395
<212> PRT
<213> Corynebacterium glutamicum

<400> 28
Val Asn Asn Ser Glu Trp Ala Asn Lys Asn Tyr Tyr Ala Asp Leu Gly
1 5 10 15

Val Ser Ser Ser Ala Ser Glu Asp Glu Ile Lys Lys Ala Tyr Arg Lys
20 25 30

Leu Ala Arg Glu Asn His Pro Asp Lys Asn Pro Gly Asp Lys Ala Ala
35 40 45

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Glu Asp Arg Phe Lys Lys Ala Ala Glu Ala Tyr Asp Val Leu Gly Asp
     50                  55                  60

Asp Lys Lys Arg Lys Glu Tyr Asp Glu Leu Lys Ala Leu Leu Ala Ser
 65                  70                  75                  80

Gly Gly Ile Arg Gly Gly Phe Gly Ser Gly Gly Ala Gly Phe Pro Gly
                 85                  90                  95

Gly Phe Arg Thr Ser Thr Gly Gly Phe Asp Thr Ser Asp Leu Phe Gly
            100                 105                 110

Gly Gly Gln Gly Gly Gly Phe Ser Thr Asp Gly Gly Leu Gly Asp Ile
        115                 120                 125

Phe Gly Gly Leu Phe Asn Arg Gly Ala Gly Ser His Gln Ser Ala Arg
    130                 135                 140

Pro Thr Arg Gly Ala Asp Val Gln Thr Glu Ile Thr Leu Ser Phe Val
145                 150                 155                 160

Glu Ala Ala Lys Gly Thr Thr Ile Pro Val Glu Leu Thr Gly Asp Ala
                165                 170                 175

Pro Cys Asn Thr Cys His Gly Ser Gly Ser Lys Ser Gly His Pro Ala
            180                 185                 190

Lys Cys Gly Thr Cys Asp Gly Thr Gly Phe Thr Ser Glu Asn Lys Gly
        195                 200                 205

Ala Phe Gly Phe Ser Ala Pro Cys Ala Thr Cys Gly Gly Thr Gly Glu
    210                 215                 220

Ile Ile Thr Asp Pro Cys Asp Asn Cys His Gly Arg Gly Thr Val Arg
225                 230                 235                 240

Lys Ser Arg Ser Ile Thr Val Arg Ile Pro Thr Gly Val Glu Asp Gly
                245                 250                 255

Gln Lys Val Arg Leu Ala Gly Gln Gly Glu Ala Gly Pro Asn Gly Lys
            260                 265                 270

Pro Ala Gly Asp Leu Phe Val Lys Val His Val Lys Lys Asp Asp Val
        275                 280                 285

Phe Thr Arg Asp Gly Ser Asn Ile Leu Ile Thr Ile Pro Val Ser Phe
    290                 295                 300

Ser Glu Leu Ala Leu Gly Gly Ala Ile Ser Val Pro Thr Leu Asn Lys
305                 310                 315                 320

Pro Val Lys Leu Lys Leu Pro Ala Gly Thr Pro Asp Gly Arg Thr Leu
                325                 330                 335

Arg Val Arg Gly Arg Gly Ile Glu Ala Arg Asp Ser Thr Gly Asp Leu
            340                 345                 350
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Leu Val Thr Val Gln Val Ser Val Pro Lys Asn Leu Asp Asp Asn Ala
        355                 360                 365

Ala Glu Ala Leu Arg Ala Tyr Ala Glu Ala Glu Thr Asn Ser Gly Phe
    370                 375                 380

Asp Pro Arg Ala Asn Trp Ala Gly Gln Asn Arg
385                 390                 395


<210> 29
<211> 777
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> RXA02542

<400> 29
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cgaagacgac gcagctgaca atggtgagga caagaagtaa atg act acc cct aac    115
                                            Met Thr Thr Pro Asn
                                            1               5

gga atg ccc gac aat cct ggg gat cct gaa aat acc gat cca gag gca    163
Gly Met Pro Asp Asn Pro Gly Asp Pro Glu Asn Thr Asp Pro Glu Ala
                10                  15                  20

acc tct gct gat cgt gct gag cag gca gct gaa gaa gca gct gcc cgc    211
Thr Ser Ala Asp Arg Ala Glu Gln Ala Ala Glu Glu Ala Ala Ala Arg
            25                  30                  35

caa gcg gag gaa tct cca ttt gga cag gcc tca gag gaa gaa att tct    259
Gln Ala Glu Glu Ser Pro Phe Gly Gln Ala Ser Glu Glu Glu Ile Ser
        40                  45                  50

cca gag ctc gaa gca gag atc aat gat ctt cta tca gat gtt gat cca    307
Pro Glu Leu Glu Ala Glu Ile Asn Asp Leu Leu Ser Asp Val Asp Pro
    55                  60                  65

gat ttg gat ggc gat ggt gaa gtg tcc gct gta gaa aca cag ctt gcc    355
Asp Leu Asp Gly Asp Gly Glu Val Ser Ala Val Glu Thr Gln Leu Ala
70                  75                  80                  85

gaa cgc act gag gat ctg cag cga gtc acc gct gag tac gcc aac tac    403
Glu Arg Thr Glu Asp Leu Gln Arg Val Thr Ala Glu Tyr Ala Asn Tyr
                90                  95                  100

cgt cga cgt acc gag cgt gaa cgc cag ggc atc atc gac acc gca cgc    451
Arg Arg Arg Thr Glu Arg Glu Arg Gln Gly Ile Ile Asp Thr Ala Arg
            105                 110                 115

gca ggt gtt gtt acc caa ctt ctg ccg ttg ctc gac gat ctt gac ctg    499
Ala Gly Val Val Thr Gln Leu Leu Pro Leu Leu Asp Asp Leu Asp Leu
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120 125 130

gct gaa cag cac ggt gac ctt aac gaa ggt ccg ctg aag tca ctg tct 547
Ala Glu Gln His Gly Asp Leu Asn Glu Gly Pro Leu Lys Ser Leu Ser
135 140 145

gac aag ctg atc aac atc ctg ggt gga ttg aag gtg gaa tcc ttc ggc 595
Asp Lys Leu Ile Asn Ile Leu Gly Gly Leu Lys Val Glu Ser Phe Gly
150 155 160 165

gag atc ggc gaa gca ttc gat cca gag atc cac gaa gca gta cag gat 643
Glu Ile Gly Glu Ala Phe Asp Pro Glu Ile His Glu Ala Val Gln Asp
170 175 180

ctc tca cag ggt gat gtc aag gtt ctg gga acg gta ctc cgc aag gga 691
Leu Ser Gln Gly Asp Val Lys Val Leu Gly Thr Val Leu Arg Lys Gly
185 190 195

tac cgc ctc ggc gac cgc gtc atc cgc acc gca atg gtc ctc att ggg 739
Tyr Arg Leu Gly Asp Arg Val Ile Arg Thr Ala Met Val Leu Ile Gly
200 205 210

gat cca gag gag agc tagagagact aagtctctta gtg 777
Asp Pro Glu Glu Ser
215

<210> 30
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 30
Met Thr Thr Pro Asn Gly Met Pro Asp Asn Pro Gly Asp Pro Glu Asn
1 5 10 15

Thr Asp Pro Glu Ala Thr Ser Ala Asp Arg Ala Glu Gln Ala Ala Glu
20 25 30

Glu Ala Ala Ala Arg Gln Ala Glu Glu Ser Pro Phe Gly Gln Ala Ser
35 40 45

Glu Glu Glu Ile Ser Pro Glu Leu Glu Ala Glu Ile Asn Asp Leu Leu
50 55 60

Ser Asp Val Asp Pro Asp Leu Asp Gly Asp Gly Glu Val Ser Ala Val
65 70 75 80

Glu Thr Gln Leu Ala Glu Arg Thr Glu Asp Leu Gln Arg Val Thr Ala
85 90 95

Glu Tyr Ala Asn Tyr Arg Arg Arg Thr Glu Arg Glu Arg Gln Gly Ile
100 105 110

Ile Asp Thr Ala Arg Ala Gly Val Val Thr Gln Leu Leu Pro Leu Leu
115 120 125

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Asp Asp Leu Asp Leu Ala Glu Gln His Gly Asp Leu Asn Glu Gly Pro
    130                 135                 140

Leu Lys Ser Leu Ser Asp Lys Leu Ile Asn Ile Leu Gly Gly Leu Lys
145                 150                 155                 160

Val Glu Ser Phe Gly Glu Ile Gly Glu Ala Phe Asp Pro Glu Ile His
                165                 170                 175

Glu Ala Val Gln Asp Leu Ser Gln Gly Asp Val Lys Val Leu Gly Thr
            180                 185                 190

Val Leu Arg Lys Gly Tyr Arg Leu Gly Asp Arg Val Ile Arg Thr Ala
        195                 200                 205

Met Val Leu Ile Gly Asp Pro Glu Glu Ser
    210                 215


<210> 31
<211> 1977
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1954)
<223> RXN02543

<400> 31
ctcaatgagg agtttttctt accggcgaaa gtcggtggga agcaagtcaa agctcaagcc 60

gtggacagta ctaaaatcac ctaaaacagg aggcaccatt atg gga cgt gca gta   115
                                            Met Gly Arg Ala Val
                                             1               5

gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc   163
Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val Ser Val Leu Glu Gly
                10                  15                  20

ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct   211
Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro
            25                  30                  35

tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc   259
Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser
        40                  45                  50

gct aag aac cag gcg gtc acc aac gtt gac cgc acc att cgc tcc gtc   307
Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val
    55                  60                  65

aag cgc cac atc ggc acc gac tgg tcc gtt gct atc gat gac aag aac   355
Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn
70                  75                  80                  85

tac acc tca cag gaa atc tcg gct cgt acc ctg atg aag ctg aag cgc   403
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Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu Met Lys Leu Lys Arg
                90                  95                  100

gac gct gaa gca tac ctg ggc gag gac gtc act gat gct gtt att acc      451
Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr Asp Ala Val Ile Thr
            105                 110                 115

gtt cct gca tac ttc gag gac tca cag cgc cag gca acc aag gaa gct      499
Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln Ala Thr Lys Glu Ala
        120                 125                 130

ggt cag atc gca ggc ctt aac gtt ctg cgt att gtt aac gag cca acc      547
Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr
    135                 140                 145

gcg gct gca ctt gca tac ggc ctt gag aag ggc gag cag gag cag acc      595
Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly Glu Gln Glu Gln Thr
150                 155                 160                 165

att ctg gta ttc gac ctc ggt ggc ggc acc ttc gac gtc tcc ctc cta      643
Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu
                170                 175                 180

gag atc ggc gac ggt gtt gtt gag gtt cgc gca acc tcc ggc gat aac      691
Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala Thr Ser Gly Asp Asn
            185                 190                 195

gag ctc ggt ggc gac gac tgg gat cag cgt atc gtt gac tgg ctg gta      739
Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile Val Asp Trp Leu Val
        200                 205                 210

gag aag ttc cag tcc tcc aac ggc att gac ctg acc aag gac aag atg      787
Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu Thr Lys Asp Lys Met
    215                 220                 225

gcc ctg cag cgt ctg cgt gag gca gct gag aag gca aag atc gag ctg      835
Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu
230                 235                 240                 245

tcc tct tcc cag agt gca aac atc aac ctt cct tac atc acc gtt gat      883
Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro Tyr Ile Thr Val Asp
                250                 255                 260

gca gac aag aac cca ctg ttc ttg gat gag acc ctt tcc cgt gcc gag      931
Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr Leu Ser Arg Ala Glu
            265                 270                 275

ttc cag cgc atc acc cag gac ctc ctg gcc cgc acc aag act cct ttc      979
Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg Thr Lys Thr Pro Phe
        280                 285                 290

aac cag gtt gtt aag gac gct ggc gtg tcc gtc tcg gag atc gac cac      1027
Asn Gln Val Val Lys Asp Ala Gly Val Ser Val Ser Glu Ile Asp His
    295                 300                 305

gtt gtt ctc gtc ggt ggt tcc acc cgt atg cct gct gtt acc gaa ctg      1075
Val Val Leu Val Gly Gly Ser Thr Arg Met Pro Ala Val Thr Glu Leu
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310                 315                 320                 325

gtc aag gaa ctg acc ggt gga cgt gag cca aac aag ggt gtt aac cca     1123
Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn Lys Gly Val Asn Pro
                330                 335                 340

gat gag gtt gtt gca gtt ggt gca gca ctt cag gcc ggt gtt ctc cgc     1171
Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln Ala Gly Val Leu Arg
            345                 350                 355

ggc gag gtc aag gat gtt ctt ctt ctt gac gtc acc cca ctg tcc ctc     1219
Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val Thr Pro Leu Ser Leu
        360                 365                 370

ggc att gag acc aag ggt ggc gtg atg acc aag ctc atc gag cgc aac     1267
Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys Leu Ile Glu Arg Asn
    375                 380                 385

acc acc atc cct acc aag cgt tcc gag acc ttc acc acc gca gag gac     1315
Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe Thr Thr Ala Glu Asp
390                 395                 400                 405

aac cag cct tct gtt cag atc cag gtc ttc cag ggc gag cgt gaa atc     1363
Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln Gly Glu Arg Glu Ile
                410                 415                 420

gca acc gcc aac aag ctg ctc gga tcc ttc gag ctc ggc ggc atc gca     1411
Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu Leu Gly Gly Ile Ala
            425                 430                 435

cct gca cca cgt ggc gtc cca cag atc gag gtc act ttc gac atc gac     1459
Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp
        440                 445                 450

gcc aac ggc atc gtc cac gtc acc gca aag gac aag ggt act ggc aag     1507
Ala Asn Gly Ile Val His Val Thr Ala Lys Asp Lys Gly Thr Gly Lys
    455                 460                 465

gaa aac acc atc acc att cag gac ggc tcc ggt ctc tcc cag gat gaa     1555
Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly Leu Ser Gln Asp Glu
470                 475                 480                 485

att gat cgc atg atc aag gat gct gaa gct cac gct gat gag gac aag     1603
Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His Ala Asp Glu Asp Lys
                490                 495                 500

aag cgc cgc gag gag cag gaa gtc cgc aac aac gct gag tcc ctg gtt     1651
Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val
            505                 510                 515

tac cag acc cgc aag ttc gtt gaa gag aac tcc gag aag gtc tcc gaa     1699
Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu
        520                 525                 530

gac ctc aag gca aag gtc gaa gag gca gcc aag ggc gtt gaa gaa gca     1747
Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala
    535                 540                 545
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ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg    1795
Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu
550                 555                 560                 565

aac acc gag tcc cag gaa atg ggt aag gct atc tac gag gct gac gct    1843
Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile Tyr Glu Ala Asp Ala
                570                 575                 580

gct gct ggt gca acc cag gct gac gca ggt gca gaa ggc gct gca gat    1891
Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala Glu Gly Ala Ala Asp
            585                 590                 595

gac aat gtt gtt gac gct gaa gtt gtc gaa gac gac gca gct gac aat    1939
Asp Asn Val Val Asp Ala Glu Val Val Glu Asp Asp Ala Ala Asp Asn
        600                 605                 610

ggt gag gac aag aag taaatgacta cccctaacgg aat                      1977
Gly Glu Asp Lys Lys
    615


<210> 32
<211> 618
<212> PRT
<213> Corynebacterium glutamicum

<400> 32
Met Gly Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
  1               5                  10                  15

Ser Val Leu Glu Gly Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly
             20                  25                  30

Ser Arg Thr Thr Pro Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val
         35                  40                  45

Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
     50                  55                  60

Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala
 65                  70                  75                  80

Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu
                 85                  90                  95

Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr
            100                 105                 110

Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln
        115                 120                 125

Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
    130                 135                 140

Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly
145                 150                 155                 160
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Glu Gln Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
165 170 175

Asp Val Ser Leu Leu Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala
180 185 190

Thr Ser Gly Asp Asn Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile
195 200 205

Val Asp Trp Leu Val Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu
210 215 220

Thr Lys Asp Lys Met Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys
225 230 235 240

Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro
245 250 255

Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr
260 265 270

Leu Ser Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg
275 280 285

Thr Lys Thr Pro Phe Asn Gln Val Val Lys Asp Ala Gly Val Ser Val
290 295 300

Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
305 310 315 320

Ala Val Thr Glu Leu Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn
325 330 335

Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
340 345 350

Ala Gly Val Leu Arg Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
355 360 365

Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys
370 375 380

Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
385 390 395 400

Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln
405 410 415

Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu
420 425 430

Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val
435 440 445

Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp
450 455 460

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Lys Gly Thr Gly Lys Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly
465                 470                 475                 480

Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His
                485                 490                 495

Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn
            500                 505                 510

Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser
        515                 520                 525

Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys
    530                 535                 540

Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala
545                 550                 555                 560

Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile
                565                 570                 575

Tyr Glu Ala Asp Ala Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala
            580                 585                 590

Glu Gly Ala Ala Asp Asp Asn Val Val Asp Ala Glu Val Val Glu Asp
        595                 600                 605

Asp Ala Ala Asp Asn Gly Glu Asp Lys Lys
    610                 615


&lt;210&gt; 33
&lt;211&gt; 1977
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(1954)
&lt;223&gt; FRXA02543

&lt;400&gt; 33
ctcaatgagg agtttttctt accggcgaaa gtcggtggga agcaagtcaa agctcaagcc 60

gtggacagta ctaaaatcac ctaaaacagg aggcaccatt atg gga cgt gca gta    115
                                            Met Gly Arg Ala Val
                                            1               5

gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc    163
Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val Ser Val Leu Glu Gly
                10                  15                  20

ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct    211
Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro
            25                  30                  35
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tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc    259
Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser
        40                  45                  50

gct aag aac cag gcg gtc acc aac gtt gac cgc acc att cgc tcc gtc    307
Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val
    55                  60                  65

aag cgc cac atc ggc acc gac tgg tcc gtt gct atc gat gac aag aac    355
Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn
70                  75                  80                  85

tac acc tca cag gaa atc tcg gct cgt acc ctg atg aag ctg aag cgc    403
Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu Met Lys Leu Lys Arg
                90                  95                  100

gac gct gaa gca tac ctg ggc gag gac gtc act gat gct gtt att acc    451
Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr Asp Ala Val Ile Thr
            105                 110                 115

gtt cct gca tac ttc gag gac tca cag cgc cag gca acc aag gaa gct    499
Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln Ala Thr Lys Glu Ala
        120                 125                 130

ggt cag atc gca ggc ctt aac gtt ctg cgt att gtt aac gag cca acc    547
Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr
    135                 140                 145

gcg gct gca ctt gca tac ggc ctt gag aag ggc gag cag gag cag acc    595
Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly Glu Gln Glu Gln Thr
150                 155                 160                 165

att ctg gta ttc gac ctc ggt ggc ggc acc ttc gac gtc tcc ctc cta    643
Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu
                170                 175                 180

gag atc ggc gac ggt gtt gtt gag gtt cgc gca acc tcc ggc gat aac    691
Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala Thr Ser Gly Asp Asn
            185                 190                 195

gag ctc ggt ggc gac gac tgg gat cag cgt atc gtt gac tgg ctg gta    739
Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile Val Asp Trp Leu Val
        200                 205                 210

gag aag ttc cag tcc tcc aac ggc att gac ctg acc aag gac aag atg    787
Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu Thr Lys Asp Lys Met
    215                 220                 225

gcc ctg cag cgt ctg cgt gag gca gct gag aag gca aag atc gag ctg    835
Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu
230                 235                 240                 245

tcc tct tcc cag agt gca aac atc aac ctt cct tac atc acc gtt gat    883
Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro Tyr Ile Thr Val Asp
                250                 255                 260

gca gac aag aac cca ctg ttc ttg gat gag acc ctt tcc cgt gcc gag    931
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Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr Leu Ser Arg Ala Glu
            265                 270                 275

ttc cag cgc atc acc cag gac ctc ctg gcc cgc acc aag act cct ttc      979
Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg Thr Lys Thr Pro Phe
        280                 285                 290

aac cag gtt gtt aag gac gct ggc gtg tcc gtc tcg gag atc gac cac     1027
Asn Gln Val Val Lys Asp Ala Gly Val Ser Val Ser Glu Ile Asp His
    295                 300                 305

gtt gtt ctc gtc ggt ggt tcc acc cgt atg cct gct gtt acc gaa ctg     1075
Val Val Leu Val Gly Gly Ser Thr Arg Met Pro Ala Val Thr Glu Leu
310                 315                 320                 325

gtc aag gaa ctg acc ggt gga cgt gag cca aac aag ggt gtt aac cca     1123
Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn Lys Gly Val Asn Pro
                330                 335                 340

gat gag gtt gtt gca gtt ggt gca gca ctt cag gcc ggt gtt ctc cgc     1171
Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln Ala Gly Val Leu Arg
            345                 350                 355

ggc gag gtc aag gat gtt ctt ctt ctt gac gtc acc cca ctg tcc ctc     1219
Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val Thr Pro Leu Ser Leu
        360                 365                 370

ggc att gag acc aag ggt ggc gtg atg acc aag ctc atc gag cgc aac     1267
Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys Leu Ile Glu Arg Asn
    375                 380                 385

acc acc atc cct acc aag cgt tcc gag acc ttc acc acc gca gag gac     1315
Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe Thr Thr Ala Glu Asp
390                 395                 400                 405

aac cag cct tct gtt cag atc cag gtc ttc cag ggc gag cgt gaa atc     1363
Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln Gly Glu Arg Glu Ile
                410                 415                 420

gca acc gcc aac aag ctg ctc gga tcc ttc gag ctc ggc ggc atc gca     1411
Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu Leu Gly Gly Ile Ala
            425                 430                 435

cct gca cca cgt ggc gtc cca cag atc gag gtc act ttc gac atc gac     1459
Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp
        440                 445                 450

gcc aac ggc atc gtc cac gtc acc gca aag gac aag ggt act ggc aag     1507
Ala Asn Gly Ile Val His Val Thr Ala Lys Asp Lys Gly Thr Gly Lys
    455                 460                 465

gaa aac acc atc acc att cag gac ggc tcc ggt ctc tcc cag gat gaa     1555
Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly Leu Ser Gln Asp Glu
470                 475                 480                 485

att gat cgc atg atc aag gat gct gaa gct cac gct gat gag gac aag     1603
Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His Ala Asp Glu Asp Lys
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                490                 495                 500

aag cgc cgc gag gag cag gaa gtc cgc aac aac gct gag tcc ctg gtt     1651
Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val
            505                 510                 515

tac cag acc cgc aag ttc gtt gaa gag aac tcc gag aag gtc tcc gaa     1699
Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu
        520                 525                 530

gac ctc aag gca aag gtc gaa gag gca gcc aag ggc gtt gaa gaa gca     1747
Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala
    535                 540                 545

ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg     1795
Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu
550                 555                 560                 565

aac acc gag tcc cag gaa atg ggt aag gnt atc tnc gag gct gac gct     1843
Asn Thr Glu Ser Gln Glu Met Gly Lys Xaa Ile Xaa Glu Ala Asp Ala
                570                 575                 580

nct gct ggt gca acc cag gct gac gca ggt gca gaa ggc gct gca gat     1891
Xaa Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala Glu Gly Ala Ala Asp
            585                 590                 595

gac aat gtt gtt gac gct gaa gtt gtc gaa gac gac gca gct gac aat     1939
Asp Asn Val Val Asp Ala Glu Val Val Glu Asp Asp Ala Ala Asp Asn
        600                 605                 610

ggt gag gac aag aag taaatgacta cccctaacgg aat                       1977
Gly Glu Asp Lys Lys
    615


<210> 34
<211> 618
<212> PRT
<213> Corynebacterium glutamicum

<400> 34
Met Gly Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
  1               5                  10                  15

Ser Val Leu Glu Gly Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly
             20                  25                  30

Ser Arg Thr Thr Pro Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val
         35                  40                  45

Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
     50                  55                  60

Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala
 65                  70                  75                  80

Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu
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                85                  90                  95

Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr
            100                 105                 110

Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln
        115                 120                 125

Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
    130                 135                 140

Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly
145                 150                 155                 160

Glu Gln Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
                165                 170                 175

Asp Val Ser Leu Leu Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala
            180                 185                 190

Thr Ser Gly Asp Asn Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile
        195                 200                 205

Val Asp Trp Leu Val Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu
    210                 215                 220

Thr Lys Asp Lys Met Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys
225                 230                 235                 240

Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro
                245                 250                 255

Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr
            260                 265                 270

Leu Ser Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg
        275                 280                 285

Thr Lys Thr Pro Phe Asn Gln Val Val Lys Asp Ala Gly Val Ser Val
    290                 295                 300

Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
305                 310                 315                 320

Ala Val Thr Glu Leu Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn
                325                 330                 335

Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
            340                 345                 350

Ala Gly Val Leu Arg Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
        355                 360                 365

Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys
    370                 375                 380

Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
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385 390 395 400

Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln
405 410 415

Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu
420 425 430

Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val
435 440 445

Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp
450 455 460

Lys Gly Thr Gly Lys Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly
465 470 475 480

Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His
485 490 495

Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn
500 505 510

Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser
515 520 525

Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys
530 535 540

Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala
545 550 555 560

Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Xaa Ile
565 570 575

Xaa Glu Ala Asp Ala Xaa Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala
580 585 590

Glu Gly Ala Ala Asp Asp Asn Val Val Asp Ala Glu Val Val Glu Asp
595 600 605

Asp Ala Ala Asp Asn Gly Glu Asp Lys Lys
610 615

<210> 35
<211> 1947
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1924)
<223> RXN02280

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cgcgattgcg tcatcgatcg ttgttgcttc catgcgcacc acactatctt tctgcacgcc 60

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ctgatgccct gtggattcaa aactgtgctt ttataggcgt atg caa gaa tcc tca    115
                                            Met Gln Glu Ser Ser
                                              1               5

cgt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt    163
Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser
                 10                  15                  20

cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag    211
Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln
             25                  30                  35

aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc    259
Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly
         40                  45                  50

tac gag ccg agt att cgt att cgg ccg gtg acc aag gat cgt gcc acg    307
Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr
     55                  60                  65

ttt tca ctg gtt gat aat ggt acg ggc ctg acc gcg cag gag gcg cgg    355
Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg
 70                  75                  80                  85

gaa ttg ctg gcg acg gtg ggg cgg acg tcg aaa cgc gat gaa ttc ggt    403
Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly
                 90                  95                 100

ctg cag cgg gaa ggt cgc ctg ggg caa ttt ggc atc ggg ctg ctt agt    451
Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly Ile Gly Leu Leu Ser
            105                 110                 115

tgt ttc atg gtg gcg gat gag atc acc atg gtg tcg cat gcg gag ggt    499
Cys Phe Met Val Ala Asp Glu Ile Thr Met Val Ser His Ala Glu Gly
        120                 125                 130

gcg tcg gcg att cgg tgg act ggt cat gcg gat ggc acc ttt aac ctg    547
Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp Gly Thr Phe Asn Leu
    135                 140                 145

gag att ctt ggg gat gac gca acg gat gtc att ccg gtg ggc acg act    595
Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile Pro Val Gly Thr Thr
150                 155                 160                 165

gtg cac ctg act ccg cgc cct gat gag cgc acg ttg ctg acg gaa aat    643
Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr Leu Leu Thr Glu Asn
                170                 175                 180

tcc gtg gtc acc att gct agt aat tat ggc cgc tac ctg ccg att cct    691
Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg Tyr Leu Pro Ile Pro
            185                 190                 195

att gtg gtg cag ggt gag aaa aac acc acc atc act aca tcg ccg gtg    739
Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile Thr Thr Ser Pro Val
        200                 205                 210
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ttt gca aag gat act gat cag cag cac agg ctg tat gcc ggc cgg gag   787
Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu Tyr Ala Gly Arg Glu
    215                 220                 225

cgc ctt ggt aaa act cct ttt gat gtc atc gat ctc acc ggt cct ggc   835
Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp Leu Thr Gly Pro Gly
230                 235                 240                 245

atc gag ggt gtg gct tat gta ttg ccg gag gcc cag gct ccg cat atg   883
Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala Gln Ala Pro His Met
                250                 255                 260

tcc agg cgt cac agt att tat gtc aac cgc atg ttg gtc tct gat ggg   931
Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met Leu Val Ser Asp Gly
            265                 270                 275

cct tcc acg gtg ctg ccc aac tgg gcg ttc ttt gtg gaa tgt gaa atc   979
Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe Val Glu Cys Glu Ile
        280                 285                 290

aat tca acc gat ttg gaa ccc acc gca tcg cgt gaa gcg ctc atg gat   1027
Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg Glu Ala Leu Met Asp
    295                 300                 305

gac acc gcg ttc gcg gca acc agg gaa cat atc ggt gag tgc att aaa   1075
Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile Gly Glu Cys Ile Lys
310                 315                 320                 325

tcg tgg ctg att aat ctc gcc atg acc aag cct cac cgc gtg cgg gaa   1123
Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro His Arg Val Arg Glu
                330                 335                 340

ttt act gcg att cat gat ctt gcc ctg cgc gag ctg tgc caa tcg gac   1171
Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu Leu Cys Gln Ser Asp
            345                 350                 355

gcg gac ctg gct gaa acc atg ttg ggt ctt ctc acc ttg gag acc tcc   1219
Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser
        360                 365                 370

cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag   1267
Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu
    375                 380                 385

gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc   1315
Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu
390                 395                 400                 405

aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att   1363
Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile
                410                 415                 420

cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt   1411
His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu
            425                 430                 435

acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt   1459
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Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu
440 445 450

ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc 1507
Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val
455 460 465

acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt 1555
Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe
470 475 480 485

gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag 1603
Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln
490 495 500

gcc tca cgg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg 1651
Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp
505 510 515

gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc 1699
Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala
520 525 530

aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac 1747
Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn
535 540 545

aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg 1795
Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val
550 555 560 565

tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg ttg tcc agc aag 1843
Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys
570 575 580

agg cca ctg cgg gtg aag gaa cgc gcg ctg ctt aat gat tcg ctg gca 1891
Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
585 590 595

gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgctaat 1944
Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
600 605

ctt 1947

<210> 36
<211> 608
<212> PRT
<213> Corynebacterium glutamicum

<400> 36
Met Gln Glu Ser Ser Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val
1 5 10 15

Val Asp Leu Leu Ser Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val
20 25 30

Arg Glu Leu Leu Gln Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu
35 40 45

Gln Gly Glu Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr
50 55 60

Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr
65 70 75 80

Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys
85 90 95

Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
100 105 110

Ile Gly Leu Leu Ser Cys Phe Met Val Ala Asp Glu Ile Thr Met Val
115 120 125

Ser His Ala Glu Gly Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp
130 135 140

Gly Thr Phe Asn Leu Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile
145 150 155 160

Pro Val Gly Thr Thr Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr
165 170 175

Leu Leu Thr Glu Asn Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg
180 185 190

Tyr Leu Pro Ile Pro Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile
195 200 205

Thr Thr Ser Pro Val Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu
210 215 220

Tyr Ala Gly Arg Glu Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp
225 230 235 240

Leu Thr Gly Pro Gly Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala
245 250 255

Gln Ala Pro His Met Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met
260 265 270

Leu Val Ser Asp Gly Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe
275 280 285

Val Glu Cys Glu Ile Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg
290 295 300

Glu Ala Leu Met Asp Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile
305 310 315 320

Gly Glu Cys Ile Lys Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro
325 330 335

His Arg Val Arg Glu Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu
340 345 350

Leu Cys Gln Ser Asp Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu
355 360 365

Thr Leu Glu Thr Ser Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr
370 375 380

Leu Ser Ile Thr Glu Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp
385 390 395 400

Asp Phe Arg Gln Leu Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile
405 410 415

Asn Gly Gly Tyr Ile His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val
420 425 430

His Tyr Pro Pro Leu Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met
435 440 445

Asp Leu Met Glu Leu Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala
450 455 460

Leu Asp Ala Gln Val Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly
465 470 475 480

Ala Thr Arg Val Phe Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile
485 490 495

Asp Ser Lys Ala Gln Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala
500 505 510

Thr Thr Asp Arg Trp Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu
515 520 525

Ser Arg Gln Thr Ala Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu
530 535 540

Cys Leu Asn Trp Asn Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp
545 550 555 560

Asp Thr Ala Val Val Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala
565 570 575

Leu Leu Ser Ser Lys Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu
580 585 590

Asn Asp Ser Leu Ala Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
595 600 605

<210> 37

<211> 436
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(436)
<223> FRXA02282

<400> 37
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cgcgattgcg tcatcgatcg ttgttgcttc catgcgcacc acactatctt tctgcacgcc 60

ctgatgccct gtggattcaa aactgtgctt ttataggcgt atg caa gaa tcc tca   115
                                          Met Gln Glu Ser Ser
                                           1               5

cgt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt   163
Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser
                10                  15                  20

cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag   211
Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln
            25                  30                  35

aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc   259
Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly
        40                  45                  50

tac gag ccg agt att cgt att cgg ccg gtg acc aag gat cgt gcc acg   307
Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr
    55                  60                  65

ttt tca ctg gtt gat aat ggt acg ggc ctg acc gcg cag gag gcg cgg   355
Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg
70                  75                  80                  85

gaa ttg ctg gcg acg gtg ggg cgg acg tcg aaa cgc gat gaa ttc ggt   403
Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly
                90                  95                  100

ctg cag cgg gaa ggt cgc ctg ggg caa ttt ggc                       436
Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
            105                 110
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<210> 38
<211> 112
<212> PRT
<213> Corynebacterium glutamicum

<400> 38
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Met Gln Glu Ser Ser Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val
1               5                   10                  15

Val Asp Leu Leu Ser Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val
            20                  25                  30
```

```
Arg Glu Leu Leu Gln Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu
        35                  40                  45

Gln Gly Glu Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr
    50                  55                  60

Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr
65                  70                  75                  80

Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys
                85                  90                  95

Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
            100                 105                 110




<210> 39
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1246)
<223> RXA00886

<400> 39
taagtatgtt ggtcgtgtgc tcgctggcga atagctgcgg gtatagttgg ccatttgttt 60

tgattaatct gtttagaagc taaaggaagt atcacccacc gtg gca cgt gac tat   115
                                           Val Ala Arg Asp Tyr
                                            1               5

tac ggc att ctc ggc gtc gat cgc aat gca acc gaa tca gag atc aaa   163
Tyr Gly Ile Leu Gly Val Asp Arg Asn Ala Thr Glu Ser Glu Ile Lys
                10                  15                  20

aag gca tac cga aag ctt gcc cgc aaa tac cac ccg gac gta aac cca   211
Lys Ala Tyr Arg Lys Leu Ala Arg Lys Tyr His Pro Asp Val Asn Pro
            25                  30                  35

ggt gag gaa gca gcg gag aaa ttc cgc gag gct tct gtt gcg cat gag   259
Gly Glu Glu Ala Ala Glu Lys Phe Arg Glu Ala Ser Val Ala His Glu
        40                  45                  50

gta ctc act gat ccg gat aag cgc cgc att gtt gat atg ggc ggt gac   307
Val Leu Thr Asp Pro Asp Lys Arg Arg Ile Val Asp Met Gly Gly Asp
    55                  60                  65

cca atg gag caa ggc ggc gga gct ggc gct ggt ggc ttc ggt gga ggc   355
Pro Met Glu Gln Gly Gly Gly Ala Gly Ala Gly Gly Phe Gly Gly Gly
70                  75                  80                  85

ttc ggc ggc agc ggt gga ctg ggc gat atc ttc gat gcc ttc ttc ggc   403
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Phe Gly Gly Ser Gly Gly Leu Gly Asp Ile Phe Asp Ala Phe Phe Gly
90 95 100

ggt ggc gcg ggc ggt tcc cgt gga cca cgt tcc cgc gtg cag cca ggc 451
Gly Gly Ala Gly Gly Ser Arg Gly Pro Arg Ser Arg Val Gln Pro Gly
105 110 115

agt gac acc ttg tgg cgc acc tcc atc acc ttg gaa gag gct tac aag 499
Ser Asp Thr Leu Trp Arg Thr Ser Ile Thr Leu Glu Glu Ala Tyr Lys
120 125 130

ggc gct aag aaa gat ctc acc ctt gac acc gca gtg ctg tgt acc aag 547
Gly Ala Lys Lys Asp Leu Thr Leu Asp Thr Ala Val Leu Cys Thr Lys
135 140 145

tgt cat ggt tct gga tct gca tcc gac aag aag cct gtt acc tgt ggc 595
Cys His Gly Ser Gly Ser Ala Ser Asp Lys Lys Pro Val Thr Cys Gly
150 155 160 165

acc tgt aat ggc gct ggt gaa att cag gaa gtg cag cgc agc ttc ctg 643
Thr Cys Asn Gly Ala Gly Glu Ile Gln Glu Val Gln Arg Ser Phe Leu
170 175 180

ggc aac gtc atg acg tcc cgc cca tgc cac acc tgc gat ggc acc ggt 691
Gly Asn Val Met Thr Ser Arg Pro Cys His Thr Cys Asp Gly Thr Gly
185 190 195

gag atc atc cca gat cct tgc act gag tgt gca gca gat ggt cgt gtg 739
Glu Ile Ile Pro Asp Pro Cys Thr Glu Cys Ala Ala Asp Gly Arg Val
200 205 210

cgt gct cgc cgc gac atc gtg gcc aac atc cca gct ggc atc cag tcc 787
Arg Ala Arg Arg Asp Ile Val Ala Asn Ile Pro Ala Gly Ile Gln Ser
215 220 225

ggc atg cgc atc cgc atg gca ggc caa ggt gag gtt ggc gct ggt ggc 835
Gly Met Arg Ile Arg Met Ala Gly Gln Gly Glu Val Gly Ala Gly Gly
230 235 240 245

ggt cct gcg ggt gac ctc tac att gaa gtc atg gtg cgc ccg cac gcc 883
Gly Pro Ala Gly Asp Leu Tyr Ile Glu Val Met Val Arg Pro His Ala
250 255 260

atc ttc acc cgc gat ggc gac gat ctg cac gcc agc atc aag gtt cca 931
Ile Phe Thr Arg Asp Gly Asp Asp Leu His Ala Ser Ile Lys Val Pro
265 270 275

atg ttc gat gca gcg ctt ggc acc gaa ttg gac gtg gaa tcc ctc acc 979
Met Phe Asp Ala Ala Leu Gly Thr Glu Leu Asp Val Glu Ser Leu Thr
280 285 290

ggc gaa gag gtg aaa att acc atc cct gca ggt act cag ccc aac gat 1027
Gly Glu Glu Val Lys Ile Thr Ile Pro Ala Gly Thr Gln Pro Asn Asp
295 300 305

gtg atc acc ttg gat ggt gaa ggc atg ccg aag ctg cgc gca gaa ggc 1075
Val Ile Thr Leu Asp Gly Glu Gly Met Pro Lys Leu Arg Ala Glu Gly

```
310                 315                 320                 325

cac ggc aac ctc atg gcg cat gtc gat cta ttt gtg cca acc gat ttg    1123
His Gly Asn Leu Met Ala His Val Asp Leu Phe Val Pro Thr Asp Leu
                330                 335                 340

gat gac cgc acc cgc gaa ttg ctt gaa gaa atc cgc aac cat cgc agc    1171
Asp Asp Arg Thr Arg Glu Leu Leu Glu Glu Ile Arg Asn His Arg Ser
            345                 350                 355

gac aac gct tcc gtg cat cgc gaa ggc gga gaa gaa tcc ggt ttc ttt    1219
Asp Asn Ala Ser Val His Arg Glu Gly Gly Glu Glu Ser Gly Phe Phe
        360                 365                 370

gac aag ctc cga aac aag ttc cgc aaa taatgtcact gccagtattt          1266
Asp Lys Leu Arg Asn Lys Phe Arg Lys
    375                 380

atc                                                                1269


<210> 40
<211> 382
<212> PRT
<213> Corynebacterium glutamicum

<400> 40
Val Ala Arg Asp Tyr Tyr Gly Ile Leu Gly Val Asp Arg Asn Ala Thr
1               5                   10                  15

Glu Ser Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ala Arg Lys Tyr His
            20                  25                  30

Pro Asp Val Asn Pro Gly Glu Glu Ala Ala Glu Lys Phe Arg Glu Ala
        35                  40                  45

Ser Val Ala His Glu Val Leu Thr Asp Pro Asp Lys Arg Arg Ile Val
    50                  55                  60

Asp Met Gly Gly Asp Pro Met Glu Gln Gly Gly Gly Ala Gly Ala Gly
65                  70                  75                  80

Gly Phe Gly Gly Gly Phe Gly Gly Ser Gly Gly Leu Gly Asp Ile Phe
                85                  90                  95

Asp Ala Phe Phe Gly Gly Gly Ala Gly Gly Ser Arg Gly Pro Arg Ser
            100                 105                 110

Arg Val Gln Pro Gly Ser Asp Thr Leu Trp Arg Thr Ser Ile Thr Leu
        115                 120                 125

Glu Glu Ala Tyr Lys Gly Ala Lys Lys Asp Leu Thr Leu Asp Thr Ala
    130                 135                 140

Val Leu Cys Thr Lys Cys His Gly Ser Gly Ser Ala Ser Asp Lys Lys
145                 150                 155                 160
```

Pro Val Thr Cys Gly Thr Cys Asn Gly Ala Gly Glu Ile Gln Glu Val
165 170 175

Gln Arg Ser Phe Leu Gly Asn Val Met Thr Ser Arg Pro Cys His Thr
180 185 190

Cys Asp Gly Thr Gly Glu Ile Ile Pro Asp Pro Cys Thr Glu Cys Ala
195 200 205

Ala Asp Gly Arg Val Arg Ala Arg Arg Asp Ile Val Ala Asn Ile Pro
210 215 220

Ala Gly Ile Gln Ser Gly Met Arg Ile Arg Met Ala Gly Gln Gly Glu
225 230 235 240

Val Gly Ala Gly Gly Gly Pro Ala Gly Asp Leu Tyr Ile Glu Val Met
245 250 255

Val Arg Pro His Ala Ile Phe Thr Arg Asp Gly Asp Asp Leu His Ala
260 265 270

Ser Ile Lys Val Pro Met Phe Asp Ala Ala Leu Gly Thr Glu Leu Asp
275 280 285

Val Glu Ser Leu Thr Gly Glu Glu Val Lys Ile Thr Ile Pro Ala Gly
290 295 300

Thr Gln Pro Asn Asp Val Ile Thr Leu Asp Gly Glu Gly Met Pro Lys
305 310 315 320

Leu Arg Ala Glu Gly His Gly Asn Leu Met Ala His Val Asp Leu Phe
325 330 335

Val Pro Thr Asp Leu Asp Asp Arg Thr Arg Glu Leu Leu Glu Glu Ile
340 345 350

Arg Asn His Arg Ser Asp Asn Ala Ser Val His Arg Glu Gly Gly Glu
355 360 365

Glu Ser Gly Phe Phe Asp Lys Leu Arg Asn Lys Phe Arg Lys
370 375 380

<210> 41
<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1447)
<223> RXS00568

<400> 41
gtttcggacg acgcgagaaa tcgcattaat cgtcggaaac cgggcttgtt tttgtaatat 60

ctgaaacttt ccctttcccg atcatccagg agatttactc gtg aag agt tct gtc 115

```
                                                Val Lys Ser Ser Val
                                                 1               5

gag aag ctg agc gac acc cgt tca aag atc acc gtt gag gtt cca ttt    163
Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr Val Glu Val Pro Phe
                 10                  15                  20

tct gaa ctg aag cca gag atc gac cag gca tac gcc gct cta gcg cag    211
Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr Ala Ala Leu Ala Gln
             25                  30                  35

caa gtc cag atc cct ggt ttc cgt aag ggc aag gca ccg cgt cag ctt    259
Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys Ala Pro Arg Gln Leu
         40                  45                  50

atc gac gca cgc ttc ggc cgt ggt gcg gtt ctg gag cag gtt gtc aac    307
Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu Glu Gln Val Val Asn
     55                  60                  65

gac atg ctt cct aac cgc tac gca cag gca atc gaa gct gag ggc atc    355
Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile Glu Ala Glu Gly Ile
 70                  75                  80                  85

aag gca atc ggc cag cct aac gta gag gtc acc aag atc gaa gac aac    403
Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr Lys Ile Glu Asp Asn
                 90                  95                  100

gag ctc gtt gag ttc gtc gct gag gtt gac gtt cgc cca gag ttc gag    451
Glu Leu Val Glu Phe Val Ala Glu Val Asp Val Arg Pro Glu Phe Glu
             105                 110                 115

ctt cct aag ttc gag gac atc act gtt gag gtc cca gct atc aag gct    499
Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val Pro Ala Ile Lys Ala
         120                 125                 130

gac gaa gag gca atc gaa gca gag ctc gag acc ctg cgt gca cgt ttc    547
Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr Leu Arg Ala Arg Phe
     135                 140                 145

tcc acc ttg aag gat cac aac cac aag ctg aag aag ggt gag ttc gtc    595
Ser Thr Leu Lys Asp His Asn His Lys Leu Lys Lys Gly Glu Phe Val
150                 155                 160                 165

acc atc aac atc acc gca agc att gac ggt gag aag att gaa gag gca    643
Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu Lys Ile Glu Glu Ala
                170                 175                 180

acc act gag ggt ctg tcc tac gaa atc gga tct gac gat ctg att gac    691
Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser Asp Asp Leu Ile Asp
            185                 190                 195

ggc ctg gac aag gct ctg atc ggc gct aag aag gat gaa acc gta gag    739
Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys Asp Glu Thr Val Glu
        200                 205                 210

ttc acc tct gag ctg gca aac ggc gag cac aag ggc aag gaa gct caa    787
Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys Gly Lys Glu Ala Gln
```

```
    215                 220                 225

atc agc gtt gag atc acc gca acc aag cag cgc gag ctg cct gag ctg      835
Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg Glu Leu Pro Glu Leu
230                 235                 240                 245

gat gat gag ttc gca cag ctg gct tct gag ttc gac acc atc gaa gag      883
Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe Asp Thr Ile Glu Glu
                250                 255                 260

ctt cgt gag tcc acc gtg tct gac gtt gag gct aag cag aag aac gag      931
Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala Lys Gln Lys Asn Glu
            265                 270                 275

cag gct gct gca atc cgc gac gaa gtt ctc gct gcg gct ctt ggc gag      979
Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala Ala Ala Leu Gly Glu
        280                 285                 290

gct gac ttc gct ctg cca cag tcc atc gtt gac gag cag gca cac tcc     1027
Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp Glu Gln Ala His Ser
    295                 300                 305

cag ctg cac cag ctc ctc ggc gag ctt gca cac gac gat gct gca ctg     1075
Gln Leu His Gln Leu Leu Gly Glu Leu Ala His Asp Asp Ala Ala Leu
310                 315                 320                 325

aac tcc ctc ctt gag gct cag ggc acc act cgt gaa gag ttc gac aag     1123
Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg Glu Glu Phe Asp Lys
                330                 335                 340

aag aac gtc gaa gat gct gag aag gct gtt cgc acc cag ctg ttc ctg     1171
Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg Thr Gln Leu Phe Leu
            345                 350                 355

gac acc ctc tct gag gtt gag gag cct gag gtt tcc cag cag gag ctc     1219
Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val Ser Gln Gln Glu Leu
        360                 365                 370

acc gac cac atc ctg ttc acc gca cag tct tac ggc atg gac cca aac     1267
Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr Gly Met Asp Pro Asn
    375                 380                 385

cag ttc atc ggt cag ctg cag cag tcc ggc cag atc gcg aac ctc ttc     1315
Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln Ile Ala Asn Leu Phe
390                 395                 400                 405

tcc gac gtt cgc cgt ggc aag gct ctt gca cag gct atc tgc cgc gta     1363
Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln Ala Ile Cys Arg Val
                410                 415                 420

aac gtg aag gac tcc gag ggt aac gag atc gac cct aag gaa tac ttc     1411
Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp Pro Lys Glu Tyr Phe
            425                 430                 435

ggt gaa gaa gaa gta gct gag act gag tct gaa gct taaaacttt           1457
Gly Glu Glu Glu Val Ala Glu Thr Glu Ser Glu Ala
        440                 445
```

aaagaaataa cgc 1470

<210> 42
<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 42
Val Lys Ser Ser Val Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr
1 5 10 15

Val Glu Val Pro Phe Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr
20 25 30

Ala Ala Leu Ala Gln Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys
35 40 45

Ala Pro Arg Gln Leu Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu
50 55 60

Glu Gln Val Val Asn Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile
65 70 75 80

Glu Ala Glu Gly Ile Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr
85 90 95

Lys Ile Glu Asp Asn Glu Leu Val Glu Phe Val Ala Glu Val Asp Val
100 105 110

Arg Pro Glu Phe Glu Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val
115 120 125

Pro Ala Ile Lys Ala Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr
130 135 140

Leu Arg Ala Arg Phe Ser Thr Leu Lys Asp His Asn His Lys Leu Lys
145 150 155 160

Lys Gly Glu Phe Val Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu
165 170 175

Lys Ile Glu Glu Ala Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser
180 185 190

Asp Asp Leu Ile Asp Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys
195 200 205

Asp Glu Thr Val Glu Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys
210 215 220

Gly Lys Glu Ala Gln Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg
225 230 235 240

Glu Leu Pro Glu Leu Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe
245 250 255

```
Asp Thr Ile Glu Glu Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala
            260                 265                 270

Lys Gln Lys Asn Glu Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala
        275                 280                 285

Ala Ala Leu Gly Glu Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp
    290                 295                 300

Glu Gln Ala His Ser Gln Leu His Gln Leu Leu Gly Glu Leu Ala His
305                 310                 315                 320

Asp Asp Ala Ala Leu Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg
                325                 330                 335

Glu Glu Phe Asp Lys Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg
            340                 345                 350

Thr Gln Leu Phe Leu Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val
        355                 360                 365

Ser Gln Gln Glu Leu Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr
    370                 375                 380

Gly Met Asp Pro Asn Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln
385                 390                 395                 400

Ile Ala Asn Leu Phe Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln
                405                 410                 415

Ala Ile Cys Arg Val Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp
            420                 425                 430

Pro Lys Glu Tyr Phe Gly Glu Glu Glu Val Ala Glu Thr Glu Ser Glu
        435                 440                 445

Ala


&lt;210&gt; 43
&lt;211&gt; 826
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(826)
&lt;223&gt; RXN03038

&lt;400&gt; 43
gcgcggaaaa caccaagtaa gccttacagt ccgacagcct catagcggat gggataagtt 60

ccaaacacgt tcaaatccgt taaagtgcct gtttaaaact atg cat tca aag gaa   115
                                          Met His Ser Lys Glu
                                          1               5
```

gag tta aca gtg cgt aaa gga att tcc cgc gtc ctc tcg gta gcg gtt 163
Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val
10 15 20

gct agt tca atc gga ttc gga act gta ctg aca ggc acc ggc atc gca 211
Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala
25 30 35

gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac 259
Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn
40 45 50

tac aac ccg atc gat gac atc aag gat cgt ccc gaa gga ttg tcc aat 307
Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn
55 60 65

ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc 355
Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala
70 75 80 85

acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat 403
Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp
90 95 100

ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac 451
Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp
105 110 115

atg gag cca gaa gtt ctt gcg cgc ctt gag cga ttc gtc ggc gtt gac 499
Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp
120 125 130

ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc 547
Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg
135 140 145

acc att cct cta gtc tgg gtt gtt cca gaa gac aac acc gtg cct ggc 595
Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val Pro Gly
150 155 160 165

cca acg gtc tac gca ctc gga ggc ggt gac ggt gga caa ggc ggc cag 643
Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly Gly Gln
170 175 180

aac tgg gtc acc cgc acc gac ctt gag gaa tta acc agt gac aac aac 691
Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu Thr Ser Asp Asn Asn
185 190 195

atc aac ctc atc atg ccg atg ctc gga tct ttt agt ttc tac tct gac 739
Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr Ser Asp
200 205 210

tgg gca cgc gaa agc caa tcc atg ggt tgt gcg caa cag tgg gaa aca 787
Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala Gln Gln Trp Glu Thr
215 220 225

ttg ctc atg cac gaa ctg cct gag ccg ctt gta gcg gcc 826
Leu Leu Met His Glu Leu Pro Glu Pro Leu Val Ala Ala
230 235 240

<210> 44
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 44
Met His Ser Lys Glu Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val
1 5 10 15

Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr
20 25 30

Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met
35 40 45

Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro
50 55 60

Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp
65 70 75 80

Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu
85 90 95

Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro
100 105 110

Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg
115 120 125

Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser
130 135 140

Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp
145 150 155 160

Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly
165 170 175

Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu
180 185 190

Thr Ser Asp Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe
195 200 205

Ser Phe Tyr Ser Asp Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala
210 215 220

Gln Gln Trp Glu Thr Leu Leu Met His Glu Leu Pro Glu Pro Leu Val
225 230 235 240

Ala Ala

<210> 45
<211> 653
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(630)
<223> RXN03039

<400> 45
gca ctc ccg caa tac acc gac cca cgc tac ccc ctc ggc aaa gac gac 48
Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp
1 5 10 15

ctg ccc aaa gca acc atc gac atg gag cca gaa gct ctt gcg cgc ctt 96
Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
20 25 30

gag cga ttc gtc ggc gtt gac ggt gat cgc atc cgc caa atc aac gcg 144
Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
35 40 45

tac tcg cca tca atg gga cgc acc att cct cta gtc tgg gtc gtg cca 192
Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
50 55 60

gaa gac aac acc gtg cct ggc cca acg gtc tac gca ctc ggc ggc ggc 240
Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
65 70 75 80

gac ggt ggc caa ggc ggc caa aac tgg gtc acc cgc acc gac ctt gat 288
Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
85 90 95

gag ttg acc agt gaa aac aac atc aac ctc atc atg ccc atg ctc gga 336
Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
100 105 110

tct ttt agt ttc tac gct gac tgg gca ggc gaa agc gaa tcc atg ggt 384
Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
115 120 125

ggt gcg caa cag tgg gaa aca ttc ctc atg cac gaa ctr ccm gag ccg 432
Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
130 135 140

cta gaa gcg gcc atc ggc gca gac ggg caa cgc agc atc gtc ggc atg 480
Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
145 150 155 160

tcc atg tcc ggg gga tcr gtg ctg aac ttt gcg acg cat gac ccc aac 528
Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
165 170 175

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ttt tay tcc tck gtc ggc tca ttt tct gga tgt gcc gaa acc aac tcc    576
Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
            180                 185                 190

tgg atg ggr cgc cgn tgg cat cgc agc cac tgc cta caa cgg caa tgt    624
Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys
        195                 200                 205

cgt gcc tgagcaaatc tttggtgaag tag                                  653
Arg Ala
    210


<210> 46
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 46
Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp
  1               5                  10                  15

Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
            20                  25                  30

Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
        35                  40                  45

Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
    50                  55                  60

Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
65                  70                  75                  80

Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
                85                  90                  95

Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
            100                 105                 110

Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
        115                 120                 125

Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
    130                 135                 140

Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
145                 150                 155                 160

Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
                165                 170                 175

Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
            180                 185                 190

Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys
```

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        195                     200                     205

Arg Ala
    210


<210> 47
<211> 432
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> RXN03040

<400> 47
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ctctacatct tcgccggttc cggtgtgttc tctgaactag atg tca tnc ggt gac    115
                                           Met Ser Xaa Gly Asp
                                           1               5

aac gca ccg att gat gag gat gcg ttc aaa aac cgc gtc ttg gtt ggg    163
Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn Arg Val Leu Val Gly
                10                  15                  20

ttt gaa atc gaa gct atg tcc aac acc tgc acc cat aac ctc aag gct    211
Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr His Asn Leu Lys Ala
            25                  30                  35

gcg acc gat caa atg ggc atc gac aac atc aac tac gat ttc cga cca    259
Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro
        40                  45                  50

acc gga acc cac gcc tgg gat tac tgg aac gaa gcg ctc cac cgc ttc    307
Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu Ala Leu His Arg Phe
    55                  60                  65

ttc ccg ttg atg atg cag ggc ttc ggc ctc gac ggt ggt ccc atc ccg    355
Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro
70                  75                  80                  85

atc tat aac cct aac ggt gtg acc tcc agc gag tct tct ntc aga act    403
Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu Ser Ser Xaa Arg Thr
                90                  95                  100

gtc ttc tgatgtgagc cttggcaccn gtg                                 432
Val Phe


<210> 48
<211> 103
<212> PRT
<213> Corynebacterium glutamicum
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<400> 48
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Met Ser Xaa Gly Asp Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn
  1               5                  10                  15

Arg Val Leu Val Gly Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr
             20                  25                  30

His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn
         35                  40                  45

Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu
     50                  55                  60

Ala Leu His Arg Phe Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp
 65                  70                  75                  80

Gly Gly Pro Ile Pro Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu
                 85                  90                  95

Ser Ser Xaa Arg Thr Val Phe
            100
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<210> 49
<211> 835
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(835)
<223> RXN03051

<400> 49
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acatccagaa gtagtcgttg agtatcacga gcaagtcaac gatagtaaag ataatgtcga 60

ggaactcccg ctgcctaagc gggacatagt tgcaggggac atg cgt tca gat gtt    115
                                           Met Arg Ser Asp Val
                                             1               5

atc gag tta ccg gag ggg gta agc aag gag aaa gct gac cag cta gaa    163
Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys Ala Asp Gln Leu Glu
                 10                  15                  20

gtt gcg gaa gcg cga ctt aac gag ggt gca cga ctg atg gca acc acc    211
Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Thr Thr
             25                  30                  35

ggg tgt gag gtt atg tgg cca acg ggc ttc tca gtt tgt ggc cga att    259
Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile
         40                  45                  50

ctt gac acc tat cgc cag gtt gga ggt cag ttg tca tgg ctt ggg cca    307
Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro
     55                  60                  65

ccg aag tca aac gag ttg acc aat ccc gac ggt gtt ggc aaa aga agt    355
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```
Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser
 70                 75                  80                  85

gaa ttt ttt ggt gga gcc atc tat tgg cac cca gac aca ggc gct tat      403
Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr
                90                  95                  100

gca gtg acc ttg gac ggt ttg cga cag tgg ggg acc ttg aac tgg gaa      451
Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu
            105                 110                 115

tca ggg cca ttg ggg tac cca acc tct ggt ccg atg gat aca aac tat      499
Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr
        120                 125                 130

ccc ctt act cag cga cag act ttt caa ggt ggt gac aac tac tac aac      547
Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn
    135                 140                 145

cca ttg act ggc ggt gct gtg tgg ggc gat att aaa cag cgc tac gaa      595
Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu
150                 155                 160                 165

gaa ctt ggc ggc tcg aat cat gcc att ggc atc ccg atc act aat gag      643
Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu
                170                 175                 180

cta cct agc ggt act gag tat ttt tac aat aat ttc tcc aat gga aca      691
Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Ser Asn Gly Thr
            185                 190                 195

att tcg tgg cga aat gat cgt cag aca cgg ttt atg tat ttg gct acg      739
Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr
        200                 205                 210

cag cgg gtg tgg gat gcg ttg ggt cgg gag acg ggt cgt tta ggt ttt      787
Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe
    215                 220                 225

cct gaa gca gat gaa aca cct gag gtt tct ggt cta ttc cat gtg gcg      835
Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly Leu Phe His Val Ala
230                 235                 240                 245


<210> 50
<211> 245
<212> PRT
<213> Corynebacterium glutamicum

<400> 50
Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys
  1               5                  10                  15

Ala Asp Gln Leu Glu Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg
             20                  25                  30

Leu Met Ala Thr Thr Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser
```

35 40 45

Val Cys Gly Arg Ile Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu
50 55 60

Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly
65 70 75 80

Val Gly Lys Arg Ser Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro
85 90 95

Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly
100 105 110

Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro
115 120 125

Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly
130 135 140

Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile
145 150 155 160

Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile
165 170 175

Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn
180 185 190

Phe Ser Asn Gly Thr Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe
195 200 205

Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr
210 215 220

Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly
225 230 235 240

Leu Phe His Val Ala
245

<210> 51
<211> 1704
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1681)
<223> RXN03054

<400> 51
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cagtttgttc acatcaacta gtaacgaaag gatcatgtga atg aaa ctg ttt tcc 115
Met Lys Leu Phe Ser

```
                                           1               5

aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata     163
Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile
            10                  15                  20

gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac     211
Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp
        25                  30                  35

caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct     259
Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro
    40                  45                  50

gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc     307
Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile
55                  60                  65

cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag     355
His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu
70                  75                  80                  85

ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act     403
Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr
                90                  95                  100

att gat aaa gca gcc gct gat gag gca gag ata gct att gca cag caa     451
Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln
            105                 110                 115

caa tct cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag     499
Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Ala Cys Gln
        120                 125                 130

acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc     547
Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg
    135                 140                 145

tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa     595
Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu
150                 155                 160                 165

ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag cgg ttt atg     643
Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met
                170                 175                 180

aat ggg ttt gtt tat tgg cat ccg aca act ggt gcg cat gct gtt aat     691
Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn
            185                 190                 195

aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg     739
Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp
        200                 205                 210

atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg     787
Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro
    215                 220                 225
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att gat ggt gag ttg agt ggg tgg gtg caa act ttc caa ggt ggg cga     835
Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg
230                 235                 240                 245

gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat     883
Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn
                250                 255                 260

ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac     931
Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp
            265                 270                 275

ctt ggt ttt ccc att gcg gat gag gct gtg aca gct gac ggt gtg ggt     979
Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly
        280                 285                 290

aga ttt tct gtt ttc cag aac gga gtt gtc tac tgg cat ccg caa cac     1027
Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His
    295                 300                 305

gga gct cac cct ata tta ggg aat ata tac agt atc tgg aga gaa gaa     1075
Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu
310                 315                 320                 325

gga gct gag agt ggg gaa ttc ggt tac cct atc ggc gat cca gaa aag     1123
Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys
                330                 335                 340

tat aca gaa aac atg gct aat cag gta ttc gaa aaa ggc gaa ctt gca     1171
Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala
            345                 350                 355

gct aac cta tac ccc aat cct ctt gag gct ttt att gag ttt tta ccc     1219
Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro
        360                 365                 370

ttt gct aat ctt gag gaa gca ata gag tat ttt gag aac gga ttg tca     1267
Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser
    375                 380                 385

aat tct cgt gta gag gcg aat tca ctt aac gcc aag aaa gat tcg att     1315
Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile
390                 395                 400                 405

caa tgt caa tcg caa tcc gct aac att cat gtg aga acg aag agt gac     1363
Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp
                410                 415                 420

gga gtc ggg att agg gtt cca aag att ggg ttt aag gct agg atg gat     1411
Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp
            425                 430                 435

tgc gac ctt cct gga act gtc tca gat gta gtg ggg tat gga tgg att     1459
Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile
        440                 445                 450
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tac tac gac tat tgg gga cga tgg gct caa gca gca tat gca caa caa 1507
Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln
455 460 465

ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt 1555
Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly
470 475 480 485

tgc agc ggg gag aag aat aca tta ttt tgg ggt act tca tat ttt cag 1603
Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln
490 495 500

gtg act tat gaa ggt cag ccg tat ttc ggt cag tca gca act aat tac 1651
Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr
505 510 515

gct tat ctt ccg tgt acg ata gac cgt agt taacataagg aatggaatag 1701
Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
520 525

gag 1704

<210> 52
<211> 527
<212> PRT
<213> Corynebacterium glutamicum

<400> 52
Met Lys Leu Phe Ser Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu
1 5 10 15

Val Ala Gly Gly Ile Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val
20 25 30

Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu
35 40 45

Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln
50 55 60

Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly
65 70 75 80

Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val
85 90 95

Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile
100 105 110

Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala
115 120 125

Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly
130 135 140

Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met

145 150 155 160

Leu Phe Pro Ser Glu Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr
165 170 175

Arg Gln Arg Phe Met Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly
180 185 190

Ala His Ala Val Asn Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly
195 200 205

Trp Glu Ser Gly Trp Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val
210 215 220

Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr
225 230 235 240

Phe Gln Gly Gly Arg Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln
245 250 255

Val Ala Ser Ile Asn Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly
260 265 270

Gly Pro Asp Ser Asp Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr
275 280 285

Ala Asp Gly Val Gly Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr
290 295 300

Trp His Pro Gln His Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser
305 310 315 320

Ile Trp Arg Glu Glu Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile
325 330 335

Gly Asp Pro Glu Lys Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu
340 345 350

Lys Gly Glu Leu Ala Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe
355 360 365

Ile Glu Phe Leu Pro Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe
370 375 380

Glu Asn Gly Leu Ser Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala
385 390 395 400

Lys Lys Asp Ser Ile Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val
405 410 415

Arg Thr Lys Ser Asp Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe
420 425 430

Lys Ala Arg Met Asp Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val
435 440 445

Gly Tyr Gly Trp Ile Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala

450 455 460

Ala Tyr Ala Gln Gln Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr
465 470 475 480

Asn Leu Glu Ala Gly Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly
485 490 495

Thr Ser Tyr Phe Gln Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln
500 505 510

Ser Ala Thr Asn Tyr Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
515 520 525

<210> 53
<211> 456
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(433)
<223> RXN02949

<400> 53
actctcgaag gttgaacaca gggctgcgat tgtgctggat caaatgtctg cacgaaaaat 60

tgttatcgcc cctggatgag tagtgattta gaggagtgct gtg agc gac gag cag 115
Val Ser Asp Glu Gln
1 5

aat tct ggc gta ggc gga acg tct cgc cca acg ggt aaa cgc cag ctg 163
Asn Ser Gly Val Gly Gly Thr Ser Arg Pro Thr Gly Lys Arg Gln Leu
10 15 20

tcg ggt gct tcc act acc tct acc tct tct tat gag gct aag cag gta 211
Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr Glu Ala Lys Gln Val
25 30 35

tct aca cag aag aag tca tcc ggt tcg gat tct aag cct ggc ggc ggt 259
Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser Lys Pro Gly Gly Gly
40 45 50

gtt att tct ttt ctg cct gag gtt gtg gga gaa gtc cgt aag gtt att 307
Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu Val Arg Lys Val Ile
55 60 65

tgg cct act gcg cgc cag atg gtc acg tac acc ctt gtc gtt ttg gga 355
Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr Leu Val Val Leu Gly
70 75 80 85

ttc ttg att gtt ttg acc gct ttg gtg tct ggt gtg gat ttc cta gct 403
Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly Val Asp Phe Leu Ala
90 95 100

ggt ctt gga gtt gag aag att ctg act ccg taggtaggat gtgtaacatc 453

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Gly Leu Gly Val Glu Lys Ile Leu Thr Pro
            105                 110

ttt                                                                     456


<210> 54
<211> 111
<212> PRT
<213> Corynebacterium glutamicum

<400> 54
Val Ser Asp Glu Gln Asn Ser Gly Val Gly Gly Thr Ser Arg Pro Thr
  1               5                  10                  15

Gly Lys Arg Gln Leu Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr
            20                  25                  30

Glu Ala Lys Gln Val Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser
        35                  40                  45

Lys Pro Gly Gly Gly Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu
    50                  55                  60

Val Arg Lys Val Ile Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr
 65                  70                  75                  80

Leu Val Val Leu Gly Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly
                 85                  90                  95

Val Asp Phe Leu Ala Gly Leu Gly Val Glu Lys Ile Leu Thr Pro
            100                 105                 110


<210> 55
<211> 1941
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1918)
<223> RXN02462

<400> 55
tccatcctca tcgacgaagc ccgcacccca ctgattatct ccgggaccag tagacggcac 60

atcgcagttc tacaacgtct tcgcacagat cgtcccacgc atg acc aag gac gtt   115
                                            Met Thr Lys Asp Val
                                              1               5

cac tac gaa gtc gac gaa cgt aaa aag acc gtc ggt gtg aaa gaa gaa   163
His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu
                 10                  15                  20

ggc gtc gaa tac gtc gaa gac caa ctc ggc atc gac aac ctc tac gca   211
Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala
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```
        25                  30                  35

cct gag cac tca cag ctg gtc agc tac ctg aac aac gcc atc aag gca     259
Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala
        40                  45                  50

cag gaa ctg ttc acc cgc gac aag gac tac atc gtc cgc aac ggc gaa     307
Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu
    55                  60                  65

gtt atg atc gtc gac ggc ttc acc ggc cgt gtc ctt gcc ggc cgc cga     355
Val Met Ile Val Asp Gly Phe Thr Gly Arg Val Leu Ala Gly Arg Arg
70                  75                  80                  85

tac aac gaa ggc atg cac cag gcg atc gaa gcc aaa gag cgc gta gag     403
Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala Lys Glu Arg Val Glu
                90                  95                  100

atc aaa aac gag aac cag acc ctg gcg acc gtt acc ctc cag aac tac     451
Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val Thr Leu Gln Asn Tyr
            105                 110                 115

ttc cgc ctc tac acc aaa ctc gcc ggc atg acc ggt acc gca gag acc     499
Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr
        120                 125                 130

gaa gca gca gag ctc aac cag atc tac aag ctc gac gtc atc gcg atc     547
Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu Asp Val Ile Ala Ile
    135                 140                 145

cca acc aac cga cca aac cag cgc gaa gac ttg acc gac ttg gtg tac     595
Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu Thr Asp Leu Val Tyr
150                 155                 160                 165

aaa acc caa gag gct aag ttc gca gca gtc gtc gac gac atc gca gaa     643
Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val Asp Asp Ile Ala Glu
                170                 175                 180

cgc acc gaa aag ggc caa cca gtc ctc gtc ggt acc gtc tcc gtc gag     691
Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly Thr Val Ser Val Glu
            185                 190                 195

cgc tcc gaa tac ctc tcc cag ctg ttg acc aaa cga ggc atc aag cac     739
Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys Arg Gly Ile Lys His
        200                 205                 210

aac gtc ctc aat gcg aag cac cac gag cag gaa gca cag atc gtt gct     787
Asn Val Leu Asn Ala Lys His His Glu Gln Glu Ala Gln Ile Val Ala
    215                 220                 225

cag gca ggt ctt cca ggc gcc gtc acc gtt gcc acc aac atg gcg ggc     835
Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala Thr Asn Met Ala Gly
230                 235                 240                 245

cgt gga acc gac atc gtg ctc ggc gga aac cca gaa atc ctc ctc gac     883
Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro Glu Ile Leu Leu Asp
                250                 255                 260
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atc aaa ctc cgc gaa cgt gga ctt gat cct ttc gaa gac gaa gaa agc      931
Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe Glu Asp Glu Glu Ser
            265                 270                 275

tac cag gaa gcc tgg gac gct gaa ctt cca gca atg aag cag cga tgc      979
Tyr Gln Glu Ala Trp Asp Ala Glu Leu Pro Ala Met Lys Gln Arg Cys
        280                 285                 290

gaa gaa cgt ggc gac aaa gtc cgc gaa gcc gga gga ctc tac gtc ctt     1027
Glu Glu Arg Gly Asp Lys Val Arg Glu Ala Gly Gly Leu Tyr Val Leu
    295                 300                 305

ggc acc gaa cgc cac gaa tcc cga cgc atc gac aac cag ctg cgc ggt     1075
Gly Thr Glu Arg His Glu Ser Arg Arg Ile Asp Asn Gln Leu Arg Gly
310                 315                 320                 325

cgt tct gca cgt cag ggc gac cca gga tcc acc cgc ttc tat ctc tct     1123
Arg Ser Ala Arg Gln Gly Asp Pro Gly Ser Thr Arg Phe Tyr Leu Ser
                330                 335                 340

atg cgc gac gac ctg atg gtt cgc ttc gtc ggc cca acc atg gaa aac     1171
Met Arg Asp Asp Leu Met Val Arg Phe Val Gly Pro Thr Met Glu Asn
            345                 350                 355

atg atg aac agg ctc aac gtc cca gac gat gtg ccc atc gaa tcc aaa     1219
Met Met Asn Arg Leu Asn Val Pro Asp Asp Val Pro Ile Glu Ser Lys
        360                 365                 370

acc gtc acc aac tcc atc aag ggc gcc caa gct cag gtg gag aac cag     1267
Thr Val Thr Asn Ser Ile Lys Gly Ala Gln Ala Gln Val Glu Asn Gln
    375                 380                 385

aac ttc gaa atg cgt aag aac gtt ctg aag tac gac gaa gtc atg aac     1315
Asn Phe Glu Met Arg Lys Asn Val Leu Lys Tyr Asp Glu Val Met Asn
390                 395                 400                 405

gaa cag cgc aag gtt atc tac agc gag cga cgc gaa atc ctc gaa tcc     1363
Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg Glu Ile Leu Glu Ser
                410                 415                 420

gca gac atc tcc cgc tac atc caa aac atg atc gaa gaa aca gtc agc     1411
Ala Asp Ile Ser Arg Tyr Ile Gln Asn Met Ile Glu Glu Thr Val Ser
            425                 430                 435

gca tac gtc gac ggc gcc acc gcc aac ggc tac gtc gaa gac tgg gac     1459
Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr Val Glu Asp Trp Asp
        440                 445                 450

ctc gac aaa ctc tgg aac gcc ctc gaa gcc ctc tac gac cca tcg atc     1507
Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu Tyr Asp Pro Ser Ile
    455                 460                 465

aac tgg acc gac ctc gtc gaa ggc agc gaa tac ggc aaa cca ggg gag     1555
Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr Gly Lys Pro Gly Glu
470                 475                 480                 485
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ctg tcc gcc gaa gat cta cgc acc gca ctc gtc aac gac gcc cac gcc     1603
Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val Asn Asp Ala His Ala
                490                 495                 500

gaa tac gca aaa ctc gaa gaa gcc gta tcc gca atc ggc ggc gaa gca     1651
Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala Ile Gly Gly Glu Ala
            505                 510                 515

cag atc cgc aac atc gaa cga atg gtg ctc atg cca gtc atc gac acc     1699
Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met Pro Val Ile Asp Thr
        520                 525                 530

aaa tgg cgc gaa cac ctc tac gaa atg gac tac ctg aaa gaa ggc atc     1747
Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr Leu Lys Glu Gly Ile
    535                 540                 545

ggc ctg cgc gca atg gca cag cgc gac cca ctg gtc gaa tac caa aag     1795
Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu Val Glu Tyr Gln Lys
550                 555                 560                 565

gaa ggc ggc gac atg ttc aac ggc atg aaa gac ggc atc aag gaa gaa     1843
Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp Gly Ile Lys Glu Glu
                570                 575                 580

acc gtc cgc cag ctc ttc ctc tcc gca agc agt tca tca agc aag acg     1891
Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser Ser Ser Ser Lys Thr
            585                 590                 595

cgg aag tcg ctg act aac tca gaa ccc tgaaattcag catccgccac           1938
Arg Lys Ser Leu Thr Asn Ser Glu Pro
        600                 605

atg                                                                 1941


&lt;210&gt; 56
&lt;211&gt; 606
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 56
Met Thr Lys Asp Val His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val
  1               5                  10                  15

Gly Val Lys Glu Glu Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile
             20                  25                  30

Asp Asn Leu Tyr Ala Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn
         35                  40                  45

Asn Ala Ile Lys Ala Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile
     50                  55                  60

Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val
 65                  70                  75                  80

Leu Ala Gly Arg Arg Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala
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                85                  90                  95

Lys Glu Arg Val Glu Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val
            100                 105                 110

Thr Leu Gln Asn Tyr Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr
        115                 120                 125

Gly Thr Ala Glu Thr Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu
    130                 135                 140

Asp Val Ile Ala Ile Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu
145                 150                 155                 160

Thr Asp Leu Val Tyr Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val
                165                 170                 175

Asp Asp Ile Ala Glu Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly
            180                 185                 190

Thr Val Ser Val Glu Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys
        195                 200                 205

Arg Gly Ile Lys His Asn Val Leu Asn Ala Lys His His Glu Gln Glu
    210                 215                 220

Ala Gln Ile Val Ala Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala
225                 230                 235                 240

Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro
                245                 250                 255

Glu Ile Leu Leu Asp Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe
            260                 265                 270

Glu Asp Glu Glu Ser Tyr Gln Glu Ala Trp Asp Ala Glu Leu Pro Ala
        275                 280                 285

Met Lys Gln Arg Cys Glu Glu Arg Gly Asp Lys Val Arg Glu Ala Gly
    290                 295                 300

Gly Leu Tyr Val Leu Gly Thr Glu Arg His Glu Ser Arg Arg Ile Asp
305                 310                 315                 320

Asn Gln Leu Arg Gly Arg Ser Ala Arg Gln Gly Asp Pro Gly Ser Thr
                325                 330                 335

Arg Phe Tyr Leu Ser Met Arg Asp Asp Leu Met Val Arg Phe Val Gly
            340                 345                 350

Pro Thr Met Glu Asn Met Met Asn Arg Leu Asn Val Pro Asp Asp Val
        355                 360                 365

Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly Ala Gln Ala
    370                 375                 380

Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val Leu Lys Tyr
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385 390 395 400

Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg
405 410 415

Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln Asn Met Ile
420 425 430

Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr
435 440 445

Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu
450 455 460

Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr
465 470 475 480

Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val
485 490 495

Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala
500 505 510

Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met
515 520 525

Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr
530 535 540

Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu
545 550 555 560

Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp
565 570 575

Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser
580 585 590

Ser Ser Ser Lys Thr Arg Lys Ser Leu Thr Asn Ser Glu Pro
595 600 605

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Val Leu Ile Val Val

1 5

ggt gtt tat gcg ttg gtg ctg ttg aca ggc gat cgt tct gcc aca cca 163
Gly Val Tyr Ala Leu Val Leu Leu Thr Gly Asp Arg Ser Ala Thr Pro
10 15 20

aaa ttg ggt att gat ctg caa ggc gga acc cga gtg acc ctc gtg ccg 211
Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr Arg Val Thr Leu Val Pro
25 30 35

cag ggg cag gat cca act cag gac cag ctg aat cag gca cgc acc att 259
Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn Gln Ala Arg Thr Ile
40 45 50

ctg gaa aac cgt gtg aac ggc atg ggc gtt tca ggt gca agc gtg gtc 307
Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser Gly Ala Ser Val Val
55 60 65

gct gac ggt aac acg ctg gtg atc act gtt ccc ggg gaa aat acc gca 355
Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro Gly Glu Asn Thr Ala
70 75 80 85

cag gcg caa tcc cta gga cag acc tcc cag ctg ctg ttc cgt ccc gtt 403
Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu Leu Phe Arg Pro Val
90 95 100

ggt cag gca gga atg ccc gat atg acc acg ttg atg cca gag ctg gaa 451
Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu Met Pro Glu Leu Glu
105 110 115

gag atg gcc aac agg tgg gtt gaa tac ggc gtc atc acc gaa gag cag 499
Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val Ile Thr Glu Glu Gln
120 125 130

gca aat gcc tcc ttg gag gaa atg aac acc gct gtt gca tcg acc act 547
Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala Val Ala Ser Thr Thr
135 140 145

gcg gtg gaa ggc gaa gaa gca act gag cca gaa ccc gtc acc gtg tcg 595
Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu Pro Val Thr Val Ser
150 155 160 165

gcg acc cct atg gat gag cca gcc aac tcc att gag gca aca cag cga 643
Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile Glu Ala Thr Gln Arg
170 175 180

cgc cag gaa atc acg gac atg ctg cgc acc gac cgc cag tcc acc gat 691
Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp Arg Gln Ser Thr Asp
185 190 195

ccc act gtc cag atc gct gca agt tct ttg atg cag tgc acc act gat 739
Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met Gln Cys Thr Thr Asp
200 205 210

gag atg gat cct ttg gcc ggc acc gat gat cca cgc ctg cca ttg gtg 787
Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro Arg Leu Pro Leu Val
215 220 225

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gca tgt gat cca gct gta ggt ggc gtg tat gta ctt gat cct gca cct    835
Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val Leu Asp Pro Ala Pro
230                 235                 240                 245

ttg ctc aac ggc gaa acc gat gag gaa aat ggt gcg cgc cta acc ggt    883
Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly Ala Arg Leu Thr Gly
                250                 255                 260

aat gag atc gat acc aac cgt ccc atc acc ggt gga ttc aac gcc cag    931
Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly Gly Phe Asn Ala Gln
            265                 270                 275

tcc ggc cag atg gaa atc agc ttt gcc ttc aaa tcc ggc gat ggg gaa    979
Ser Gly Gln Met Glu Ile Ser Phe Ala Phe Lys Ser Gly Asp Gly Glu
        280                 285                 290

gaa ggc tct gca act tgg tcc tct ctg acc agc cag tac ctg cag cag    1027
Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser Gln Tyr Leu Gln Gln
    295                 300                 305

cag atc gcc atc acc ctg gac tct cag gtg att tct gca ccc gtg att    1075
Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile Ser Ala Pro Val Ile
310                 315                 320                 325

cag tca gca acc cct gtg ggt tct gca aca tcc atc acc ggt gac ttc    1123
Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser Ile Thr Gly Asp Phe
                330                 335                 340

act caa act gaa gcc caa gat ctg gcg aac aac ctg cgc tac ggt gca    1171
Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn Leu Arg Tyr Gly Ala
            345                 350                 355

ttg ccc ctg agc ttc gca ggt gaa aac ggc gag cgc ggc gga act acc    1219
Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu Arg Gly Gly Thr Thr
        360                 365                 370

acc acc gtt ccg cca tca cta ggc gca gca tcc ttg aag gcc gga ctg    1267
Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser Leu Lys Ala Gly Leu
    375                 380                 385

atc gca ggc atc gtc ggc atc gcg ctg gtc gcc atc ttc gtg ttc gcc    1315
Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala Ile Phe Val Phe Ala
390                 395                 400                 405

tac tac cgc gtc ttc gga ttc gtt tcc ctg ttc acc ctg ttt gcc gca    1363
Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe Thr Leu Phe Ala Ala
                410                 415                 420

ggc gtg ttg gtc tac ggc ctt ctg gta ctg ctg gga cgc tgg atc gga    1411
Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu Gly Arg Trp Ile Gly
            425                 430                 435

tat tcc cta gac ctt gct ggt atc gcc ggt ttg atc atc ggt atc ggt    1459
Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu Ile Ile Gly Ile Gly
        440                 445                 450
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acc acc gcc gac tcc ttc gtg gtg ttc tat gag cgc atc aag gat gag 1507
Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu Arg Ile Lys Asp Glu
455 460 465

atc cgt gaa gga aga tcc ttt aga tct gca gta cct cgt gca tgg gaa 1555
Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val Pro Arg Ala Trp Glu
470 475 480 485

agc gcc aag cgc acc atc gtc aca ggc aac atg gtc act ttg ctc ggc 1603
Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met Val Thr Leu Leu Gly
490 495 500

gct atc gtg att tac ttg ctc gcg gtc ggc gaa gtc aag ggc ttt gcc 1651
Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu Val Lys Gly Phe Ala
505 510 515

ttc acc ctg ggt ctg acc acc gta ttc gat ctc gtt gtc acc ttc ctg 1699
Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu Val Val Thr Phe Leu
520 525 530

atc acg gca cca ctg gtt atc ctg gca tca cgc aac cca ttc ttt gcc 1747
Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg Asn Pro Phe Phe Ala
535 540 545

aag tca tcg gtc aac ggc atg gga cga gtg atg aag ctc gtt gaa gaa 1795
Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu
550 555 560 565

cgc cgc gcc aac ggt gaa ttg gat gag cct gag tac ctg aaa aag atc 1843
Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile
570 575 580

cat gcc aag aat gcg gca gct gat aag gct tcc act gac aat tct tcc 1891
His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser
585 590 595

act gac aat tct gaa gca cct ggc acc gat acg aac caa gag gag gag 1939
Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr Asn Gln Glu Glu Glu
600 605 610

aag tagccatgac tgattcccag act 1965
Lys

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Arg Ser Ala Thr Pro Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr Arg
20 25 30

Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn
35 40 45

Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser
50 55 60

Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro
65 70 75 80

Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu
85 90 95

Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu
100 105 110

Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val
115 120 125

Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala
130 135 140

Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu
145 150 155 160

Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile
165 170 175

Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp
180 185 190

Arg Gln Ser Thr Asp Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met
195 200 205

Gln Cys Thr Thr Asp Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro
210 215 220

Arg Leu Pro Leu Val Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val
225 230 235 240

Leu Asp Pro Ala Pro Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly
245 250 255

Ala Arg Leu Thr Gly Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly
260 265 270

Gly Phe Asn Ala Gln Ser Gly Gln Met Glu Ile Ser Phe Ala Phe Lys
275 280 285

Ser Gly Asp Gly Glu Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser
290 295 300

Gln Tyr Leu Gln Gln Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile
305 310 315 320

Ser Ala Pro Val Ile Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser
325 330 335

Ile Thr Gly Asp Phe Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn
340 345 350

Leu Arg Tyr Gly Ala Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu
355 360 365

Arg Gly Gly Thr Thr Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser
370 375 380

Leu Lys Ala Gly Leu Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala
385 390 395 400

Ile Phe Val Phe Ala Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe
405 410 415

Thr Leu Phe Ala Ala Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu
420 425 430

Gly Arg Trp Ile Gly Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu
435 440 445

Ile Ile Gly Ile Gly Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu
450 455 460

Arg Ile Lys Asp Glu Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val
465 470 475 480

Pro Arg Ala Trp Glu Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met
485 490 495

Val Thr Leu Leu Gly Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu
500 505 510

Val Lys Gly Phe Ala Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu
515 520 525

Val Val Thr Phe Leu Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg
530 535 540

Asn Pro Phe Phe Ala Lys Ser Ser Val Asn Gly Met Gly Arg Val Met
545 550 555 560

Lys Leu Val Glu Glu Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu
565 570 575

Tyr Leu Lys Lys Ile His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser
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Thr Asp Asn Ser Ser Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr
595 600 605

Asn Gln Glu Glu Glu Lys
610

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<223> RXN00046

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acctaaaacg ctgttctcaa cacaggagtt tccttaaata atg gac tta aat act   115
                                           Met Asp Leu Asn Thr
                                           1               5

caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc   163
Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser
                10                  15                  20

gtg caa gct ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc   211
Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr
            25                  30                  35

cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt   259
His Val Ala Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys
        40                  45                  50

ggc ggt tac ggc ggt ttg gaa gat atc cgt tca atc tcc aac cgt gtc   307
Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser Ile Ser Asn Arg Val
    55                  60                  65

gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac   355
Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr
70                  75                  80                  85

atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc   403
Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala
                90                  95                  100

act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc   451
Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser
            105                 110                 115

acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc   499
Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile
        120                 125                 130

atg gcg gac tgc gca act ccc gaa gaa gtt ctc agt gcg cat aag gct   547
Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu Ser Ala His Lys Ala
    135                 140                 145

ggc gcg gat ttt gtg tcc acc acg ctt gct gga tac acc gaa cac cgc   595
Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly Tyr Thr Glu His Arg
150                 155                 160                 165

gag aaa aca gtc ggt cca gat ttc gat tgc ctc cgc gaa gca cgt gag   643
Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu Arg Glu Ala Arg Glu
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170 175 180

tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct 691
Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly Arg Phe Ser Asn Pro
185 190 195

gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg 739
Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val
200 205 210

ggc acc gca atc act gac cct ggt ttc atc act gga cag ttc gcg tca 787
Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr Gly Gln Phe Ala Ser
215 220 225

ctg ttg cac tagcacttag tccagcgctg cac 819
Leu Leu His
230

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Gln Leu Ile Val Ser Val Gln Ala Pro Asp Gly His Ala Met Arg Asp
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Thr His Thr Leu Thr His Val Ala Ala Ala Cys Val Asp Gly Gly Ala
35 40 45

Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser
50 55 60

Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly
65 70 75 80

Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val
85 90 95

Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro
100 105 110

Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp
115 120 125

Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu
130 135 140

Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly
145 150 155 160

Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu
165 170 175

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Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly
            180                 185                 190

Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala
        195                 200                 205

Asn Ala Ile Ile Val Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr
    210                 215                 220

Gly Gln Phe Ala Ser Leu Leu His
225                 230


<210> 61
<211> 1219
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (48)..(1196)
<223> RXN01863

<400> 61
ggtatcatac cgatatgaac caaatagaaa gaaggaagtt taagacgatg aat agc      56
                                                       Met Asn Ser
                                                       1

gtc aaa ttg aag caa cct gtt agc att tac aat gat cca tgg gaa tca    104
Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro Trp Glu Ser
    5                   10                  15

tat aac gat gtt aaa gaa cat ggc caa tta act tta agt aac atc gaa    152
Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser Asn Ile Glu
 20                 25                  30                  35

ttt aca act aca aat ctt tgt aat atg cgt tgt agc cac tgt gca gtt    200
Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His Cys Ala Val
                40                  45                  50

ggt tat act tta caa act gtc gac ccc gag cct tta gat atg gac tta    248
Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp Met Asp Leu
            55                  60                  65

att tat cgt aga ctt gat gaa att cca aat ctg cga acg atg tca att    296
Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr Met Ser Ile
        70                  75                  80

aca ggt ggc gaa cca atg ttt tct aaa aag tct att aga aat gtt gtt    344
Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg Asn Val Val
    85                  90                  95

aaa cct cta tta aag tat gca cat cat cga ggt ata tat aca caa atg    392
Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr Thr Gln Met
100                 105                 110                 115
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aat tca aac cta aca ttg cct caa gat cgt tat tta gat att gct gaa    440
Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp Ile Ala Glu
                120                 125                 130

tat atc gat gtt atg cat atc tca cat aac tgg gga aca act gat gaa    488
Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr Thr Asp Glu
            135                 140                 145

ttc gca aat gtt ggc ttt ggc gca atg aag aag caa cca ccg tta aaa    536
Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu Lys
        150                 155                 160

gct aag tta aaa tta tat gaa caa atg att tcg aat gca cgt aca tta    584
Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr Leu
    165                 170                 175

tca gaa caa gga atg ttt gta tct gcg gaa aca atg ctc aat caa agt    632
Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln Ser
180                 185                 190                 195

acg cta cca cat tta cga aaa ata cat caa gaa gtc gtt cat gat atg    680
Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp Met
                200                 205                 210

aaa tgt agc aga cac gag att cac cct atg tat cca gct gac ttt gca    728
Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe Ala
            215                 220                 225

agt caa tta aat gtg tta act cta gcg gaa atg aaa aag aca att cat    776
Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile His
        230                 235                 240

gat ata ttg gat ttc aga gat gaa gat att tgg atg tta ttt ggt act    824
Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly Thr
    245                 250                 255

ttg cct gtg ttt cca tgc tta aag gat gat gaa gat caa aag tta cta    872
Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu Leu
260                 265                 270                 275

tca cgt tta aga aat gct aac aat gta acg act aga aat gac ccg gat    920
Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro Asp
                280                 285                 290

ggc cgt agt cgt tta aat gtc aat gta ttt aca ggt aat gta atc gta    968
Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile Val
            295                 300                 305

act gat ttc gga gat gaa aca ggt aca att tcg aat ata caa aaa gat    1016
Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys Asp
        310                 315                 320

aaa tta aca gat gta ttt gat aaa tgg tta tcc tct gat ctt gct aaa    1064
Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala Lys
    325                 330                 335

tca tta aat tgt cat tgt tcc gag ttt agt tgt tta gga cca aat gtt    1112
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Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn Val
340 345 350 355

ctt gtt aaa aat atg tac tat ccg aat atg gat ttt aaa gat aat gag 1160
Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn Glu
360 365 370

cgt cat atg cac aaa caa cca caa att ata caa ttt taaaactct 1206
Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
375 380

taattatgcg gag 1219

<210> 62
<211> 383
<212> PRT
<213> Corynebacterium glutamicum

<400> 62
Met Asn Ser Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro
1 5 10 15

Trp Glu Ser Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser
20 25 30

Asn Ile Glu Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His
35 40 45

Cys Ala Val Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp
50 55 60

Met Asp Leu Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr
65 70 75 80

Met Ser Ile Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg
85 90 95

Asn Val Val Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr
100 105 110

Thr Gln Met Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp
115 120 125

Ile Ala Glu Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr
130 135 140

Thr Asp Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro
145 150 155 160

Pro Leu Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala
165 170 175

Arg Thr Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu
180 185 190

Asn Gln Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val

```
        195                 200                 205

His Asp Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala
    210                 215                 220

Asp Phe Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys
225                 230                 235                 240

Thr Ile His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu
                245                 250                 255

Phe Gly Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln
            260                 265                 270

Lys Leu Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn
        275                 280                 285

Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn
    290                 295                 300

Val Ile Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile
305                 310                 315                 320

Gln Lys Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp
                325                 330                 335

Leu Ala Lys Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly
            340                 345                 350

Pro Asn Val Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys
        355                 360                 365

Asp Asn Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
    370                 375                 380


<210> 63
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(595)
<223> RXN00833

<400> 63
agctttttgc atgtgtcata tcgtaccgtt tgcataggcc tgttcgcgct tggtgaacct  60

tttctagcac caaaacaaaa ctctccctag tatggggtcc atg gct aaa aca cat   115
                                            Met Ala Lys Thr His
                                            1               5

ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc   163
Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly
                10                  15                  20
```

gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211
Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val
25 30 35

tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259
Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro
40 45 50

tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307
Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu
55 60 65

gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355
Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp
70 75 80 85

ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403
Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn
90 95 100

gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451
Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly
105 110 115

atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc gtc 499
Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser Val
120 125 130

atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat 547
Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr Thr Gln Leu Val Asp
135 140 145

gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac 595
Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala Leu Ala Gly Leu Asn
150 155 160 165

taatttactt cgctcagggg aat 618

<210> 64
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 64
Met Ala Lys Thr His Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu
1 5 10 15

Leu Pro Gln Val Gly Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr
20 25 30

Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
35 40 45

Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
50 55 60

```
Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
65                  70                  75                  80

Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
                85                  90                  95

Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
            100                 105                 110

Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu
        115                 120                 125

Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr
    130                 135                 140

Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala
145                 150                 155                 160

Leu Ala Gly Leu Asn
                165


<210> 65
<211> 879
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(856)
<223> RXN01676

<400> 65
agttacagct tttctcggtg gcacactcgc gctacttagc ccttgtgccg cactcctttt 60

accagcattt tttgcatcct cagtgggtgc tggcccgcgc atg atc ctt cac ggt   115
                                            Met Ile Leu His Gly
                                            1               5

gtt gtg ttc tac gca gga ctt cta gta ctt ctc gtg cca ctt ggc ctt   163
Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu
                10                  15                  20

ggt gcg gga atc ctc ggc gag ctg ttt atc acc caa cgc cag acc atc   211
Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile
            25                  30                  35

atc gtg gtt tca tcg atc gtg ctg att atc cta ggt ttt gtc cag atc   259
Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu Gly Phe Val Gln Ile
        40                  45                  50

ttc ggc ggc gga ttc gac ttc gga aaa gca ctc cca gga tta gat cgt   307
Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu Pro Gly Leu Asp Arg
    55                  60                  65

ctg caa tct aag gcc act gtg acc tca ggt cta gga aag agc ttt tta   355
Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu Gly Lys Ser Phe Leu
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 70                75                80                85

cta gga atg acc agt agt att gcc ggt ttt tgt tcc gga cca atc ctc    403
Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys Ser Gly Pro Ile Leu
                 90                  95                 100

ggc gcc gtt ctt act ttg gct gcc acc agt gga aac tcc atc acc tca    451
Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly Asn Ser Ile Thr Ser
            105                 110                 115

gca ctc att ttg agt gct tat ggt gcg gga atg gtg ctg ccc ctg atg    499
Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met Val Leu Pro Leu Met
        120                 125                 130

gct att gca gcg ctc tgg gcc aaa ctc gga cag cgt gga cag cag atg    547
Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln Arg Gly Gln Gln Met
    135                 140                 145

ctc cgc ggc cgg gaa ttc acc ttc ttg ggc agg cag tgg cac att gtt    595
Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg Gln Trp His Ile Val
150                 155                 160                 165

tct gtc att agc ggt gcc ctg atc atc gct gtc gga atc ctc ttt tgg    643
Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val Gly Ile Leu Phe Trp
                170                 175                 180

tcc acg aac ggc ctt gtc agc atg ccg gag ctc gtt cca atg gac acc    691
Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu Val Pro Met Asp Thr
            185                 190                 195

cag atc tgg cta cag gaa gcc aca ttc tca ctc ggg tca cca ctc ttt    739
Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu Gly Ser Pro Leu Phe
        200                 205                 210

gac atc gca ttg atc att gtc gcc gct ggc ttg ttc ttg tac ttc tgg    787
Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu Phe Leu Tyr Phe Trp
    215                 220                 225

aac aaa cga caa aag cga aaa gaa gaa gct cag cga ccc aaa gaa agt    835
Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser
230                 235                 240                 245

gga tgg gtt att aac cct cgc taattattag ttttggagcg agg              879
Gly Trp Val Ile Asn Pro Arg
                250
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<210> 66
<211> 252
<212> PRT
<213> Corynebacterium glutamicum

<400> 66

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Met Ile Leu His Gly Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu
  1               5                  10                  15

Val Pro Leu Gly Leu Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr
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```
                20                  25                  30

Gln Arg Gln Thr Ile Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu
        35                  40                  45

Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu
    50                  55                  60

Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu
65                  70                  75                  80

Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys
                85                  90                  95

Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly
            100                 105                 110

Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met
        115                 120                 125

Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln
    130                 135                 140

Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg
145                 150                 155                 160

Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val
                165                 170                 175

Gly Ile Leu Phe Trp Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu
            180                 185                 190

Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu
        195                 200                 205

Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu
    210                 215                 220

Phe Leu Tyr Phe Trp Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln
225                 230                 235                 240

Arg Pro Lys Glu Ser Gly Trp Val Ile Asn Pro Arg
                245                 250


<210> 67
<211> 744
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(721)
<223> RXN00380

<400> 67
caggcaatgc gacctcgcct cagtgacatc cttggtgttc caagacgatc aaattgtcgg 60
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cgtgcattac aacgaaccag ctcaggagat ttgatcactc gtg cgt ttg acc aaa     115
                                            Val Arg Leu Thr Lys
                                             1               5

cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta     163
Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val
                 10                  15                  20

gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc     211
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly
             25                  30                  35

gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac     259
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr
         40                  45                  50

gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc     307
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu
     55                  60                  65

atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt     355
Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val
 70                  75                  80                  85

gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa     403
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu
                 90                  95                 100

tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac     451
Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn
            105                 110                 115

ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac     499
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr
        120                 125                 130

tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac     547
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr
    135                 140                 145

cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt     595
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly
150                 155                 160                 165

gtt ccc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac     643
Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His
                170                 175                 180

cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg     691
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu
            185                 190                 195

gat gtt gcg ttg cca ttg gta gat gag gcc taaatgtctg agattgtggt       741
Asp Val Ala Leu Pro Leu Val Asp Glu Ala
        200                 205
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agc 744

<210> 68
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 68
Val Arg Leu Thr Lys Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser
1 5 10 15

Gly Leu Ala Leu Val Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp
20 25 30

Ala Val Ala Val Gly Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys
35 40 45

Met Glu Ile Phe Tyr Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile
50 55 60

Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp
65 70 75 80

Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
85 90 95

Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
100 105 110

Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile
115 120 125

Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp
130 135 140

Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
145 150 155 160

Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
165 170 175

Leu Asp Lys Gln His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr
180 185 190

Ser Lys Asp Val Leu Asp Val Ala Leu Pro Leu Val Asp Glu Ala
195 200 205

<210> 69
<211> 495
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(472)

<223> RXN00937

<400> 69
agctgccggt caatgaagaa aatccttggc cgggaataac tacagtccgc tgaaagttgg 60

tctatatata gaccttacaa atcttgaacg gagattctta atg gca acc atc gat 115
Met Ala Thr Ile Asp
1 5

gta acc gaa gaa aca ttt gag agc aca gtt acc ggc gac gga att gtc 163
Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr Gly Asp Gly Ile Val
10 15 20

ctc gta gac gca tgg gca tcc tgg tgc gga cct tgc cgc cag ttc gcc 211
Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro Cys Arg Gln Phe Ala
25 30 35

cca acc tac gag aag gtt tcc gaa acc cac acc gac gca acc ttc gcc 259
Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr Asp Ala Thr Phe Ala
40 45 50

aag ctt gat acc gaa gca aac cag ggc ctg gct gca gca ctg cag atc 307
Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala Ala Ala Leu Gln Ile
55 60 65

cag tcc atc cca act ctg atg gtt ttc cgc gac ggc atc atg gtc tac 355
Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp Gly Ile Met Val Tyr
70 75 80 85

cgc gaa gcc ggc acc atg cca gct cct gca ctg gat gat ctg gtc aac 403
Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu Val Asn
90 95 100

cag gtt aag gca ctc gac atg gat gac gtt cgt cgc cag gtc gca gag 451
Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val Ala Glu
105 110 115

cag cag ggt tct gca gag gca taagcttcca attgtgtttt ggt 495
Gln Gln Gly Ser Ala Glu Ala
120

<210> 70
<211> 124
<212> PRT
<213> Corynebacterium glutamicum

<400> 70
Met Ala Thr Ile Asp Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr
1 5 10 15

Gly Asp Gly Ile Val Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro
20 25 30

Cys Arg Gln Phe Ala Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr
35 40 45

Asp Ala Thr Phe Ala Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala
50 55 60

Ala Ala Leu Gln Ile Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp
65 70 75 80

Gly Ile Met Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu
85 90 95

Asp Asp Leu Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg
100 105 110

Arg Gln Val Ala Glu Gln Gln Gly Ser Ala Glu Ala
115 120

<210> 71
<211> 990
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(967)
<223> RXN02325

<400> 71
cagagatttg aagatggaga ccaaggctca aagggaatcc atgccgtctt ggtttaatac 60

tgcacccgtc taatgaaaat cattactatt aggtgtcatg atg gac cat gca cac 115
Met Asp His Ala His
1 5

gat tcc tgc tca cca act ctg cgc cgt gat ttg gag gtc act ggc cag 163
Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu Glu Val Thr Gly Gln
10 15 20

ctc caa cct gag aaa gct gtc gat tta gca gcg ccg cac gaa ggg aag 211
Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala Pro His Glu Gly Lys
25 30 35

gtt gcc aat ata acg aag gtg acc tcc tca aat atg gag cac acc atc 259
Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn Met Glu His Thr Ile
40 45 50

acg cag gcc tca aaa gct aag gag gtg gtg gtg ctc att ggt cac tcc 307
Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val Leu Ile Gly His Ser
55 60 65

ctg ctg ccc aca ttt cag gat ttg gaa aaa gac att ctg cac ttt cag 355
Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp Ile Leu His Phe Gln
70 75 80 85

gca ggt aat aaa ggg cga ttt tct gta gcg att gtt gat cct gat cgc 403
Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile Val Asp Pro Asp Arg
90 95 100

agt gca gat gtg gtt gcc aga ttt agg cca aaa cag att ccg gtg gca 451
Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys Gln Ile Pro Val Ala
105 110 115

tac gtg gtg aaa gat ggc gcc agc att gcg gag ttc aac tcg ctc aac 499
Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu Phe Asn Ser Leu Asn
120 125 130

aag gag ccg gtt gca caa tgg ctt gat cat ttt gtg tcg cgg gaa acg 547
Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe Val Ser Arg Glu Thr
135 140 145

atc ccc aat gaa aaa gag ggg gac gtc gat aag caa ata gac ccg cgc 595
Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys Gln Ile Asp Pro Arg
150 155 160 165

ctg tgg cgg gca gcg gaa ttg gtg aac gcc ggt gat ttt cgc gcg gcg 643
Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly Asp Phe Arg Ala Ala
170 175 180

ttg gcg ttg tat gag cag ttg ccg cag gat gcg acg gtg aag cgg gcg 691
Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala Thr Val Lys Arg Ala
185 190 195

cac gcg gcg gtg tcg gta ttg gcg cgg atg tct gtg gcg gat cgg gga 739
His Ala Ala Val Ser Val Leu Ala Arg Met Ser Val Ala Asp Arg Gly
200 205 210

gag gat ccg atc gag aag tcg cgc cgg gat cca gac gat gtg aac aag 787
Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn Lys
215 220 225

gcg ctg gcg gcg gcg gat atg tat gtg ttg atg aat cag ccg gac aca 835
Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp Thr
230 235 240 245

gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc cgg 883
Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala Arg
250 255 260

cgg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc gca 931
Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val Ala
265 270 275

ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaca 977
Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met Ser
280 285

ctttaaatat tct 990

<210> 72
<211> 289
<212> PRT
<213> Corynebacterium glutamicum

<400> 72

Met Asp His Ala His Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu
1 5 10 15

Glu Val Thr Gly Gln Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala
20 25 30

Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn
35 40 45

Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val
50 55 60

Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp
65 70 75 80

Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile
85 90 95

Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys
100 105 110

Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu
115 120 125

Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe
130 135 140

Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys
145 150 155 160

Gln Ile Asp Pro Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly
165 170 175

Asp Phe Arg Ala Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala
180 185 190

Thr Val Lys Arg Ala His Ala Ala Val Ser Val Leu Ala Arg Met Ser
195 200 205

Val Ala Asp Arg Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro
210 215 220

Asp Asp Val Asn Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met
225 230 235 240

Asn Gln Pro Asp Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys
245 250 255

Pro Glu Ala Ala Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro
260 265 270

Leu Asp Leu Val Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met
275 280 285

Ser

<210> 73
<211> 900
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(877)
<223> RXN01837

<400> 73
cccccatcat tccctcaagg tgtgaagata cggttaggat agaaaagaat tttttgacg 60

ttggacattc tcaaaatcaa gtagcaaggg atcaaactct gtg agt act aat aag 115
Val Ser Thr Asn Lys
1 5

gaa cga cgc caa cag gcg ctt tcc cag ctg gag aaa gaa atc aaa agc 163
Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu Lys Glu Ile Lys Ser
10 15 20

cgg gac cgc aaa gaa aag acc aag cca cta acc gtg gtc ttt gct tcc 211
Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr Val Val Phe Ala Ser
25 30 35

ctg gct gtc atc ctg gtt gtc gtt ggc ggt atc tgg tac gca gct acc 259
Leu Ala Val Ile Leu Val Val Val Gly Gly Ile Trp Tyr Ala Ala Thr
40 45 50

cgc agc acc gaa gac gaa gtc atc acc gct gat gaa aca tcc acc acc 307
Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp Glu Thr Ser Thr Thr
55 60 65

gca gag acc cct gac tac cag cca ctg gcg ctg acc cgc acc acc gcg 355
Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu Thr Arg Thr Thr Ala
70 75 80 85

ctc ggc gac tcc gtg acc tgt gag tac cca gat gct ggc gag gct tcc 403
Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp Ala Gly Glu Ala Ser
90 95 100

aag gat gtc tcc aag cct gct act gaa aac gtg cca gca acc ggc acc 451
Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val Pro Ala Thr Gly Thr
105 110 115

gtg acc gtc aac ctg acc acc gcc cag ggc aac atc ggc atg gaa ctt 499
Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn Ile Gly Met Glu Leu
120 125 130

gat cgc tcc gta tcc cct tgt acc gtc aac gct gtt gag cac atg gct 547
Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala Val Glu His Met Ala
135 140 145

tcc gag ggc tac tac aac gat act gtc tgc cac cgc atc acc acc tct 595
Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser
150 155 160 165

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ggc att tac gtt ctc cag tgc ggc gat cca agc agc acc ggc gca ggc    643
Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly
                170                 175                 180

ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act    691
Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr
            185                 190                 195

gac cta acc acc cca gtc atc tac gag cgc ggc acc atc gcc atg gcc    739
Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala
        200                 205                 210

aac gct ggc gct gac acc aac ggg ctc cca gtt ctt cct caa cta cga    787
Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val Leu Pro Gln Leu Arg
    215                 220                 225

gga ttc ccc act ggc acc gaa cta cac cta ctt cgg cca gat cac cga    835
Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu Arg Pro Asp His Arg
230                 235                 240                 245

aga agg cct tgc aac cct cga cgc cat cgc aga agt tgg cac            877
Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg Ser Trp His
                250                 255

tgaaggtgga accggcgacg gag                                          900


<210> 74
<211> 259
<212> PRT
<213> Corynebacterium glutamicum

<400> 74
Val Ser Thr Asn Lys Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu
  1               5                  10                  15

Lys Glu Ile Lys Ser Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr
             20                  25                  30

Val Val Phe Ala Ser Leu Ala Val Ile Leu Val Val Val Gly Gly Ile
         35                  40                  45

Trp Tyr Ala Ala Thr Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp
     50                  55                  60

Glu Thr Ser Thr Thr Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu
 65                  70                  75                  80

Thr Arg Thr Thr Ala Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp
                 85                  90                  95

Ala Gly Glu Ala Ser Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val
            100                 105                 110

Pro Ala Thr Gly Thr Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn
        115                 120                 125
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```
Ile Gly Met Glu Leu Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala
    130                 135                 140

Val Glu His Met Ala Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His
145                 150                 155                 160

Arg Ile Thr Thr Ser Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser
                165                 170                 175

Ser Thr Gly Ala Gly Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro
            180                 185                 190

Thr Asp Glu Ala Thr Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly
        195                 200                 205

Thr Ile Ala Met Ala Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val
    210                 215                 220

Leu Pro Gln Leu Arg Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu
225                 230                 235                 240

Arg Pro Asp His Arg Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg
                245                 250                 255

Ser Trp His


<210> 75
<211> 741
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(741)
<223> RXN01926

<400> 75
ctg cga agc ttc tac acc cca gaa caa gcc atc gaa cgc gaa ggc gac      48
Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp
  1               5                  10                  15

gtc tgg aaa gcc gcc acc gaa gaa gca gaa ctc ctc gca gct gac ggc      96
Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
             20                  25                  30

gcc gtc cac gac cag gaa ctc ttc ctc aac tgc acc acc tcc cca ctg     144
Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
         35                  40                  45

atc ttc gcc tcc gcg atg ctc aac ttc ggc gtc cac caa atc ctg gac     192
Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
     50                  55                  60

acc ctc tgc caa ctc gca cca tcc ccc gcc ggc cgc gac gca gac ccc     240
```

```
Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
 65                 70                  75                  80

aaa gcc ctc gaa gcc gcc acc tcc gca atg gac gac cac cgc gac acc    288
Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
                 85                  90                  95

acc gac gac ttc tcc ggc gtc gtc ttc aaa gtc caa gcc ggc atg gac    336
Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
            100                 105                 110

aaa aac cac cgc gat acc ctc gcc ttc atg cgc gtc gtc tcc ggc gaa    384
Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
        115                 120                 125

ttc gac cgc ggc atg caa gtc acc cac tcc caa tcc ggc cgc agc ttc    432
Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
    130                 135                 140

tcc acc aaa tac gcc ctc acc gtc ttc ggc cgc acc cgc tct acc gtc    480
Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
145                 150                 155                 160

gaa acc gcc ttc ccc ggc gac atc gtc ggc ctc gtc aac gcc ggc gcc    528
Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
                165                 170                 175

ctc gca cca ggc gac acc atc ttc gaa ggc cga aaa atc caa tac cca    576
Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
            180                 185                 190

cca atg cca aaa ttc gcg cca gaa cac ttc cgc atc ctg cgc gcc aaa    624
Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
        195                 200                 205

tca ctc ggc aaa tac aaa cag ttc cgc aaa gcc ctc gag cag ctg gac    672
Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
    210                 215                 220

tcc gaa ggt gtc gtc cag atc ctc aag aac gac ctg cgt ggc gac gcc    720
Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
225                 230                 235                 240

aac cca ggt cat ggc cgg tgt                                        741
Asn Pro Gly His Gly Arg Cys
                245


&lt;210&gt; 76
&lt;211&gt; 247
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 76
Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp
  1               5                  10                  15
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Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
            20                  25                  30

Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
        35                  40                  45

Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
    50                  55                  60

Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
65                  70                  75                  80

Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
                85                  90                  95

Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
            100                 105                 110

Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
        115                 120                 125

Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
    130                 135                 140

Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
145                 150                 155                 160

Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
                165                 170                 175

Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
            180                 185                 190

Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
        195                 200                 205

Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
    210                 215                 220

Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
225                 230                 235                 240

Asn Pro Gly His Gly Arg Cys
                245


<210> 77
<211> 478
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> RXN02002

<400> 77
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aagtggcaaa aaacgtttca agcaggcaac gccggcgtac aacttcgctg agctggggcg 60

attatggccc agcgcccaca acccgctatt cttaataccc atg agc aac gcc aat   115
                                            Met Ser Asn Ala Asn
                                             1               5

tcc gac acc acc gcc gcc gag gca cat cgc cgc aga aca ttc gcc gta   163
Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg Arg Thr Phe Ala Val
                10                  15                  20

atc gca cac ccc gac gcc ggt aaa tcc acc ctc acc gag gca ttg gcg   211
Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu Thr Glu Ala Leu Ala
            25                  30                  35

ctg cat gca cac atc atc tcc gaa gcc ggc gcc acc cac ggc aaa gca   259
Leu His Ala His Ile Ile Ser Glu Ala Gly Ala Thr His Gly Lys Ala
        40                  45                  50

ggc cgc aaa gcc acc gtt tcc gac tgg atg gaa atg gaa aaa gac cgc   307
Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu Met Glu Lys Asp Arg
    55                  60                  65

ggc atc tcc atc gcc tcc tcc gca ctc caa ttc gag tac gca cca gaa   355
Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu
70                  75                  80                  85

ggc cac gca ggc gag ccc ttc atg atc aac ctc gtg gac acc cca ggc   403
Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly
                90                  95                  100

cac gcc gac ttc tcc gaa gac acc tac cgc gtc ctc atg gcc gtc gac   451
His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp
            105                 110                 115

gca gca gtc atg ctt atg cac tcc gtc                               478
Ala Ala Val Met Leu Met His Ser Val
        120                 125


<210> 78
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 78
Met Ser Asn Ala Asn Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg
 1               5                  10                  15

Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu
            20                  25                  30

Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala
        35                  40                  45

Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu
    50                  55                  60
```

```
Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe
 65                 70                  75                  80

Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu
                85                  90                  95

Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val
            100                 105                 110

Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val
        115                 120                 125


<210> 79
<211> 1080
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1057)
<223> RXN02736

<400> 79
cagaggatta cccagcgggt acgtggggtc caaagagcgc tgatgaaatg ctttcccgca 60

acggtcacac ctggcgcagg ccataattta ggggcaaaaa atg atc ttt gaa ctt    115
                                           Met Ile Phe Glu Leu
                                           1               5

ccg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt    163
Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg
                10                  15                  20

gaa tcg ggc acc cag gtc acc acc ggc cga gtg ctc acc ctc atc gtg    211
Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val
            25                  30                  35

gtc act gac tcc gaa agc gat gtc gct gca gtt acc gag tcc acc aat    259
Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn
        40                  45                  50

gaa gcc tcg cgc gag cac cca tct cgc gtg atc att ttg gtg gtt ggc    307
Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile Ile Leu Val Val Gly
    55                  60                  65

gat aaa act gca gaa aac aaa gtt gac gca gaa gtc cgt atc ggt ggc    355
Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu Val Arg Ile Gly Gly
70                  75                  80                  85

gac gct ggt gct tcc gag atg atc atc atg cat ctc aac gga cct gtc    403
Asp Ala Gly Ala Ser Glu Met Ile Ile Met His Leu Asn Gly Pro Val
                90                  95                  100

gct gac aag ctc cag tat gtc gtc aca cca ctg ttg ctt cct gac acc    451
Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu Leu Leu Pro Asp Thr
            105                 110                 115
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ccc atc gtt gct tgg tgg cca ggt gaa tca cca aag aat cct tcc cag 499
Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro Lys Asn Pro Ser Gln
120 125 130

gac cca att gga cgc atc gca caa cga cgc atc act gat gct ttg tac 547
Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile Thr Asp Ala Leu Tyr
135 140 145

gac cgt gat gac gca cta gaa gat cgt gtt gag aac tat cac cca ggt 595
Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu Asn Tyr His Pro Gly
150 155 160 165

gat acc gac atg acg tgg gcg cgc ctt acc cag tgg cgg gga ctt gtt 643
Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln Trp Arg Gly Leu Val
170 175 180

gcc tcc tca ttg gat cac cca cca cac agc gaa atc act tcc gtg agg 691
Ala Ser Ser Leu Asp His Pro Pro His Ser Glu Ile Thr Ser Val Arg
185 190 195

ctg acc ggt gca agc ggc agt acc tcg gtg gat ttg gct gca ggc tgg 739
Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp Leu Ala Ala Gly Trp
200 205 210

ttg gcg cgg agg ctg aaa gtg cct gtg atc cgc gag gtg aca gat gct 787
Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg Glu Val Thr Asp Ala
215 220 225

ccc acc gtg cca acc gat gag ttt ggt act cca ctg ctg gct atc cag 835
Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro Leu Leu Ala Ile Gln
230 235 240 245

cgc ctg gag atc gtt cgc acc acc ggc tcg atc atc atc acc atc tat 883
Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile Ile Ile Thr Ile Tyr
250 255 260

gac gct cat acc ctt cag gta gag atg ccg gaa tcc ggc aat gcc cca 931
Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro
265 270 275

tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag 979
Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu
280 285 290

gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc 1027
Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser
295 300 305

ggc ttg tcc agc gtc aag ctg gaa acc gtc taaggagaaa tacaacacta 1077
Gly Leu Ser Ser Val Lys Leu Glu Thr Val
310 315

tgg 1080

<210> 80

<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 80
Met Ile Phe Glu Leu Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr
1   5   10   15

Leu Thr Arg Leu Arg Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val
            20   25   30

Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val
        35   40   45

Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile
    50   55   60

Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
65   70   75   80

Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
                85   90   95

Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
            100   105   110

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro
        115   120   125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile
    130   135   140

Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu
145   150   155   160

Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln
                165   170   175

Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu
            180   185   190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp
        195   200   205

Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg
    210   215   220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro
225   230   235   240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile
                245   250   255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu
            260   265   270

Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser

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        275                 280                 285

Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr
    290                 295                 300

Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val
305                 310                 315


<210> 81
<211> 331
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> RXS03217

<400> 81
tctgtgaagg tagatggttt gacgaggagt tccaacgact cggacgctgg tgaatcatgc 60

tggcgaacgt agcatcacct gattaggaaa aggtacaaat atg gca cag ggt act    115
                                          Met Ala Gln Gly Thr
                                           1               5

gtg aaa tgg ttc aac ggc gaa aag gga ttt ggt ttc atc gct ccc aac    163
Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly Phe Ile Ala Pro Asn
                10                  15                  20

gat ggc tcc gca gat ctc ttc gtc cac tac tct gag att cag ggc tcc    211
Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser
            25                  30                  35

ggt ttc cgt aat ctt gag gaa aac cag cca gtt gaa ttt gag gtc ggc    259
Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly
        40                  45                  50

gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctc            301
Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val Arg Ala Leu
    55                  60                  65

taagctctaa ctgctagcta aaaattccgc                                   331


<210> 82
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 82
Met Ala Gln Gly Thr Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly
1               5                   10                  15

Phe Ile Ala Pro Asn Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser
            20                  25                  30
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Glu Ile Gln Gly Ser Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val
35 40 45

Glu Phe Glu Val Gly Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val
50 55 60

Arg Ala Leu
65

<210> 83
<211> 324
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> FRXA01917

<400> 83
tctgtgaagg tagatggttt gacgaggagt tccaacgact cggacgctgg tgaatcatgc 60

tggcgaacgt agcatcacct gattaggaaa aggtacaaat atg gca cag ggt act 115
Met Ala Gln Gly Thr
1 5

gtg aaa tgg ttc aac ggc gaa aag gga ttt ggt ttc atc gct ccc aac 163
Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly Phe Ile Ala Pro Asn
10 15 20

gat ggc tcc gca gat ctc ttc gtc cac tac tct gag att cag ggc tcc 211
Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser
25 30 35

ggt ttc cgt aat ctt gag gaa aac cag cca gtt gaa ttt gag gtc ggc 259
Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly
40 45 50

gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctc 301
Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val Arg Ala Leu
55 60 65

taagctctaa ctgctagcta aaa 324

<210> 84
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 84
Met Ala Gln Gly Thr Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly
1 5 10 15

Phe Ile Ala Pro Asn Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser
20 25 30

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Glu Ile Gln Gly Ser Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val
        35                  40                  45

Glu Phe Glu Val Gly Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val
    50                  55                  60

Arg Ala Leu
65


&lt;210&gt; 85
&lt;211&gt; 504
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(481)
&lt;223&gt; RXA02184

&lt;400&gt; 85
tttaccgcga tgcttgcggt gtataataat ttcttctggt caaaaatagt tgatcaattt 60

gaatcagcat atgaattagg aatgaaagtg gtgaggacaa gtg cct gtc gga aca   115
                                          Val Pro Val Gly Thr
                                          1               5

gtg aag tgg tac gac gcg gag cgt ggt ttc ggc ttt gtc tcc aat cca   163
Val Lys Trp Tyr Asp Ala Glu Arg Gly Phe Gly Phe Val Ser Asn Pro
                10                  15                  20

ggt ggt gaa gat tgc ttc gta ggt aag caa gta ctt ccc aag gga gtc   211
Gly Gly Glu Asp Cys Phe Val Gly Lys Gln Val Leu Pro Lys Gly Val
            25                  30                  35

acc gaa ttg cac aag gga cag cga atc gat ttt gac ttc gcc gca ggc   259
Thr Glu Leu His Lys Gly Gln Arg Ile Asp Phe Asp Phe Ala Ala Gly
        40                  45                  50

cgt aag ggc cct caa gca ctt cga ata aag att ctt gaa act cca cgc   307
Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile Leu Glu Thr Pro Arg
    55                  60                  65

agg cgt cca cag cac aaa tac aag cca gaa gag ctc aac gga atg atc   355
Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu Leu Asn Gly Met Ile
70                  75                  80                  85

tct gac ctc atc acg ctt cta gaa agt gga gtg caa cca ggc ctt gcc   403
Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val Gln Pro Gly Leu Ala
                90                  95                  100

aaa ggg caa tac ccg gag cac aaa gct gga gcg cag gta gca gaa att   451
Lys Gly Gln Tyr Pro Glu His Lys Ala Gly Ala Gln Val Ala Glu Ile
            105                 110                 115

ctt cgc gtt gtt gcg aag gag ctt gag tct taaaacaata aggagaggat     501
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Leu Arg Val Val Ala Lys Glu Leu Glu Ser
        120                 125

ccg                                                                504


<210> 86
<211> 127
<212> PRT
<213> Corynebacterium glutamicum

<400> 86
Val Pro Val Gly Thr Val Lys Trp Tyr Asp Ala Glu Arg Gly Phe Gly
  1               5                  10                  15

Phe Val Ser Asn Pro Gly Gly Glu Asp Cys Phe Val Gly Lys Gln Val
            20                  25                  30

Leu Pro Lys Gly Val Thr Glu Leu His Lys Gly Gln Arg Ile Asp Phe
        35                  40                  45

Asp Phe Ala Ala Gly Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile
    50                  55                  60

Leu Glu Thr Pro Arg Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu
65                  70                  75                  80

Leu Asn Gly Met Ile Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val
                85                  90                  95

Gln Pro Gly Leu Ala Lys Gly Gln Tyr Pro Glu His Lys Ala Gly Ala
            100                 105                 110

Gln Val Ala Glu Ile Leu Arg Val Val Ala Lys Glu Leu Glu Ser
        115                 120                 125


<210> 87
<211> 324
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> RXA00810

<400> 87
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tcgaacccgg tagtaattcc aatcagtaaa ggtaagacaa atg gca cag ggc act   115
                                           Met Ala Gln Gly Thr
                                           1               5

gtt aag tgg ttc aac cca gag aag ggc ttc ggc ttc atc gct cct tcc   163
Val Lys Trp Phe Asn Pro Glu Lys Gly Phe Gly Phe Ile Ala Pro Ser
            10                  15                  20
```

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gac gga tcc gct gac gtt ttc gtc cac tac tcc gag atc gag ggc aac    211
Asp Gly Ser Ala Asp Val Phe Val His Tyr Ser Glu Ile Glu Gly Asn
            25                  30                  35

ggc ttc cgt acc ctc gag gag aac cag ctc gtc gag ttc gaa atc ggc    259
Gly Phe Arg Thr Leu Glu Glu Asn Gln Leu Val Glu Phe Glu Ile Gly
        40                  45                  50

gag ggc gct aag ggc ctt cag gct cag gct gtt cgt gca atc            301
Glu Gly Ala Lys Gly Leu Gln Ala Gln Ala Val Arg Ala Ile
    55                  60                  65

taattgcatc tgagttcgaa acc                                          324


&lt;210&gt; 88
&lt;211&gt; 67
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 88
Met Ala Gln Gly Thr Val Lys Trp Phe Asn Pro Glu Lys Gly Phe Gly
1               5                   10                  15

Phe Ile Ala Pro Ser Asp Gly Ser Ala Asp Val Phe Val His Tyr Ser
            20                  25                  30

Glu Ile Glu Gly Asn Gly Phe Arg Thr Leu Glu Glu Asn Gln Leu Val
        35                  40                  45

Glu Phe Glu Ile Gly Glu Gly Ala Lys Gly Leu Gln Ala Gln Ala Val
    50                  55                  60

Arg Ala Ile
65


&lt;210&gt; 89
&lt;211&gt; 1017
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(994)
&lt;223&gt; RXA01674

&lt;400&gt; 89
cggcgtcgat tccagaaggt ttgtagacat gcttcaaggt tgcgctaatt gaaaagaacg 60

cggtagacgg tactttcata tccacccata taatgttgat atg gat aat ggg tgg   115
                                            Met Asp Asn Gly Trp
                                            1               5

ccg aac ctg caa act ctc gca ctc ttt gtg gcg att gtg gaa gag ggg   163
Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala Ile Val Glu Glu Gly
```

10 15 20

agc ctc ggt gcc ggt gct cga aaa gtc gga atg gcc caa cct aat gcc 211
Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met Ala Gln Pro Asn Ala
25 30 35

agt cgg gct atc gca gag ctt gag gca gac atg aaa gcc gaa ttg ttg 259
Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met Lys Ala Glu Leu Leu
40 45 50

gta cgt cat cct cga gga tca cat cca aca gct gct gga ctt gcg ctt 307
Val Arg His Pro Arg Gly Ser His Pro Thr Ala Ala Gly Leu Ala Leu
55 60 65

gtt gag cat tcg cgc gat ctg ctt caa tct gta caa gaa ttt act gaa 355
Val Glu His Ser Arg Asp Leu Leu Gln Ser Val Gln Glu Phe Thr Glu
70 75 80 85

tgg gtg aca gag gga cga act gag cag ccg ctg aaa ttg cat gtt ggg 403
Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu Lys Leu His Val Gly
90 95 100

gcc agt atg acc att gcc gag gct cta ctt cca gct tgg gtt gcg gac 451
Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro Ala Trp Val Ala Asp
105 110 115

atg cgc acg cgt ttt cct gcc tgc cgt gtc gac gtc tct gtg atg aat 499
Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp Val Ser Val Met Asn
120 125 130

tct tct caa gta att gaa gcc gtc cag aaa ggg cac ttg caa cta ggt 547
Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly His Leu Gln Leu Gly
135 140 145

ttt att gaa aca ccg cat gtt ccc gta cgg ctt cat gct cgt gtg gtg 595
Phe Ile Glu Thr Pro His Val Pro Val Arg Leu His Ala Arg Val Val
150 155 160 165

caa gag gac aag ctg att gtg gtg att tct cct aat cat gag tgg gct 643
Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro Asn His Glu Trp Ala
170 175 180

aat cgc acg ggt agg atc agt ctt cgg gag ttg tcg gaa act ccg ctg 691
Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu Ser Glu Thr Pro Leu
185 190 195

ata gtg agg gaa gtc ggc tca ggt acc cga gaa gca tta caa gaa tta 739
Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu Ala Leu Gln Glu Leu
200 205 210

ctt gcg gat tat gac atg gct gag ccg att caa gtg tta aac agc aat 787
Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln Val Leu Asn Ser Asn
215 220 225

gct gcg gta cgt gtt gtt gtt gaa gca ggg gca ggt cct gca gta ctt 835
Ala Ala Val Arg Val Val Val Glu Ala Gly Ala Gly Pro Ala Val Leu
230 235 240 245

ggt gaa tta gcc ttg cgt gat cat ctt gcg ctc ggc agg ctg ttg agt 883
Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu Gly Arg Leu Leu Ser
250 255 260

gtg cca ttt gaa ggc agt gga gtt act cgt cct ctt aca gct gtg tgg 931
Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro Leu Thr Ala Val Trp
265 270 275

agt gga ccc cgc aga ttg ccg att cta gcg gga gaa tta gtg tcc atc 979
Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile
280 285 290

gca tcg aac cac atc tgattttgag ccctggctaa cgg 1017
Ala Ser Asn His Ile
295

<210> 90
<211> 298
<212> PRT
<213> Corynebacterium glutamicum

<400> 90
Met Asp Asn Gly Trp Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala
1 5 10 15

Ile Val Glu Glu Gly Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met
20 25 30

Ala Gln Pro Asn Ala Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met
35 40 45

Lys Ala Glu Leu Leu Val Arg His Pro Arg Gly Ser His Pro Thr Ala
50 55 60

Ala Gly Leu Ala Leu Val Glu His Ser Arg Asp Leu Leu Gln Ser Val
65 70 75 80

Gln Glu Phe Thr Glu Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu
85 90 95

Lys Leu His Val Gly Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro
100 105 110

Ala Trp Val Ala Asp Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp
115 120 125

Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly
130 135 140

His Leu Gln Leu Gly Phe Ile Glu Thr Pro His Val Pro Val Arg Leu
145 150 155 160

His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro
165 170 175

Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu
180 185 190

Ser Glu Thr Pro Leu Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu
195 200 205

Ala Leu Gln Glu Leu Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln
210 215 220

Val Leu Asn Ser Asn Ala Ala Val Arg Val Val Val Glu Ala Gly Ala
225 230 235 240

Gly Pro Ala Val Leu Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu
245 250 255

Gly Arg Leu Leu Ser Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro
260 265 270

Leu Thr Ala Val Trp Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly
275 280 285

Glu Leu Val Ser Ile Ala Ser Asn His Ile
290 295

<210> 91
<211> 1214
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1191)
<223> RXA02431

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Val Val Val Thr Pro Arg His Ile Val Tyr Ser Ala Ala Ser Arg Arg
1 5 10 15

gtg ttc caa atc gtg gaa aaa cgc gcc gga att gtc gaa cgc ctc agc 96
Val Phe Gln Ile Val Glu Lys Arg Ala Gly Ile Val Glu Arg Leu Ser
20 25 30

atc gat gaa ggc ttc atg gaa cca gag gct ctc gtt gga gcc acc cca 144
Ile Asp Glu Gly Phe Met Glu Pro Glu Ala Leu Val Gly Ala Thr Pro
35 40 45

gaa gag gtg aaa cag tgg gcg gaa gaa tta cgc gcg gaa att aaa gaa 192
Glu Glu Val Lys Gln Trp Ala Glu Glu Leu Arg Ala Glu Ile Lys Glu
50 55 60

gtt act ggc tta ccc tcc tcg gtt ggt gct ggc tcc ggt aag cag atc 240
Val Thr Gly Leu Pro Ser Ser Val Gly Ala Gly Ser Gly Lys Gln Ile
65 70 75 80

gcc aaa att ggt tca ggc gaa gca aag cca gat ggt gtg ttt gtc gtg 288

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Ala Lys Ile Gly Ser Gly Glu Ala Lys Pro Asp Gly Val Phe Val Val
                85                  90                  95

cca gta gac aag caa cat gac ttg ctt gat cca ctt cct gtg ggc gca    336
Pro Val Asp Lys Gln His Asp Leu Leu Asp Pro Leu Pro Val Gly Ala
            100                 105                 110

ctt tgg gga gtg ggt cct gtg aca ggc tcc aag ctt gcc tca atg ggg    384
Leu Trp Gly Val Gly Pro Val Thr Gly Ser Lys Leu Ala Ser Met Gly
        115                 120                 125

gtg gaa aca att ggt gat cta gca gcg cta acc caa aaa gaa gta gaa    432
Val Glu Thr Ile Gly Asp Leu Ala Ala Leu Thr Gln Lys Glu Val Glu
    130                 135                 140

atc agc ctc ggt gca acc atc gga ata tca ctg tgg aac ctt gcc cga    480
Ile Ser Leu Gly Ala Thr Ile Gly Ile Ser Leu Trp Asn Leu Ala Arg
145                 150                 155                 160

gga atc gac gac cgc cct gtg gaa ccc cgc gcc gaa gca aaa cag atc    528
Gly Ile Asp Asp Arg Pro Val Glu Pro Arg Ala Glu Ala Lys Gln Ile
                165                 170                 175

tcc caa gag cac acc tat gaa aaa gac ctc ctc acc agg caa caa gta    576
Ser Gln Glu His Thr Tyr Glu Lys Asp Leu Leu Thr Arg Gln Gln Val
            180                 185                 190

gat gct gcc atc att cga tca gcc gaa ggc gca cac cga cgg ctc ctc    624
Asp Ala Ala Ile Ile Arg Ser Ala Glu Gly Ala His Arg Arg Leu Leu
        195                 200                 205

aaa gac gga cgc ggt gcc aga act gtc agc gtg aaa ctg cgg atg gcc    672
Lys Asp Gly Arg Gly Ala Arg Thr Val Ser Val Lys Leu Arg Met Ala
    210                 215                 220

gac ttt cgt att gag tct cgt tcc tac acc ttg tcc tat gcc acc gat    720
Asp Phe Arg Ile Glu Ser Arg Ser Tyr Thr Leu Ser Tyr Ala Thr Asp
225                 230                 235                 240

gat tac gca act ctt gag gca aca gca ttc cga ctt gcc cgc tac ccc    768
Asp Tyr Ala Thr Leu Glu Ala Thr Ala Phe Arg Leu Ala Arg Tyr Pro
                245                 250                 255

gga gaa gta ggc ccc atc cgc ctt gtc gga gta agt ttt tct ggt ttg    816
Gly Glu Val Gly Pro Ile Arg Leu Val Gly Val Ser Phe Ser Gly Leu
            260                 265                 270

gaa gaa tcc cgc caa gac atc ctc ttc ccg gaa ctt gac caa caa atc    864
Glu Glu Ser Arg Gln Asp Ile Leu Phe Pro Glu Leu Asp Gln Gln Ile
        275                 280                 285

atc gta cca cca gca ccc gac acc gat tat gag gta ggc gtg caa tcc    912
Ile Val Pro Pro Ala Pro Asp Thr Asp Tyr Glu Val Gly Val Gln Ser
    290                 295                 300

tct tct agt tcc gaa agt act caa gtt gaa gcg ccg caa gat gtc gcg    960
Ser Ser Ser Ser Glu Ser Thr Gln Val Glu Ala Pro Gln Asp Val Ala
```

305 310 315 320

ttg agt atg tgg tgc gca acg caa gat gtc tac cac cca gaa tat ggc 1008
Leu Ser Met Trp Cys Ala Thr Gln Asp Val Tyr His Pro Glu Tyr Gly
325 330 335

cac ggt tgg gta caa ggt gcc ggt cac ggt gtt gta tca gta cgt ttt 1056
His Gly Trp Val Gln Gly Ala Gly His Gly Val Val Ser Val Arg Phe
340 345 350

gaa acc cgc agc acc aca aaa ggg cga act aaa agt ttt tcc atg gat 1104
Glu Thr Arg Ser Thr Thr Lys Gly Arg Thr Lys Ser Phe Ser Met Asp
355 360 365

gac ccg gac ctc acc ccg gca gac cct cta gat agt ttg gat tgg gct 1152
Asp Pro Asp Leu Thr Pro Ala Asp Pro Leu Asp Ser Leu Asp Trp Ala
370 375 380

gac tgg ttt gct gaa aat ggt gaa acg ggg gat gac gaa tagggtttca 1201
Asp Trp Phe Ala Glu Asn Gly Glu Thr Gly Asp Asp Glu
385 390 395

tcgggtttcg ggg 1214

<210> 92
<211> 397
<212> PRT
<213> Corynebacterium glutamicum

<400> 92
Val Val Val Thr Pro Arg His Ile Val Tyr Ser Ala Ala Ser Arg Arg
1 5 10 15

Val Phe Gln Ile Val Glu Lys Arg Ala Gly Ile Val Glu Arg Leu Ser
20 25 30

Ile Asp Glu Gly Phe Met Glu Pro Glu Ala Leu Val Gly Ala Thr Pro
35 40 45

Glu Glu Val Lys Gln Trp Ala Glu Glu Leu Arg Ala Glu Ile Lys Glu
50 55 60

Val Thr Gly Leu Pro Ser Ser Val Gly Ala Gly Ser Gly Lys Gln Ile
65 70 75 80

Ala Lys Ile Gly Ser Gly Glu Ala Lys Pro Asp Gly Val Phe Val Val
85 90 95

Pro Val Asp Lys Gln His Asp Leu Leu Asp Pro Leu Pro Val Gly Ala
100 105 110

Leu Trp Gly Val Gly Pro Val Thr Gly Ser Lys Leu Ala Ser Met Gly
115 120 125

Val Glu Thr Ile Gly Asp Leu Ala Ala Leu Thr Gln Lys Glu Val Glu
130 135 140

Ile Ser Leu Gly Ala Thr Ile Gly Ile Ser Leu Trp Asn Leu Ala Arg
145 150 155 160

Gly Ile Asp Asp Arg Pro Val Glu Pro Arg Ala Glu Ala Lys Gln Ile
165 170 175

Ser Gln Glu His Thr Tyr Glu Lys Asp Leu Leu Thr Arg Gln Gln Val
180 185 190

Asp Ala Ala Ile Ile Arg Ser Ala Glu Gly Ala His Arg Arg Leu Leu
195 200 205

Lys Asp Gly Arg Gly Ala Arg Thr Val Ser Val Lys Leu Arg Met Ala
210 215 220

Asp Phe Arg Ile Glu Ser Arg Ser Tyr Thr Leu Ser Tyr Ala Thr Asp
225 230 235 240

Asp Tyr Ala Thr Leu Glu Ala Thr Ala Phe Arg Leu Ala Arg Tyr Pro
245 250 255

Gly Glu Val Gly Pro Ile Arg Leu Val Gly Val Ser Phe Ser Gly Leu
260 265 270

Glu Glu Ser Arg Gln Asp Ile Leu Phe Pro Glu Leu Asp Gln Gln Ile
275 280 285

Ile Val Pro Pro Ala Pro Asp Thr Asp Tyr Glu Val Gly Val Gln Ser
290 295 300

Ser Ser Ser Ser Glu Ser Thr Gln Val Glu Ala Pro Gln Asp Val Ala
305 310 315 320

Leu Ser Met Trp Cys Ala Thr Gln Asp Val Tyr His Pro Glu Tyr Gly
325 330 335

His Gly Trp Val Gln Gly Ala Gly His Gly Val Val Ser Val Arg Phe
340 345 350

Glu Thr Arg Ser Thr Thr Lys Gly Arg Thr Lys Ser Phe Ser Met Asp
355 360 365

Asp Pro Asp Leu Thr Pro Ala Asp Pro Leu Asp Ser Leu Asp Trp Ala
370 375 380

Asp Trp Phe Ala Glu Asn Gly Glu Thr Gly Asp Asp Glu
385 390 395

<210> 93
<211> 558
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

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<222> (101)..(535)
<223> RXA02446

<400> 93
caggaaatct tgctgtctaa tgcacaacgg aaaactgctc acggacgaac tagttgtagc 60

gagcgtattc tttgtgttct ctcacgacag gaatactgct atg gcg atc gag tcc   115
                                           Met Ala Ile Glu Ser
                                            1               5

atc gcg tac acc agt gaa gca ctc tca acc ggc agt ggc cgg ctg ggg   163
Ile Ala Tyr Thr Ser Glu Ala Leu Ser Thr Gly Ser Gly Arg Leu Gly
                10                  15                  20

cat gtg cgc tcc aca gat ggt gcg ctc gaa ttt gaa atg aca ccg cca   211
His Val Arg Ser Thr Asp Gly Ala Leu Glu Phe Glu Met Thr Pro Pro
            25                  30                  35

aag gct ttg ggc gga tcc ggt gaa ggc acc aat cca gaa cag ctg ttc   259
Lys Ala Leu Gly Gly Ser Gly Glu Gly Thr Asn Pro Glu Gln Leu Phe
        40                  45                  50

gcg gta ggt tac gca gcc tgt ttc cac tct gcc atg cac tct gtc gca   307
Ala Val Gly Tyr Ala Ala Cys Phe His Ser Ala Met His Ser Val Ala
    55                  60                  65

cgc agc cgc aag atc act ctt gaa gac aca gcg gtt ggt gcc cga gtt   355
Arg Ser Arg Lys Ile Thr Leu Glu Asp Thr Ala Val Gly Ala Arg Val
70                  75                  80                  85

agc atc ggg cca aac ggc gct ggt gga ttt gag att gcc gta gaa ctc   403
Ser Ile Gly Pro Asn Gly Ala Gly Gly Phe Glu Ile Ala Val Glu Leu
                90                  95                  100

gaa gta tcg att cct caa ttg cca caa gca gaa gcc cag gaa ctt gct   451
Glu Val Ser Ile Pro Gln Leu Pro Gln Ala Glu Ala Gln Glu Leu Ala
            105                 110                 115

gat gcc gcg cac cag gtg tgc ccg tat tcc aac gcc aca cga ggc aat   499
Asp Ala Ala His Gln Val Cys Pro Tyr Ser Asn Ala Thr Arg Gly Asn
        120                 125                 130

atc tcg gta act gtg tca gtc atc gac gaa gag gct taaaaccaca        545
Ile Ser Val Thr Val Ser Val Ile Asp Glu Glu Ala
    135                 140                 145

ggattaacaa aac                                                    558

<210> 94
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
Met Ala Ile Glu Ser Ile Ala Tyr Thr Ser Glu Ala Leu Ser Thr Gly
 1               5                  10                  15
```

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Ser Gly Arg Leu Gly His Val Arg Ser Thr Asp Gly Ala Leu Glu Phe
            20                  25                  30

Glu Met Thr Pro Pro Lys Ala Leu Gly Gly Ser Gly Glu Gly Thr Asn
        35                  40                  45

Pro Glu Gln Leu Phe Ala Val Gly Tyr Ala Ala Cys Phe His Ser Ala
    50                  55                  60

Met His Ser Val Ala Arg Ser Arg Lys Ile Thr Leu Glu Asp Thr Ala
65                  70                  75                  80

Val Gly Ala Arg Val Ser Ile Gly Pro Asn Gly Ala Gly Gly Phe Glu
                85                  90                  95

Ile Ala Val Glu Leu Glu Val Ser Ile Pro Gln Leu Pro Gln Ala Glu
            100                 105                 110

Ala Gln Glu Leu Ala Asp Ala Ala His Gln Val Cys Pro Tyr Ser Asn
        115                 120                 125

Ala Thr Arg Gly Asn Ile Ser Val Thr Val Ser Val Ile Asp Glu Glu
    130                 135                 140

Ala
145


<210> 95
<211> 1206
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1183)
<223> RXA02861

<400> 95
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gaaggtatta atacttcttt aagggtcgga ggattttcgt atg tct act aga aca    115
                                          Met Ser Thr Arg Thr
                                          1               5

acg cca caa gac cgt tat acc gac gaa tac ggc atc gaa cgc gtc aac    163
Thr Pro Gln Asp Arg Tyr Thr Asp Glu Tyr Gly Ile Glu Arg Val Asn
                10                  15                  20

aag gat gaa ccc ggc ctg gtg gac aaa ctc cgg gac aag cac gac tgg    211
Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg Asp Lys His Asp Trp
            25                  30                  35

ttt gat cat ctc atg cgc atg aat gaa cgt ttc ggc gca aaa ggt ggc    259
Phe Asp His Leu Met Arg Met Asn Glu Arg Phe Gly Ala Lys Gly Gly
        40                  45                  50
```

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aac caa ttg tcg gcg ggt att acg tat ttc tcc gtg ctg tcg atc ttc    307
Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser Val Leu Ser Ile Phe
     55                  60                  65

ccg att gcc atg ctt gtc ttc ggt att gca ggt gtc atc ctt gcc gga    355
Pro Ile Ala Met Leu Val Phe Gly Ile Ala Gly Val Ile Leu Ala Gly
 70                  75                  80                  85

aac cct gaa gtt ctc aca gat att caa aat cga atc aac gat gct tta    403
Asn Pro Glu Val Leu Thr Asp Ile Gln Asn Arg Ile Asn Asp Ala Leu
                 90                  95                 100

gaa ggc gag atc ggt aac acc gtc aac ggc atc att gat tcc gcg att    451
Glu Gly Glu Ile Gly Asn Thr Val Asn Gly Ile Ile Asp Ser Ala Ile
            105                 110                 115

gcg cag cgt ggt gct gtg ttg ggc att ggt ggt gta act gcc ctg tgg    499
Ala Gln Arg Gly Ala Val Leu Gly Ile Gly Gly Val Thr Ala Leu Trp
        120                 125                 130

tct gga ctg ggg tgg atg gcg aac ctg cgc ttt gga gtt tcc cgc atg    547
Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe Gly Val Ser Arg Met
    135                 140                 145

tgg gcc att gac cca act gaa ggc aac ttc att caa aag aag ctc acc    595
Trp Ala Ile Asp Pro Thr Glu Gly Asn Phe Ile Gln Lys Lys Leu Thr
150                 155                 160                 165

gac ttg gtc gcg ctg atc gtc ttg ctg ctg gcc atg ggc gta gcc ttc    643
Asp Leu Val Ala Leu Ile Val Leu Leu Leu Ala Met Gly Val Ala Phe
                170                 175                 180

ggt atc acg gcg ctc ggt gct tcc gga cta acc aaa aac ctg ctg gac    691
Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr Lys Asn Leu Leu Asp
            185                 190                 195

ttt gtg ggc ctg ggg gag att ccg ggc att agc tac atc acc tgg gtg    739
Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser Tyr Ile Thr Trp Val
        200                 205                 210

gtc gca gca ctt gtt ggt gtc ttg gct aac ttc ctg gtg ttc atg tgg    787
Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe Leu Val Phe Met Trp
    215                 220                 225

ctg att ttc tcc ctg cca cgt acc aaa gtt ccc atg aaa ccg ggt ctt    835
Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro Met Lys Pro Gly Leu
230                 235                 240                 245

cag gca gca ctg ctt ggc gca atc ggt ttt gag gtg gtc aag cag gtt    883
Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu Val Val Lys Gln Val
                250                 255                 260

gga tcg ctg ttg gct tca aat gca ttg agt aac ccc gcg ggt gca gca    931
Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn Pro Ala Gly Ala Ala
            265                 270                 275
```

ttc ggt ccg atc atc ggc atc atg gtt gtg ctg tat ttg atc tgg cgc 979
Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu Tyr Leu Ile Trp Arg
280 285 290

atc ctc atg tat tgc tct gcg tgg gct gcc acc agt gaa gaa gcg ttg 1027
Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr Ser Glu Glu Ala Leu
295 300 305

cgt ctt gcg act gtt cca gca cca gag cct gcg atc att cgg gtt cgc 1075
Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala Ile Ile Arg Val Arg
310 315 320 325

cat gaa att gat cca ggt gaa gaa gtc tcc caa tct gct cga aaa gtg 1123
His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln Ser Ala Arg Lys Val
330 335 340

ggc att gga gtg gcc gtg ggt gcc gcg act gcg ggt gct ttt gcg ctg 1171
Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala Gly Ala Phe Ala Leu
345 350 355

ttg cgt aaa aaa tagtttttat taagggcatt ccc 1206
Leu Arg Lys Lys
360

<210> 96
<211> 361
<212> PRT
<213> Corynebacterium glutamicum

<400> 96
Met Ser Thr Arg Thr Thr Pro Gln Asp Arg Tyr Thr Asp Glu Tyr Gly
1 5 10 15

Ile Glu Arg Val Asn Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg
20 25 30

Asp Lys His Asp Trp Phe Asp His Leu Met Arg Met Asn Glu Arg Phe
35 40 45

Gly Ala Lys Gly Gly Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser
50 55 60

Val Leu Ser Ile Phe Pro Ile Ala Met Leu Val Phe Gly Ile Ala Gly
65 70 75 80

Val Ile Leu Ala Gly Asn Pro Glu Val Leu Thr Asp Ile Gln Asn Arg
85 90 95

Ile Asn Asp Ala Leu Glu Gly Glu Ile Gly Asn Thr Val Asn Gly Ile
100 105 110

Ile Asp Ser Ala Ile Ala Gln Arg Gly Ala Val Leu Gly Ile Gly Gly
115 120 125

Val Thr Ala Leu Trp Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe
130 135 140

```
Gly Val Ser Arg Met Trp Ala Ile Asp Pro Thr Glu Gly Asn Phe Ile
145                 150                 155                 160

Gln Lys Lys Leu Thr Asp Leu Val Ala Leu Ile Val Leu Leu Leu Ala
                165                 170                 175

Met Gly Val Ala Phe Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr
            180                 185                 190

Lys Asn Leu Leu Asp Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser
        195                 200                 205

Tyr Ile Thr Trp Val Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe
    210                 215                 220

Leu Val Phe Met Trp Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro
225                 230                 235                 240

Met Lys Pro Gly Leu Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu
                245                 250                 255

Val Val Lys Gln Val Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn
            260                 265                 270

Pro Ala Gly Ala Ala Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu
        275                 280                 285

Tyr Leu Ile Trp Arg Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr
    290                 295                 300

Ser Glu Glu Ala Leu Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala
305                 310                 315                 320

Ile Ile Arg Val Arg His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln
                325                 330                 335

Ser Ala Arg Lys Val Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala
            340                 345                 350

Gly Ala Phe Ala Leu Leu Arg Lys Lys
        355                 360
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<210> 97
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(730)
<223> RXA00981

<400> 97
aaccaatggc tgggtactga tgtggtgatc agtgcccagt ttcttctttc tactagtgtc 60

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ggatagaagt acccccagtc cagaatgaag gtcaccacca atg tca gag aat ttg    115
                                            Met Ser Glu Asn Leu
                                             1               5

cca gcg ccc gag aat ctc ctg gac gcc gag aga att cag atg atc aag    163
Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg Ile Gln Met Ile Lys
                10                  15                  20

aac ttc cgc aac gaa tta acg ggg ttc atg ctc aac tac caa ttt ggc    211
Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu Asn Tyr Gln Phe Gly
            25                  30                  35

att gat gag atc ctg acc aag atc aac atc ctg aaa act gaa ttc agc    259
Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu Lys Thr Glu Phe Ser
        40                  45                  50

cag ctg cac gaa tac gca cct atc gag cac gta tct tca cga ttg aag    307
Gln Leu His Glu Tyr Ala Pro Ile Glu His Val Ser Ser Arg Leu Lys
    55                  60                  65

aca cca gaa agc atc gtc aaa aag gtc atc cga aaa gga gac gag ctc    355
Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg Lys Gly Asp Glu Leu
 70                  75                  80                  85

tcc ctc gca gct atc aaa gac aca gtg ttt gat atc gca ggc att cga    403
Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp Ile Ala Gly Ile Arg
                90                  95                 100

atc gtc tgc agt ttc ctc aaa gat gcc tac gca atc gcc gat atg ctg    451
Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala Ile Ala Asp Met Leu
            105                 110                 115

acc aac caa aaa gac gtc acg gtc atc gag gcc aaa gac tac atc gct    499
Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala Lys Asp Tyr Ile Ala
        120                 125                 130

aac cca aag ccg aac ggc tac aag agt ttg cac ctt atc ctc caa gtg    547
Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His Leu Ile Leu Gln Val
    135                 140                 145

cct gtc ttc ctg tct aac tcc gtg gaa aag gtc aat gtt gaa gtc cag    595
Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val Asn Val Glu Val Gln
150                 155                 160                 165

atc cgc acc att gcc atg gac ttc tgg gca agc ctc gag cac aaa atc    643
Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser Leu Glu His Lys Ile
                170                 175                 180

tac tac aaa ttt gaa caa gaa gtt cct cag tca atc ctt gat gag ctc    691
Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
            185                 190                 195

agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca    740
Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr
        200                 205                 210

gttgaaacca ctg                                                    753
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<210> 98
<211> 210
<212> PRT
<213> Corynebacterium glutamicum

<400> 98
Met Ser Glu Asn Leu Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg
1 5 10 15

Ile Gln Met Ile Lys Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu
20 25 30

Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
35 40 45

Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
50 55 60

Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
65 70 75 80

Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
85 90 95

Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
100 105 110

Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
115 120 125

Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
130 135 140

Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
145 150 155 160

Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
165 170 175

Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
180 185 190

Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu
195 200 205

Val Thr
210

<210> 99
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>

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<221> CDS
<222> (101)..(1075)
<223> RXN00786

<400> 99
tccttcttcc accagctaaa agtgaattac cccgcctttg tcggggtggt tgcattccca 60

gtctaggtgt ttagcctcaa cgttggatac gctgggaggc atg agc tca cct gtt    115
                                            Met Ser Ser Pro Val
                                            1               5

atc agc ccc gaa acc aaa acc gga aag aag atc ctg ctt gca gcc cct    163
Ile Ser Pro Glu Thr Lys Thr Gly Lys Lys Ile Leu Leu Ala Ala Pro
                10                  15                  20

cgc gga tac tgt gcc ggc gta gac cgt gca gtg gaa acc gtc gag cgc    211
Arg Gly Tyr Cys Ala Gly Val Asp Arg Ala Val Glu Thr Val Glu Arg
            25                  30                  35

gcg ctc gag gaa tac ggc gcc cca att tat gtc cgt aaa gaa atc gtg    259
Ala Leu Glu Glu Tyr Gly Ala Pro Ile Tyr Val Arg Lys Glu Ile Val
        40                  45                  50

cac aac cgt tac gtt gtg gac acc ctg gca gaa aag ggc gcg att ttt    307
His Asn Arg Tyr Val Val Asp Thr Leu Ala Glu Lys Gly Ala Ile Phe
    55                  60                  65

gtc aac gaa gca tct gaa gca cca gaa ggt gcc aac atg gtg ttc tct    355
Val Asn Glu Ala Ser Glu Ala Pro Glu Gly Ala Asn Met Val Phe Ser
70                  75                  80                  85

gca cac ggc gtg agc cca atg gtc cac gaa gaa gct gca gct aaa aac    403
Ala His Gly Val Ser Pro Met Val His Glu Glu Ala Ala Ala Lys Asn
                90                  95                  100

atc aag gct att gac gcg gcc tgc ccg ctg gtc acc aaa gtg cac aag    451
Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val Thr Lys Val His Lys
            105                 110                 115

gaa gtc cag cgc ttt gat aag cag gga ttc cac att ctc ttc atc ggt    499
Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His Ile Leu Phe Ile Gly
        120                 125                 130

cac gaa ggc cat gaa gaa gta gag ggc acc atg ggt cat tcc gtt gag    547
His Glu Gly His Glu Glu Val Glu Gly Thr Met Gly His Ser Val Glu
    135                 140                 145

aaa acc cac ctg gtt gac ggc gtt gct ggc att gcc acc ctg cct gaa    595
Lys Thr His Leu Val Asp Gly Val Ala Gly Ile Ala Thr Leu Pro Glu
150                 155                 160                 165

ttc tta aac gat gaa cca aac ctg atc tgg ctg tct cag acc acg ctt    643
Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu Ser Gln Thr Thr Leu
                170                 175                 180

tct gtg gac gag acc atg gag atc gtc cgc gag ctg aag gtg aag ttc    691
Ser Val Asp Glu Thr Met Glu Ile Val Arg Glu Leu Lys Val Lys Phe
```

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            185                 190                 195

cct cag ctg cag gat cca ccg tca gat gat att tgc tac gcc acg cag      739
Pro Gln Leu Gln Asp Pro Pro Ser Asp Asp Ile Cys Tyr Ala Thr Gln
        200                 205                 210

aac cgc cag gtt gcc gtc aag gct atc gct gag cgc tgc gag ctg atg      787
Asn Arg Gln Val Ala Val Lys Ala Ile Ala Glu Arg Cys Glu Leu Met
    215                 220                 225

att gtg gtc ggt tcc cgc aac tcc tcc aac tcg gtt cgt ctg gtt gag      835
Ile Val Val Gly Ser Arg Asn Ser Ser Asn Ser Val Arg Leu Val Glu
230                 235                 240                 245

gtc gct aag caa aac ggt gcc gat aac gcc tac ctg gtg gat tac gcc      883
Val Ala Lys Gln Asn Gly Ala Asp Asn Ala Tyr Leu Val Asp Tyr Ala
                250                 255                 260

cgc gaa atc gac cca gca tgg ttc gaa ggc gta gag acc atc ggt atc      931
Arg Glu Ile Asp Pro Ala Trp Phe Glu Gly Val Glu Thr Ile Gly Ile
            265                 270                 275

tcc tcc ggc gct tcc gtg cct gag atc ctc gtc cag ggc gtc att gag      979
Ser Ser Gly Ala Ser Val Pro Glu Ile Leu Val Gln Gly Val Ile Glu
        280                 285                 290

cgc ctg gct gag ttc ggc tac gac gac gtc gag gaa gtc acc tcc gcc      1027
Arg Leu Ala Glu Phe Gly Tyr Asp Asp Val Glu Glu Val Thr Ser Ala
    295                 300                 305

gct gag aag att gtt ttc gcg ctg cct cgc gtg ctg cgc cac aag aat      1075
Ala Glu Lys Ile Val Phe Ala Leu Pro Arg Val Leu Arg His Lys Asn
310                 315                 320                 325

taattgcaag aatgaaaaat ccc                                            1098


<210> 100
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 100
Met Ser Ser Pro Val Ile Ser Pro Glu Thr Lys Thr Gly Lys Lys Ile
  1               5                  10                  15

Leu Leu Ala Ala Pro Arg Gly Tyr Cys Ala Gly Val Asp Arg Ala Val
             20                  25                  30

Glu Thr Val Glu Arg Ala Leu Glu Glu Tyr Gly Ala Pro Ile Tyr Val
         35                  40                  45

Arg Lys Glu Ile Val His Asn Arg Tyr Val Val Asp Thr Leu Ala Glu
     50                  55                  60

Lys Gly Ala Ile Phe Val Asn Glu Ala Ser Glu Ala Pro Glu Gly Ala
 65                  70                  75                  80
```

```
Asn Met Val Phe Ser Ala His Gly Val Ser Pro Met Val His Glu Glu
                85                  90                  95

Ala Ala Ala Lys Asn Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val
            100                 105                 110

Thr Lys Val His Lys Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His
        115                 120                 125

Ile Leu Phe Ile Gly His Glu Gly His Glu Glu Val Glu Gly Thr Met
    130                 135                 140

Gly His Ser Val Glu Lys Thr His Leu Val Asp Gly Val Ala Gly Ile
145                 150                 155                 160

Ala Thr Leu Pro Glu Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu
                165                 170                 175

Ser Gln Thr Thr Leu Ser Val Asp Glu Thr Met Glu Ile Val Arg Glu
            180                 185                 190

Leu Lys Val Lys Phe Pro Gln Leu Gln Asp Pro Pro Ser Asp Asp Ile
        195                 200                 205

Cys Tyr Ala Thr Gln Asn Arg Gln Val Ala Val Lys Ala Ile Ala Glu
    210                 215                 220

Arg Cys Glu Leu Met Ile Val Val Gly Ser Arg Asn Ser Ser Asn Ser
225                 230                 235                 240

Val Arg Leu Val Glu Val Ala Lys Gln Asn Gly Ala Asp Asn Ala Tyr
                245                 250                 255

Leu Val Asp Tyr Ala Arg Glu Ile Asp Pro Ala Trp Phe Glu Gly Val
            260                 265                 270

Glu Thr Ile Gly Ile Ser Ser Gly Ala Ser Val Pro Glu Ile Leu Val
        275                 280                 285

Gln Gly Val Ile Glu Arg Leu Ala Glu Phe Gly Tyr Asp Asp Val Glu
    290                 295                 300

Glu Val Thr Ser Ala Ala Glu Lys Ile Val Phe Ala Leu Pro Arg Val
305                 310                 315                 320

Leu Arg His Lys Asn
                325
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<210> 101
<211> 1131
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

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<222> (101)..(1108)
<223> RXS01027

<400> 101
aatagatgga agtagttttt cattcactta tgtgcgcgtt tttaatctgg tttctaccaa 60

gaactgtgtg caccacaacg cggaaggtga atcgcaccca atg gca aat aag aac   115
                                            Met Ala Asn Lys Asn
                                            1               5

aat aag cct cat gag gtg gac aaa gac caa gat tca gcc atg ctg atc   163
Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp Ser Ala Met Leu Ile
                10                  15                  20

aac ggt cgc ctg caa cag atc ccg gcg cgt ccc act gag gaa ttc acc   211
Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro Thr Glu Glu Phe Thr
            25                  30                  35

cgc cca act ctt gca gca ggt gca gta ctg tgg cgc ggc gac atc acc   259
Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp Arg Gly Asp Ile Thr
        40                  45                  50

aac ccg gac agc atc gag gtc gct gtc atc cac cgc ccg cac tat gat   307
Asn Pro Asp Ser Ile Glu Val Ala Val Ile His Arg Pro His Tyr Asp
    55                  60                  65

gac tgg tcc ctg gcc aag ggc aaa gtc gat ccc ggc gag tct att ccg   355
Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro Gly Glu Ser Ile Pro
70                  75                  80                  85

aca acc gcg gcc cgt gaa atc ctt gaa gaa act ggc tac gac atc cgt   403
Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr Gly Tyr Asp Ile Arg
                90                  95                  100

ctg ggc aag ctg atc ggc aag gtt act tac cct gtg ctc gac cga acc   451
Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro Val Leu Asp Arg Thr
            105                 110                 115

aaa gtg gtc tac tac tgg act gcc cag gtt ctt ggt gga gag ttt gtc   499
Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu Gly Gly Glu Phe Val
        120                 125                 130

ccc aac gat gaa gtt gat gaa atc cgt tgg ctg tct gtt gat gaa gca   547
Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu Ser Val Asp Glu Ala
    135                 140                 145

tgc gag ttg ctc agc tac caa gta gat acc gaa gtt ctg gcc aag gca   595
Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu Val Leu Ala Lys Ala
150                 155                 160                 165

gca aag cgt ttc cgc act cct tcc acc act cgg gtg ctg tat gtt cgc   643
Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg Val Leu Tyr Val Arg
                170                 175                 180

cat gct cat gca cat ggt cgc caa acc tgg ggt ggc gac gac aat aag   691
His Ala His Ala His Gly Arg Gln Thr Trp Gly Gly Asp Asp Asn Lys
            185                 190                 195
```

```
cgc cca ttg gac aaa aag ggg cgt cga caa gca gaa atg ctc gta ccc     739
Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala Glu Met Leu Val Pro
        200                 205                 210

atg ttg ttg ccc ttc aaa ccc acc gca att tac tcg gcg gtg ccc gat     787
Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr Ser Ala Val Pro Asp
    215                 220                 225

cgc tgc caa gcc acc gcg ctc ccc ctt gcc gat gag ctc ggc ctc gac     835
Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp Glu Leu Gly Leu Asp
230                 235                 240                 245

gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc     883
Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro
                250                 255                 260

gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg     931
Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val
            265                 270                 275

ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg     979
Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
        280                 285                 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa     1027
Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
    295                 300                 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc     1075
Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
310                 315                 320                 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg tttaaggcct 1128
Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
                330                 335

cca                                                                 1131
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<210> 102
<211> 336
<212> PRT
<213> Corynebacterium glutamicum

<400> 102

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Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp
1               5                   10                  15

Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro
            20                  25                  30

Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp
        35                  40                  45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
    50                  55                  60
```

```
Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
 65                  70                  75                  80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
                 85                  90                  95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
            100                 105                 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
        115                 120                 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
    130                 135                 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
145                 150                 155                 160

Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
                165                 170                 175

Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
            180                 185                 190

Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
        195                 200                 205

Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
    210                 215                 220

Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
225                 230                 235                 240

Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
                245                 250                 255

Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
            260                 265                 270

Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
        275                 280                 285

Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
    290                 295                 300

Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp
305                 310                 315                 320

Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
                325                 330                 335
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<210> 103

<211> 651
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(628)
<223> RXS01528

<400> 103
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cacccaaacc caaacctctc agtcgaataa gcagaagtct caggacaacc gcaggggtaa 60

gggtcgtagg tctccaacca ggaggcgttc caacacgagg gtg aat cag gcg tgg   115
                                            Val Asn Gln Ala Trp
                                             1               5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc   163
Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
                10                  15                  20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat   211
Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
            25                  30                  35

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt   259
Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
        40                  45                  50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat   307
Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp
    55                  60                  65

aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac   355
Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
70                  75                  80                  85

ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg   403
Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
                90                  95                  100

gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat   451
Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
            105                 110                 115

gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg   499
Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
        120                 125                 130

tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag   547
Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
    135                 140                 145

cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg   595
Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
150                 155                 160                 165

aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaacccg 648
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Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
170 175

aac 651

<210> 104
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 104
Val Asn Gln Ala Trp Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr
1 5 10 15

Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
20 25 30

Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
35 40 45

Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
50 55 60

Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
65 70 75 80

Glu Thr Gly Ile His Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp
85 90 95

Tyr Trp Phe Val Ser Glu Gly Lys Arg Ile His Lys Thr Val His His
100 105 110

His Leu Leu Arg Tyr Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu
115 120 125

Val Thr Glu Val Ala Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu
130 135 140

Ala Phe Ala Asp Glu Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu
145 150 155 160

Pro Glu Phe Ala Leu Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
165 170 175

<210> 105
<211> 509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(486)

<223> RXS01716

<400> 105
gaa gtc act cct gag gga ttc aaa gag atc acc cgt gaa aac acc atc 48
Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile
1 5 10 15

gtt cgc ctg ggc aaa ggc gtc gac gcc acc ggt cag cta gac ccc gag 96
Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu
20 25 30

gca atc gag cgc act cgt gtc gct ttg gaa aac tac gtt gaa ctc atg 144
Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met
35 40 45

gaa acc cat ggg gta gag gcc gta cga atg gtt gcc acc tcc gca acc 192
Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr
50 55 60

cgc gat gcg tcc aac cgc gat gaa ttc ttt tcg atg acc cgc cag ctt 240
Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu
65 70 75 80

ctg tcc aag atc cgt cct gga tac caa gct gaa gta att tcc ggc gaa 288
Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu
85 90 95

gag gaa gct ctg ctg tcc ttc cga ggt gca atc gtt gac ctg cct gaa 336
Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu
100 105 110

gac caa ggt cct ttc tgt gtt atc gac ctt ggc ggt gga tcc act gag 384
Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu
115 120 125

ttc atc gtt ggc acc tac gac ggt gaa atc cta ggc tcc cac tca acc 432
Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr
130 135 140

caa atg gga tgc gtg cgc ctg acc gaa cga atc atg cgc agc gac cca 480
Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
145 150 155 160

ccc gac tgaaaccgaa gtggaaatcg ccc 509
Pro Asp

<210> 106
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 106
Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile
1 5 10 15

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Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu
            20                  25                  30

Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met
        35                  40                  45

Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr
    50                  55                  60

Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu
65                  70                  75                  80

Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu
                85                  90                  95

Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu
            100                 105                 110

Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu
        115                 120                 125

Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr
    130                 135                 140

Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
145                 150                 155                 160

Pro Asp


<210> 107
<211> 654
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(631)
<223> RXS01835

<400> 107
tcaacatcta ttcctcctgc gatttgcatg ggatatatat taaaaattct agccgaaagt    60

ttcctgcgtg aatacacttt ccccgcgcct tcgcaaagct atg aat act gcc gcg    115
                                            Met Asn Thr Ala Ala
                                            1               5

tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc    163
Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val
                10                  15                  20

agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat    211
Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp
            25                  30                  35

gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta    259
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Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
        40                  45                  50

ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg     307
Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
    55                  60                  65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg     355
Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
70                  75                  80                  85

aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc     403
Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
                90                  95                  100

tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg     451
Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met
            105                 110                 115

tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc     499
Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg
        120                 125                 130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat     547
Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
    135                 140                 145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg     595
Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
150                 155                 160                 165

ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg          641
Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala
                170                 175

gcggcgtcga taa                                                      654


<210> 108
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 108
Met Asn Thr Ala Ala Trp Ala His Arg His His Val Arg Lys Gly Gly
 1               5                  10                  15

Gly Ile Pro Tyr Val Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala
            20                  25                  30

Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp
        35                  40                  45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
    50                  55                  60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln
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65 70 75 80

Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu
85 90 95

Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys
100 105 110

Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu
115 120 125

Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp
130 135 140

Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu
145 150 155 160

Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser
165 170 175

Ala

<210> 109
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> RXS02497

<400> 109
tcgatgccgc cgctggcgaa gactcgggga aacctaaaaa taccgaagaa gaatttgacc 60

gattcacact ttgccaccct agaccgtcta acctttaggt gtg aga tta ggt gta 115
Val Arg Leu Gly Val
1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
55 60 65

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ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc     355
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser
 70                  75                  80                  85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc     403
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly
                 90                  95                 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc     451
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe
            105                 110                 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac     499
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn
        120                 125                 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa     547
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu
    135                 140                 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc     595
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr
150                 155                 160                 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc     643
His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu
                170                 175                 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg     691
Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met
            185                 190                 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc     739
Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe
        200                 205                 210

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca     787
Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro
    215                 220                 225

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca     835
His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
230                 235                 240                 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc     883
Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
                250                 255                 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa     931
Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
            265                 270                 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg     979
Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
        280                 285                 290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag    1027
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Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
295 300 305

taacatttac ccggaaagga gtt 1050

<210> 110
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 110
Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
1 5 10 15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
65 70 75 80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
85 90 95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
100 105 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
115 120 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
130 135 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
145 150 155 160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
165 170 175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
180 185 190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
195 200 205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
210 215 220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
225 230 235 240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
245 250 255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
260 265 270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
275 280 285

Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
290 295 300

Asp Lys Gly Leu Glu
305

<210> 111
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(511)
<223> RXS02972

<400> 111
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gaacgaatca tgcgcagcga cccacccgac tgaaaccgaa gtg gaa atc gcc cgc 115
Val Glu Ile Ala Arg
1 5

gac tac gtt gca gaa cgc atc cag gaa gta aaa gcc atc gtc cca att 163
Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys Ala Ile Val Pro Ile
10 15 20

tca aag gca aaa acc ttt gtg gga tgc gca ggc acc ttc acc aca atc 211
Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly Thr Phe Thr Thr Ile
25 30 35

tcc gcc tgg gtg caa ggc cta gaa agc tac gac cgc gac gcg atc cac 259
Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp Arg Asp Ala Ile His
40 45 50

ctc tct gca ctc aac ttc gat gca ctg cga gtt gtc acc gat gag atc 307
Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val Val Thr Asp Glu Ile
55 60 65

att tca gaa tca tca tca cag cgc gcc agc aac cca gtt gtt gat cca 355
Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn Pro Val Val Asp Pro
70 75 80 85

ggt cgc gcc gac gtc atc ggt ggc gga tcc gtt gtt gtc caa gca gcg 403
Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val Val Val Gln Ala Ala
90 95 100

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atc gac tta gcc tcc aaa gaa gcc ggt gta gac tac atc att att tcc    451
Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp Tyr Ile Ile Ile Ser
            105                 110                 115

gaa aaa gac atc ctc gac ggc ctc atc ctt ggc ctg gta gaa gcc gac    499
Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly Leu Val Glu Ala Asp
        120                 125                 130

tct ttg aag aaa taggacccta gttttaaacc act                           534
Ser Leu Lys Lys
    135


<210> 112
<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 112
Val Glu Ile Ala Arg Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys
 1               5                  10                  15

Ala Ile Val Pro Ile Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly
            20                  25                  30

Thr Phe Thr Thr Ile Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp
        35                  40                  45

Arg Asp Ala Ile His Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val
    50                  55                  60

Val Thr Asp Glu Ile Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn
65                  70                  75                  80

Pro Val Val Asp Pro Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val
                85                  90                  95

Val Val Gln Ala Ala Ile Asp Leu Ala Ser Lys Glu Ala Gly Val Asp
            100                 105                 110

Tyr Ile Ile Ile Ser Glu Lys Asp Ile Leu Asp Gly Leu Ile Leu Gly
        115                 120                 125

Leu Val Glu Ala Asp Ser Leu Lys Lys
    130                 135


<210> 113
<211> 636
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(613)
<223> RXA02159
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<400> 113
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actgctggtg tggctgctgg ccaaccagcc gaggtaagac atg tcc ctt ggc tca 115
Met Ser Leu Gly Ser
1 5

acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163
Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg
10 15 20

caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag 211
Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln
25 30 35

gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259
Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln
40 45 50

gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc 307
Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg
55 60 65

ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355
Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile
70 75 80 85

gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt 403
Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu
90 95 100

gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451
Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu
105 110 115

cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg 499
Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg
120 125 130

gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547
Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val
135 140 145

ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595
Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu
150 155 160 165

ctc agc ggg cgc acc act taaagcgccc ctagttcaag gct 636
Leu Ser Gly Arg Thr Thr
170

<210> 114
<211> 171
<212> PRT
<213> Corynebacterium glutamicum

<400> 114
Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val
1   5   10   15

Thr Arg Thr Ala Arg Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln
            20   25   30

Lys Val Thr Ser Gln Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly
        35   40   45

Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly
    50   55   60

Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly
65   70   75   80

Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys
                85   90   95

Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly
            100   105   110

Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala
        115   120   125

Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala
    130   135   140

Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys
145   150   155   160

Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr
                165   170

<210> 115
<211> 486
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(463)
<223> RXA02201

<400> 115
tctaccagcc aaatcatcaa ctcatagcga aggaatcaac ttcatgaata atcaaccatc 60

agtacttttc gtttgcgtcg gcaatggtgg aaaatctcaa atg gcc gca gcg cta 115
                                            Met Ala Ala Ala Leu
                                            1   5

gcc aaa aaa cat gcc ggg gac gct ctc aaa gtt tat tca gct ggc aca 163
Ala Lys Lys His Ala Gly Asp Ala Leu Lys Val Tyr Ser Ala Gly Thr
                10   15   20

aag cca ggt acg aaa tta aat caa cag tcc ctt gat tcc att gct gaa 211

Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu Asp Ser Ile Ala Glu
25 30 35

gtt ggc gca gat atg tct caa ggg ttt cca aag ggc att gac cag gag 259
Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys Gly Ile Asp Gln Glu
40 45 50

tta att aag cga gta gac cgc gtg gtc att ctt ggt gcc gaa gct caa 307
Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu Gly Ala Glu Ala Gln
55 60 65

cta gaa atg cct atc gat gca aac ggc ata cta cag cgc tgg gta act 355
Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu Gln Arg Trp Val Thr
70 75 80 85

gac gaa ccc tct gaa cgt gga att gaa ggt atg gaa cgc atg cgc ctg 403
Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met Glu Arg Met Arg Leu
90 95 100

gtc cga gat gat att gac gcc cga gtc caa aac ctc gtc gct gaa cta 451
Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn Leu Val Ala Glu Leu
105 110 115

acc caa aac gca tagcagtttt ctaatctcac aca 486
Thr Gln Asn Ala
120

<210> 116
<211> 121
<212> PRT
<213> Corynebacterium glutamicum

<400> 116
Met Ala Ala Ala Leu Ala Lys Lys His Ala Gly Asp Ala Leu Lys Val
1 5 10 15

Tyr Ser Ala Gly Thr Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu
20 25 30

Asp Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys
35 40 45

Gly Ile Asp Gln Glu Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu
50 55 60

Gly Ala Glu Ala Gln Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu
65 70 75 80

Gln Arg Trp Val Thr Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met
85 90 95

Glu Arg Met Arg Leu Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn
100 105 110

Leu Val Ala Glu Leu Thr Gln Asn Ala
115 120

<210> 117
<211> 510
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> RXA00599

<400> 117
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gaacgatcgg ccctttgatt gaagtcccag tattagtcgg attggtttat gtcatgttgt 60

ggcttggacc aaaaatcttt aaaaaggaga atgcaggatc atg aaa tca gtt ttg   115
                                            Met Lys Ser Val Leu
                                             1               5

ttt gtg tgc gtc ggt aat ggc gga aaa tca cag atg gcg gcg gcg ctg   163
Phe Val Cys Val Gly Asn Gly Gly Lys Ser Gln Met Ala Ala Ala Leu
                 10                  15                  20

gca cag aag tat gca tca gat tca gta gag atc cat tct gct gga acc   211
Ala Gln Lys Tyr Ala Ser Asp Ser Val Glu Ile His Ser Ala Gly Thr
             25                  30                  35

aag cct gca cag ggg cta aac caa ttg tct gtg gaa tcc atc gct gag   259
Lys Pro Ala Gln Gly Leu Asn Gln Leu Ser Val Glu Ser Ile Ala Glu
         40                  45                  50

gtg ggc gct gat atg tcg caa gga att ccc aaa gcg atc gat ccg gag   307
Val Gly Ala Asp Met Ser Gln Gly Ile Pro Lys Ala Ile Asp Pro Glu
     55                  60                  65

ctg ctg cgc act gtc gat cgt gtg gtt att ttg ggc gat gac gca cag   355
Leu Leu Arg Thr Val Asp Arg Val Val Ile Leu Gly Asp Asp Ala Gln
 70                  75                  80                  85

gta gat atg cct gaa tct gca cag ggc gct ctt gag cgt tgg tca att   403
Val Asp Met Pro Glu Ser Ala Gln Gly Ala Leu Glu Arg Trp Ser Ile
                 90                  95                 100

gag gaa ccg gat gct caa ggt atg gaa cgt atg cgt att gtg cgg gat   451
Glu Glu Pro Asp Ala Gln Gly Met Glu Arg Met Arg Ile Val Arg Asp
            105                 110                 115

cag atc gat aac cga gtc caa gct ttg cta gcg gga taagcgccga        497
Gln Ile Asp Asn Arg Val Gln Ala Leu Leu Ala Gly
        120                 125

aaaaggggca tgt                                                    510
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<210> 118
<211> 129
<212> PRT

<213> Corynebacterium glutamicum

<400> 118
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Met Lys Ser Val Leu Phe Val Cys Val Gly Asn Gly Gly Lys Ser Gln
1               5                   10                  15

Met Ala Ala Ala Leu Ala Gln Lys Tyr Ala Ser Asp Ser Val Glu Ile
            20                  25                  30

His Ser Ala Gly Thr Lys Pro Ala Gln Gly Leu Asn Gln Leu Ser Val
        35                  40                  45

Glu Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Ile Pro Lys
    50                  55                  60

Ala Ile Asp Pro Glu Leu Leu Arg Thr Val Asp Arg Val Val Ile Leu
65                  70                  75                  80

Gly Asp Asp Ala Gln Val Asp Met Pro Glu Ser Ala Gln Gly Ala Leu
                85                  90                  95

Glu Arg Trp Ser Ile Glu Glu Pro Asp Ala Gln Gly Met Glu Arg Met
            100                 105                 110

Arg Ile Val Arg Asp Gln Ile Asp Asn Arg Val Gln Ala Leu Leu Ala
        115                 120                 125

Gly
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<210> 119
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA00600

<400> 119
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cggagttaat gagcggtagg tggatgggtg cggtcatgtc cgtcattata tattgacgca 60

catcgatatt gaaggtattt ttatatcggc aaacatcaat atg att gaa ggc tgg   115
                                           Met Ile Glu Gly Trp
                                           1               5

ctc atg acc ctt act aaa gag cat tcg aca cct cga gcg gct ggc tca   163
Leu Met Thr Leu Thr Lys Glu His Ser Thr Pro Arg Ala Ala Gly Ser
                10                  15                  20

atg tcg ttt ctt gac cgc tgg tta gct gcc tgg att ttc ttg gct atg   211
Met Ser Phe Leu Asp Arg Trp Leu Ala Ala Trp Ile Phe Leu Ala Met
            25                  30                  35

gct gct ggg ttg tta atc ggc aag gtc ttt cca gga att ggg gcg ctt   259
```

```
Ala Ala Gly Leu Leu Ile Gly Lys Val Phe Pro Gly Ile Gly Ala Leu
        40                  45                  50

ttg agc gcg gtg gaa att ggt gga att tcc att cca att gct atc ggt     307
Leu Ser Ala Val Glu Ile Gly Gly Ile Ser Ile Pro Ile Ala Ile Gly
    55                  60                  65

ttg atc gtc atg atg tat cca cct ttg gcc aag gtg cgc tac gac aaa     355
Leu Ile Val Met Met Tyr Pro Pro Leu Ala Lys Val Arg Tyr Asp Lys
70                  75                  80                  85

act aaa gaa atc agc aca gac cgc gct ctc atg gtg gtg tcg att atg     403
Thr Lys Glu Ile Ser Thr Asp Arg Ala Leu Met Val Val Ser Ile Met
                90                  95                  100

ttg aac tgg atc gtt gga cca gca ctt atg ttt agc ctg gcg tgg ctg     451
Leu Asn Trp Ile Val Gly Pro Ala Leu Met Phe Ser Leu Ala Trp Leu
            105                 110                 115

ttt ctt cca gat caa cca gag ctt cgc act ggg cta att atc gtg ggc     499
Phe Leu Pro Asp Gln Pro Glu Leu Arg Thr Gly Leu Ile Ile Val Gly
        120                 125                 130

ctt gcg cgc tgt atc gcg atg gtt ttg gta tgg agt gat ctc gct tgt     547
Leu Ala Arg Cys Ile Ala Met Val Leu Val Trp Ser Asp Leu Ala Cys
    135                 140                 145

ggt gac cgg gaa gca act gct gtg ctg gtt gca atc aac tcg gtg ttc     595
Gly Asp Arg Glu Ala Thr Ala Val Leu Val Ala Ile Asn Ser Val Phe
150                 155                 160                 165

cag atc ctt atg ttc ggt gtg ctt ggt tgg ttt tac ctg cag att ctt     643
Gln Ile Leu Met Phe Gly Val Leu Gly Trp Phe Tyr Leu Gln Ile Leu
                170                 175                 180

ccc tcg tgg ctg gga tta gac acc acg tcg gtg act ttc tct gtg gta     691
Pro Ser Trp Leu Gly Leu Asp Thr Thr Ser Val Thr Phe Ser Val Val
            185                 190                 195

tca atc gtg act tcc gtt ctc gtg ttc ttg ggc ata cca ctt gta gct     739
Ser Ile Val Thr Ser Val Leu Val Phe Leu Gly Ile Pro Leu Val Ala
        200                 205                 210

gga gtt tta tct cgc gtc att ggt gaa aaa aca aag gga cgg cgc tgg     787
Gly Val Leu Ser Arg Val Ile Gly Glu Lys Thr Lys Gly Arg Arg Trp
    215                 220                 225

tac gag gac acg ttc ctg cct aag att tca ccc ttg gcg ctg att ggc     835
Tyr Glu Asp Thr Phe Leu Pro Lys Ile Ser Pro Leu Ala Leu Ile Gly
230                 235                 240                 245

ttg cta tac aca att gtt ctg ctg ttt tcg ttg cag ggg gat gaa atc     883
Leu Leu Tyr Thr Ile Val Leu Leu Phe Ser Leu Gln Gly Asp Glu Ile
                250                 255                 260

aca gcg cag cct tgg aca gta gct cgt ctt gca ttg ccg ctg ctg atg     931
Thr Ala Gln Pro Trp Thr Val Ala Arg Leu Ala Leu Pro Leu Leu Met
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```
            265                 270                 275

tac ttt gtg ggc atg ttt ttc att tcc ctg gtg gta tcc aaa ctg tcc    979
Tyr Phe Val Gly Met Phe Phe Ile Ser Leu Val Val Ser Lys Leu Ser
        280                 285                 290

ggg tta act tat gag cga gct gct tcc gtg tct ttt act gca gca gga    1027
Gly Leu Thr Tyr Glu Arg Ala Ala Ser Val Ser Phe Thr Ala Ala Gly
    295                 300                 305

aac aac ttt gaa tta gcg att gcg gta tcg atc gga acc ttt ggt gcg    1075
Asn Asn Phe Glu Leu Ala Ile Ala Val Ser Ile Gly Thr Phe Gly Ala
310                 315                 320                 325

aca tca ccg cag gca tta gct gga acg atc ggc cct ttg att gaa gtc    1123
Thr Ser Pro Gln Ala Leu Ala Gly Thr Ile Gly Pro Leu Ile Glu Val
                330                 335                 340

cca gta tta gtc gga ttg gtt tat gtc atg ttg tgg ctt gga cca aaa    1171
Pro Val Leu Val Gly Leu Val Tyr Val Met Leu Trp Leu Gly Pro Lys
            345                 350                 355

atc ttt aaa aag gag aat gca gga tca tgaaatcagt tttgtttgtg          1218
Ile Phe Lys Lys Glu Asn Ala Gly Ser
        360                 365

tgc                                                                1221


<210> 120
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 120
Met Ile Glu Gly Trp Leu Met Thr Leu Thr Lys Glu His Ser Thr Pro
1               5                   10                  15

Arg Ala Ala Gly Ser Met Ser Phe Leu Asp Arg Trp Leu Ala Ala Trp
            20                  25                  30

Ile Phe Leu Ala Met Ala Ala Gly Leu Leu Ile Gly Lys Val Phe Pro
        35                  40                  45

Gly Ile Gly Ala Leu Leu Ser Ala Val Glu Ile Gly Gly Ile Ser Ile
    50                  55                  60

Pro Ile Ala Ile Gly Leu Ile Val Met Met Tyr Pro Pro Leu Ala Lys
65                  70                  75                  80

Val Arg Tyr Asp Lys Thr Lys Glu Ile Ser Thr Asp Arg Ala Leu Met
                85                  90                  95

Val Val Ser Ile Met Leu Asn Trp Ile Val Gly Pro Ala Leu Met Phe
            100                 105                 110

Ser Leu Ala Trp Leu Phe Leu Pro Asp Gln Pro Glu Leu Arg Thr Gly
```

```
        115                 120                 125

Leu Ile Ile Val Gly Leu Ala Arg Cys Ile Ala Met Val Leu Val Trp
    130                 135                 140

Ser Asp Leu Ala Cys Gly Asp Arg Glu Ala Thr Ala Val Leu Val Ala
145                 150                 155                 160

Ile Asn Ser Val Phe Gln Ile Leu Met Phe Gly Val Leu Gly Trp Phe
                165                 170                 175

Tyr Leu Gln Ile Leu Pro Ser Trp Leu Gly Leu Asp Thr Thr Ser Val
            180                 185                 190

Thr Phe Ser Val Val Ser Ile Val Thr Ser Val Leu Val Phe Leu Gly
        195                 200                 205

Ile Pro Leu Val Ala Gly Val Leu Ser Arg Val Ile Gly Glu Lys Thr
    210                 215                 220

Lys Gly Arg Arg Trp Tyr Glu Asp Thr Phe Leu Pro Lys Ile Ser Pro
225                 230                 235                 240

Leu Ala Leu Ile Gly Leu Leu Tyr Thr Ile Val Leu Leu Phe Ser Leu
                245                 250                 255

Gln Gly Asp Glu Ile Thr Ala Gln Pro Trp Thr Val Ala Arg Leu Ala
            260                 265                 270

Leu Pro Leu Leu Met Tyr Phe Val Gly Met Phe Phe Ile Ser Leu Val
        275                 280                 285

Val Ser Lys Leu Ser Gly Leu Thr Tyr Glu Arg Ala Ala Ser Val Ser
    290                 295                 300

Phe Thr Ala Ala Gly Asn Asn Phe Glu Leu Ala Ile Ala Val Ser Ile
305                 310                 315                 320

Gly Thr Phe Gly Ala Thr Ser Pro Gln Ala Leu Ala Gly Thr Ile Gly
                325                 330                 335

Pro Leu Ile Glu Val Pro Val Leu Val Gly Leu Val Tyr Val Met Leu
            340                 345                 350

Trp Leu Gly Pro Lys Ile Phe Lys Lys Glu Asn Ala Gly Ser
        355                 360                 365
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<210> 121
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1210)
<223> RXA02200

<400> 121
attgtgtgga gagtggtcat aaatccacta tatattgacg aatgtcgata ttgaaagtat 60

tttgaatatc gacaggtatc aatataccga aaggtgtcgc atg aca aac tca act 115
Met Thr Asn Ser Thr
1 5

cag acg cgg gcc aag cca gcc cga atc tca ttt ctt gat aaa tac att 163
Gln Thr Arg Ala Lys Pro Ala Arg Ile Ser Phe Leu Asp Lys Tyr Ile
10 15 20

cca ctt tgg att att ttg gcg atg gcg ttt ggg cta ttt tta ggc cgg 211
Pro Leu Trp Ile Ile Leu Ala Met Ala Phe Gly Leu Phe Leu Gly Arg
25 30 35

agc gtt tcg gga ctc tca ggc ttt cta ggc gca atg gaa gtc gga ggg 259
Ser Val Ser Gly Leu Ser Gly Phe Leu Gly Ala Met Glu Val Gly Gly
40 45 50

atc tcc ttg cca atc gct tta ggc ctc ctt gta atg atg tac cca ccg 307
Ile Ser Leu Pro Ile Ala Leu Gly Leu Leu Val Met Met Tyr Pro Pro
55 60 65

ttg gcc aaa gtt cgg tat gac aaa act aaa caa att gcc act gat aag 355
Leu Ala Lys Val Arg Tyr Asp Lys Thr Lys Gln Ile Ala Thr Asp Lys
70 75 80 85

cat ttg atg ggc gtg tca ctc att ctc aat tgg gtg gtg ggt cct gcc 403
His Leu Met Gly Val Ser Leu Ile Leu Asn Trp Val Val Gly Pro Ala
90 95 100

tta atg ttc gcg cta gct tgg ttg ttc ctc cca gac caa ccg gaa tta 451
Leu Met Phe Ala Leu Ala Trp Leu Phe Leu Pro Asp Gln Pro Glu Leu
105 110 115

cga acc ggc ctg att att gta gga ctc gca cga tgt att gcg atg gtc 499
Arg Thr Gly Leu Ile Ile Val Gly Leu Ala Arg Cys Ile Ala Met Val
120 125 130

ttg gtt tgg tct gat atg tcc tgt gga gac cgc gag gct aca gca gtt 547
Leu Val Trp Ser Asp Met Ser Cys Gly Asp Arg Glu Ala Thr Ala Val
135 140 145

ctc gta gcc att aat tca gtt ttt caa gtc gca atg ttt ggt gca ctt 595
Leu Val Ala Ile Asn Ser Val Phe Gln Val Ala Met Phe Gly Ala Leu
150 155 160 165

ggc tgg ttc tat ctg caa gtt tta cca tcc tgg cta gga tta cca act 643
Gly Trp Phe Tyr Leu Gln Val Leu Pro Ser Trp Leu Gly Leu Pro Thr
170 175 180

acc acc gct caa ttc tct ttc tgg tca att gtg act tcg gtt ttg gtg 691
Thr Thr Ala Gln Phe Ser Phe Trp Ser Ile Val Thr Ser Val Leu Val
185 190 195

ttc ctc gga ata cct cta ctt gct gga gtt ttc tcg cga att att ggc 739

Phe Leu Gly Ile Pro Leu Leu Ala Gly Val Phe Ser Arg Ile Ile Gly
200 205 210

gaa aag atc aag gga cgt gag tgg tat gaa caa aag ttc ctt ccg gca 787
Glu Lys Ile Lys Gly Arg Glu Trp Tyr Glu Gln Lys Phe Leu Pro Ala
215 220 225

atc tct cca ttt gca cta atc ggt ctg ctt tat acg atc gtc ttg ttg 835
Ile Ser Pro Phe Ala Leu Ile Gly Leu Leu Tyr Thr Ile Val Leu Leu
230 235 240 245

ttt tca ttg caa ggt gat cag atc gtc tct caa cca tgg gct gta gtt 883
Phe Ser Leu Gln Gly Asp Gln Ile Val Ser Gln Pro Trp Ala Val Val
250 255 260

cgt ctc gcg ata cca ttg gtt atc tat ttc gtt gga atg ttt ttc att 931
Arg Leu Ala Ile Pro Leu Val Ile Tyr Phe Val Gly Met Phe Phe Ile
265 270 275

tca ctc att gcg tca aaa cta tct ggc atg aac tat gca aag tct gca 979
Ser Leu Ile Ala Ser Lys Leu Ser Gly Met Asn Tyr Ala Lys Ser Ala
280 285 290

tcc gtc tct ttc act gca gct ggc aac aat ttt gaa ctt gcg att gcg 1027
Ser Val Ser Phe Thr Ala Ala Gly Asn Asn Phe Glu Leu Ala Ile Ala
295 300 305

gtg tcg atc gga acg ttt ggc gca act tct gca cag gct atg gca gga 1075
Val Ser Ile Gly Thr Phe Gly Ala Thr Ser Ala Gln Ala Met Ala Gly
310 315 320 325

acg att ggt ccc ttg att gaa att cca gta ctt gtc ggc ttg gtc tac 1123
Thr Ile Gly Pro Leu Ile Glu Ile Pro Val Leu Val Gly Leu Val Tyr
330 335 340

gcc atg ctg tgg cta ggc ccc aag ttg ttc cca aat gac ccc acg ctg 1171
Ala Met Leu Trp Leu Gly Pro Lys Leu Phe Pro Asn Asp Pro Thr Leu
345 350 355

cca tca tca gct cgt tct acc agc caa atc atc aac tca tagcgaagga 1220
Pro Ser Ser Ala Arg Ser Thr Ser Gln Ile Ile Asn Ser
360 365 370

atcaacttca tga 1233

<210> 122
<211> 370
<212> PRT
<213> Corynebacterium glutamicum

<400> 122
Met Thr Asn Ser Thr Gln Thr Arg Ala Lys Pro Ala Arg Ile Ser Phe
1 5 10 15

Leu Asp Lys Tyr Ile Pro Leu Trp Ile Ile Leu Ala Met Ala Phe Gly
20 25 30

Leu Phe Leu Gly Arg Ser Val Ser Gly Leu Ser Gly Phe Leu Gly Ala
35 40 45

Met Glu Val Gly Gly Ile Ser Leu Pro Ile Ala Leu Gly Leu Leu Val
50 55 60

Met Met Tyr Pro Pro Leu Ala Lys Val Arg Tyr Asp Lys Thr Lys Gln
65 70 75 80

Ile Ala Thr Asp Lys His Leu Met Gly Val Ser Leu Ile Leu Asn Trp
85 90 95

Val Val Gly Pro Ala Leu Met Phe Ala Leu Ala Trp Leu Phe Leu Pro
100 105 110

Asp Gln Pro Glu Leu Arg Thr Gly Leu Ile Ile Val Gly Leu Ala Arg
115 120 125

Cys Ile Ala Met Val Leu Val Trp Ser Asp Met Ser Cys Gly Asp Arg
130 135 140

Glu Ala Thr Ala Val Leu Val Ala Ile Asn Ser Val Phe Gln Val Ala
145 150 155 160

Met Phe Gly Ala Leu Gly Trp Phe Tyr Leu Gln Val Leu Pro Ser Trp
165 170 175

Leu Gly Leu Pro Thr Thr Thr Ala Gln Phe Ser Phe Trp Ser Ile Val
180 185 190

Thr Ser Val Leu Val Phe Leu Gly Ile Pro Leu Leu Ala Gly Val Phe
195 200 205

Ser Arg Ile Ile Gly Glu Lys Ile Lys Gly Arg Glu Trp Tyr Glu Gln
210 215 220

Lys Phe Leu Pro Ala Ile Ser Pro Phe Ala Leu Ile Gly Leu Leu Tyr
225 230 235 240

Thr Ile Val Leu Leu Phe Ser Leu Gln Gly Asp Gln Ile Val Ser Gln
245 250 255

Pro Trp Ala Val Val Arg Leu Ala Ile Pro Leu Val Ile Tyr Phe Val
260 265 270

Gly Met Phe Phe Ile Ser Leu Ile Ala Ser Lys Leu Ser Gly Met Asn
275 280 285

Tyr Ala Lys Ser Ala Ser Val Ser Phe Thr Ala Ala Gly Asn Asn Phe
290 295 300

Glu Leu Ala Ile Ala Val Ser Ile Gly Thr Phe Gly Ala Thr Ser Ala
305 310 315 320

Gln Ala Met Ala Gly Thr Ile Gly Pro Leu Ile Glu Ile Pro Val Leu
325 330 335

Val Gly Leu Val Tyr Ala Met Leu Trp Leu Gly Pro Lys Leu Phe Pro
340 345 350

Asn Asp Pro Thr Leu Pro Ser Ser Ala Arg Ser Thr Ser Gln Ile Ile
355 360 365

Asn Ser
370

<210> 123
<211> 762
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(739)
<223> RXA02202

<400> 123
cgctgaacta acccaaaacg catagcagtt ttctaatctc acacatcttc aacaccgtta 60

aatctattgg tttccccgta aaatcttcga aaggaagaac atg acc ggg caa gct 115
Met Thr Gly Gln Ala
1 5

gca cca aac ttg cat acc aat att ttg aac cgt atc gca aat gaa ctg 163
Ala Pro Asn Leu His Thr Asn Ile Leu Asn Arg Ile Ala Asn Glu Leu
10 15 20

gcg ttg acc tat caa gga gtt ttc tct gca gag act atc aac cgc tat 211
Ala Leu Thr Tyr Gln Gly Val Phe Ser Ala Glu Thr Ile Asn Arg Tyr
25 30 35

att ttt gaa tcg tat gtg tcg ttg gcg aga aca gca aaa atc cat acg 259
Ile Phe Glu Ser Tyr Val Ser Leu Ala Arg Thr Ala Lys Ile His Thr
40 45 50

cac ctg cca att ttg gca gaa ggt ttt gct aaa gac cgg ctg cac gca 307
His Leu Pro Ile Leu Ala Glu Gly Phe Ala Lys Asp Arg Leu His Ala
55 60 65

ctt gcg gta gct gaa ggt aag gtg gct tca cct gtg cct cag gtc cta 355
Leu Ala Val Ala Glu Gly Lys Val Ala Ser Pro Val Pro Gln Val Leu
70 75 80 85

ttt att tgc gtc cac aac gca ggt cgt tca caa att gct tcg gcg ttg 403
Phe Ile Cys Val His Asn Ala Gly Arg Ser Gln Ile Ala Ser Ala Leu
90 95 100

ttg tct cac tat gcc ggt agt tct gta gag gta cgt tct gca ggt tct 451
Leu Ser His Tyr Ala Gly Ser Ser Val Glu Val Arg Ser Ala Gly Ser
105 110 115

tta cct gct tct gaa att cac cca ctg gtg ttg gaa att ttg tca gag 499

Leu Pro Ala Ser Glu Ile His Pro Leu Val Leu Glu Ile Leu Ser Glu
120 125 130

cga gga gtg aac att tct gat gca ttt ccg aaa ccg cta acc gat gat 547
Arg Gly Val Asn Ile Ser Asp Ala Phe Pro Lys Pro Leu Thr Asp Asp
135 140 145

gtt att cgc gca tct gac tat gtc ata aca atg gga tgt gga gat gtg 595
Val Ile Arg Ala Ser Asp Tyr Val Ile Thr Met Gly Cys Gly Asp Val
150 155 160 165

tgc cca atg tat cca gga aag cac tat ctc gat tgg gag ctc gct gat 643
Cys Pro Met Tyr Pro Gly Lys His Tyr Leu Asp Trp Glu Leu Ala Asp
170 175 180

ccg tca gat gaa ggt gag gac aag ata cag gaa ata att gag gaa att 691
Pro Ser Asp Glu Gly Glu Asp Lys Ile Gln Glu Ile Ile Glu Glu Ile
185 190 195

gac ggt cga atc cgc gag ctt tgg aaa agc att caa tta tcg caa aac 739
Asp Gly Arg Ile Arg Glu Leu Trp Lys Ser Ile Gln Leu Ser Gln Asn
200 205 210

taggcagtca aaggtctggc acc 762

<210> 124
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 124
Met Thr Gly Gln Ala Ala Pro Asn Leu His Thr Asn Ile Leu Asn Arg
1 5 10 15

Ile Ala Asn Glu Leu Ala Leu Thr Tyr Gln Gly Val Phe Ser Ala Glu
20 25 30

Thr Ile Asn Arg Tyr Ile Phe Glu Ser Tyr Val Ser Leu Ala Arg Thr
35 40 45

Ala Lys Ile His Thr His Leu Pro Ile Leu Ala Glu Gly Phe Ala Lys
50 55 60

Asp Arg Leu His Ala Leu Ala Val Ala Glu Gly Lys Val Ala Ser Pro
65 70 75 80

Val Pro Gln Val Leu Phe Ile Cys Val His Asn Ala Gly Arg Ser Gln
85 90 95

Ile Ala Ser Ala Leu Leu Ser His Tyr Ala Gly Ser Ser Val Glu Val
100 105 110

Arg Ser Ala Gly Ser Leu Pro Ala Ser Glu Ile His Pro Leu Val Leu
115 120 125

Glu Ile Leu Ser Glu Arg Gly Val Asn Ile Ser Asp Ala Phe Pro Lys

```
    130                 135                 140

Pro Leu Thr Asp Asp Val Ile Arg Ala Ser Asp Tyr Val Ile Thr Met
145                 150                 155                 160

Gly Cys Gly Asp Val Cys Pro Met Tyr Pro Gly Lys His Tyr Leu Asp
                165                 170                 175

Trp Glu Leu Ala Asp Pro Ser Asp Glu Gly Glu Asp Lys Ile Gln Glu
            180                 185                 190

Ile Ile Glu Glu Ile Asp Gly Arg Ile Arg Glu Leu Trp Lys Ser Ile
        195                 200                 205

Gln Leu Ser Gln Asn
    210


<210> 125
<211> 1002
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(979)
<223> RXA02205

<400> 125
gcccaaaccg agcctggata cccgcaaacc acttgaaccg accattcgct gtttcacgcc 60

caccacacta ctgaggtcat aaggtagtac ggtagatcgg gtg aat gaa gag ata    115
                                          Val Asn Glu Glu Ile
                                          1               5

acc ctc cta gcc gca gca gca gat cct gcc gca act gaa aat att ggc    163
Thr Leu Leu Ala Ala Ala Ala Asp Pro Ala Ala Thr Glu Asn Ile Gly
                10                  15                  20

tgg gta caa acc att gtg ctc tcc atc gtt caa ggc ctc aca gag ttc    211
Trp Val Gln Thr Ile Val Leu Ser Ile Val Gln Gly Leu Thr Glu Phe
            25                  30                  35

ctg ccg atc agc tcc agc gga cac ctc cga atc atc tct gag ctg ttc    259
Leu Pro Ile Ser Ser Ser Gly His Leu Arg Ile Ile Ser Glu Leu Phe
        40                  45                  50

tgg ggt gcc gat gcc ggc gcg tcc ttt acc gcc gtg gtt cag ctt ggt    307
Trp Gly Ala Asp Ala Gly Ala Ser Phe Thr Ala Val Val Gln Leu Gly
    55                  60                  65

acc gaa gcc gca gtg ctg gtg ttt ttt gcc aag gaa atc tgg caa atc    355
Thr Glu Ala Ala Val Leu Val Phe Phe Ala Lys Glu Ile Trp Gln Ile
70                  75                  80                  85

atc aca ggt tgg ttc gct ggc gta ttc aat aag gaa cgc cgc gga ttt    403
Ile Thr Gly Trp Phe Ala Gly Val Phe Asn Lys Glu Arg Arg Gly Phe
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            90                      95                      100

gaa tac cgc atg ggc tgg atg atc att gtt gcc acc att ccc gtc gtg     451
Glu Tyr Arg Met Gly Trp Met Ile Ile Val Ala Thr Ile Pro Val Val
            105                     110                     115

atc ttg ggt gtg ttg ggc aag gac ctg atc cgt gag gcg ctg cga aat     499
Ile Leu Gly Val Leu Gly Lys Asp Leu Ile Arg Glu Ala Leu Arg Asn
        120                     125                     130

atg tgg atc act gca tcc gtg ctg atc ctg ttc tcc ctg gtg ttc att     547
Met Trp Ile Thr Ala Ser Val Leu Ile Leu Phe Ser Leu Val Phe Ile
    135                     140                     145

ttg gcc gag aag atg ggc aag aag gaa cgc gac tac gac aaa ctg acc     595
Leu Ala Glu Lys Met Gly Lys Lys Glu Arg Asp Tyr Asp Lys Leu Thr
150                     155                     160                     165

atg aaa gat gcc atc atc atg ggt ctt gca cag tgt ctt gcg ctg atc     643
Met Lys Asp Ala Ile Ile Met Gly Leu Ala Gln Cys Leu Ala Leu Ile
                170                     175                     180

cct ggc gtg tct cgc tcc ggc ggc acc atc tct gct ggt ttg ttc ctt     691
Pro Gly Val Ser Arg Ser Gly Gly Thr Ile Ser Ala Gly Leu Phe Leu
            185                     190                     195

ggt ctc aag cgt gaa gta gcc acc aag ttc tcc ttc ctg ctg gca atc     739
Gly Leu Lys Arg Glu Val Ala Thr Lys Phe Ser Phe Leu Leu Ala Ile
        200                     205                     210

cct gca gtg ctt ggc tcc ggt ttg tac tcc ctg cct gac gct ttt gcg     787
Pro Ala Val Leu Gly Ser Gly Leu Tyr Ser Leu Pro Asp Ala Phe Ala
    215                     220                     225

cca agc tcc gga caa gct gcc tcc ggc cta cag ctc acc gtg ggt acc     835
Pro Ser Ser Gly Gln Ala Ala Ser Gly Leu Gln Leu Thr Val Gly Thr
230                     235                     240                     245

ctg gtt gcc ttc gta gtt ggc tac att tcc att gcg tgg ctg atg aag     883
Leu Val Ala Phe Val Val Gly Tyr Ile Ser Ile Ala Trp Leu Met Lys
                250                     255                     260

ttc gtg gca aac cac tcc ttc agc tgg ttt gct gca tac cgt att cct     931
Phe Val Ala Asn His Ser Phe Ser Trp Phe Ala Ala Tyr Arg Ile Pro
            265                     270                     275

gca ggt ctg ctc gtg atg ctg ctg ctc gca ctg ggc atg ctc aac cca     979
Ala Gly Leu Leu Val Met Leu Leu Leu Ala Leu Gly Met Leu Asn Pro
        280                     285                     290

taaaattcct gtacatctta aaa                                           1002
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<210> 126
<211> 293
<212> PRT
<213> Corynebacterium glutamicum

<400> 126
Val Asn Glu Glu Ile Thr Leu Leu Ala Ala Ala Ala Asp Pro Ala Ala
1 5 10 15

Thr Glu Asn Ile Gly Trp Val Gln Thr Ile Val Leu Ser Ile Val Gln
20 25 30

Gly Leu Thr Glu Phe Leu Pro Ile Ser Ser Ser Gly His Leu Arg Ile
35 40 45

Ile Ser Glu Leu Phe Trp Gly Ala Asp Ala Gly Ala Ser Phe Thr Ala
50 55 60

Val Val Gln Leu Gly Thr Glu Ala Ala Val Leu Val Phe Phe Ala Lys
65 70 75 80

Glu Ile Trp Gln Ile Ile Thr Gly Trp Phe Ala Gly Val Phe Asn Lys
85 90 95

Glu Arg Arg Gly Phe Glu Tyr Arg Met Gly Trp Met Ile Ile Val Ala
100 105 110

Thr Ile Pro Val Val Ile Leu Gly Val Leu Gly Lys Asp Leu Ile Arg
115 120 125

Glu Ala Leu Arg Asn Met Trp Ile Thr Ala Ser Val Leu Ile Leu Phe
130 135 140

Ser Leu Val Phe Ile Leu Ala Glu Lys Met Gly Lys Lys Glu Arg Asp
145 150 155 160

Tyr Asp Lys Leu Thr Met Lys Asp Ala Ile Ile Met Gly Leu Ala Gln
165 170 175

Cys Leu Ala Leu Ile Pro Gly Val Ser Arg Ser Gly Gly Thr Ile Ser
180 185 190

Ala Gly Leu Phe Leu Gly Leu Lys Arg Glu Val Ala Thr Lys Phe Ser
195 200 205

Phe Leu Leu Ala Ile Pro Ala Val Leu Gly Ser Gly Leu Tyr Ser Leu
210 215 220

Pro Asp Ala Phe Ala Pro Ser Ser Gly Gln Ala Ala Ser Gly Leu Gln
225 230 235 240

Leu Thr Val Gly Thr Leu Val Ala Phe Val Val Gly Tyr Ile Ser Ile
245 250 255

Ala Trp Leu Met Lys Phe Val Ala Asn His Ser Phe Ser Trp Phe Ala
260 265 270

Ala Tyr Arg Ile Pro Ala Gly Leu Leu Val Met Leu Leu Leu Ala Leu
275 280 285

Gly Met Leu Asn Pro

290

<210> 127
<211> 975
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(952)
<223> RXA00900

<400> 127
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tagtgatcgc acgcctggtg caggggcttg gcggcggtgc gtg cgt ggt att gcg 115
Val Arg Gly Ile Ala
1 5

cgc gcg atc gtg cca gac ctt gaa cgc gga caa aag gct gcg cac gcc 163
Arg Ala Ile Val Pro Asp Leu Glu Arg Gly Gln Lys Ala Ala His Ala
10 15 20

ttt gca ctg ctg atg att att cag gga att gct ccc gtg gta gct ccg 211
Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala Pro Val Val Ala Pro
25 30 35

ctc att ggt ggt gtg ctg gtc ggg cct ttt ggc tgg cgg gga att ttc 259
Leu Ile Gly Gly Val Leu Val Gly Pro Phe Gly Trp Arg Gly Ile Phe
40 45 50

tgg gca ctt gca ctg gtg aat ttt gcg cag ctg ctt gtt gct ttg ctg 307
Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu Leu Val Ala Leu Leu
55 60 65

cag att aag gag tcg aag cca gtt gaa gag cgt acc gca gca gga ctt 355
Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg Thr Ala Ala Gly Leu
70 75 80 85

ggc gga atg ctg tcc aac tat gtc ttt gtg ctg aag aat cct caa ttt 403
Gly Gly Met Leu Ser Asn Tyr Val Phe Val Leu Lys Asn Pro Gln Phe
90 95 100

ttg gca tat gta ttc aca ttg ggg ctg tct ttt ggg gcg atg ttc tcc 451
Leu Ala Tyr Val Phe Thr Leu Gly Leu Ser Phe Gly Ala Met Phe Ser
105 110 115

tac att tcg gcg tcg ccg ttc gtg ctg cag aat caa atg ggc att ccg 499
Tyr Ile Ser Ala Ser Pro Phe Val Leu Gln Asn Gln Met Gly Ile Pro
120 125 130

gta ctg ctg tat tcc att att ttc gga gtg aat gct ttt ggt ttg att 547
Val Leu Leu Tyr Ser Ile Ile Phe Gly Val Asn Ala Phe Gly Leu Ile
135 140 145

gtg ggc gga atg gtc aat agg cga ctt ctg cag cgg att cat cca cac 595

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Val Gly Gly Met Val Asn Arg Arg Leu Leu Gln Arg Ile His Pro His
150                 155                 160                 165

cgc atc atg caa act gtg ctg gcc agt ttt act gtg ctg tgt gcg ctt      643
Arg Ile Met Gln Thr Val Leu Ala Ser Phe Thr Val Leu Cys Ala Leu
                170                 175                 180

ttg ctg att gaa gtg ctg ttt att aat tgg ata ccg ctg ttc ctg ttg      691
Leu Leu Ile Glu Val Leu Phe Ile Asn Trp Ile Pro Leu Phe Leu Leu
            185                 190                 195

ctg ctg ttt ctt atc gtt tcc cat att ccg atg gtt atg gct aac gcg      739
Leu Leu Phe Leu Ile Val Ser His Ile Pro Met Val Met Ala Asn Ala
        200                 205                 210

aca gct ctg gga act gaa gtg gtg cga agc agg gcg gga tcg ggt tct      787
Thr Ala Leu Gly Thr Glu Val Val Arg Ser Arg Ala Gly Ser Gly Ser
    215                 220                 225

gca att ttg ggt ttc gtg caa ttc acg atg ggt gct ttg gtg agt tca      835
Ala Ile Leu Gly Phe Val Gln Phe Thr Met Gly Ala Leu Val Ser Ser
230                 235                 240                 245

ctg gtc gga tta ggc tct gat aag gct ttg act atg gga atc gca atg      883
Leu Val Gly Leu Gly Ser Asp Lys Ala Leu Thr Met Gly Ile Ala Met
                250                 255                 260

act gct tgt gca ctg ctg gcg tgt ggg tgt gcg tac ctg gca ggt cga      931
Thr Ala Cys Ala Leu Leu Ala Cys Gly Cys Ala Tyr Leu Ala Gly Arg
            265                 270                 275

aaa ggt att cca gaa atg aag tagctctagg tggcgtttta agg                975
Lys Gly Ile Pro Glu Met Lys
        280


&lt;210&gt; 128
&lt;211&gt; 284
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 128
Val Arg Gly Ile Ala Arg Ala Ile Val Pro Asp Leu Glu Arg Gly Gln
 1               5                  10                  15

Lys Ala Ala His Ala Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala
            20                  25                  30

Pro Val Val Ala Pro Leu Ile Gly Gly Val Leu Val Gly Pro Phe Gly
        35                  40                  45

Trp Arg Gly Ile Phe Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu
    50                  55                  60

Leu Val Ala Leu Leu Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg
65                  70                  75                  80
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Thr Ala Ala Gly Leu Gly Gly Met Leu Ser Asn Tyr Val Phe Val Leu
85 90 95

Lys Asn Pro Gln Phe Leu Ala Tyr Val Phe Thr Leu Gly Leu Ser Phe
100 105 110

Gly Ala Met Phe Ser Tyr Ile Ser Ala Ser Pro Phe Val Leu Gln Asn
115 120 125

Gln Met Gly Ile Pro Val Leu Leu Tyr Ser Ile Ile Phe Gly Val Asn
130 135 140

Ala Phe Gly Leu Ile Val Gly Gly Met Val Asn Arg Arg Leu Leu Gln
145 150 155 160

Arg Ile His Pro His Arg Ile Met Gln Thr Val Leu Ala Ser Phe Thr
165 170 175

Val Leu Cys Ala Leu Leu Leu Ile Glu Val Leu Phe Ile Asn Trp Ile
180 185 190

Pro Leu Phe Leu Leu Leu Leu Phe Leu Ile Val Ser His Ile Pro Met
195 200 205

Val Met Ala Asn Ala Thr Ala Leu Gly Thr Glu Val Val Arg Ser Arg
210 215 220

Ala Gly Ser Gly Ser Ala Ile Leu Gly Phe Val Gln Phe Thr Met Gly
225 230 235 240

Ala Leu Val Ser Ser Leu Val Gly Leu Gly Ser Asp Lys Ala Leu Thr
245 250 255

Met Gly Ile Ala Met Thr Ala Cys Ala Leu Leu Ala Cys Gly Cys Ala
260 265 270

Tyr Leu Ala Gly Arg Lys Gly Ile Pro Glu Met Lys
275 280

<210> 129
<211> 537
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(514)
<223> RXN00901

<400> 129
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aaataccccc aaatcttcga tatagataca cgagacagtg atg cag aaa aaa caa 115
Met Gln Lys Lys Gln
1 5

cag ctg agc acc gcc ctg att atg gga ttg gca tta ttg tca gcc agc 163
Gln Leu Ser Thr Ala Leu Ile Met Gly Leu Ala Leu Leu Ser Ala Ser
10 15 20

tcc gcg cta gcg act gat atg tat ttg ccg gca atg cct ggt att gcg 211
Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala Met Pro Gly Ile Ala
25 30 35

gaa gat ttg ggg aca act gca ccg atg gtg cag tta act ctt tct tcc 259
Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln Leu Thr Leu Ser Ser
40 45 50

ttt atg gct gga atg gcg att ggc caa ttg atc att ggt cct ttg tcg 307
Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile Ile Gly Pro Leu Ser
55 60 65

gat caa ttg gga agg aaa ggc ctg ctc gtt gca ggt gcg gtg gct gcg 355
Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala Gly Ala Val Ala Ala
70 75 80 85

ctg gtc gct agt gtg gtg tgc gcg ctg gcg ccg tcg ata agc gta tta 403
Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro Ser Ile Ser Val Leu
90 95 100

gtg atc gca cgc ctg gtg cag ggg ctt ggc ggc ggt gcg tgc gtg gta 451
Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly Gly Ala Cys Val Val
105 110 115

ttg cgc gcg cga tcg tgc cag acc ttg aac gcg gac aaa agg ctg cgc 499
Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala Asp Lys Arg Leu Arg
120 125 130

acg cct ttg cac tgc tgatgattat tcagggaatt gct 537
Thr Pro Leu His Cys
135

<210> 130
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 130
Met Gln Lys Lys Gln Gln Leu Ser Thr Ala Leu Ile Met Gly Leu Ala
1 5 10 15

Leu Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala
20 25 30

Met Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln
35 40 45

Leu Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile
50 55 60

Ile Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala
65 70 75 80

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Gly Ala Val Ala Ala Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro
                85                  90                  95

Ser Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly
            100                 105                 110

Gly Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala
        115                 120                 125

Asp Lys Arg Leu Arg Thr Pro Leu His Cys
    130                 135


<210> 131
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(478)
<223> FRXA00901

<400> 131
acctgaatga aaatttctaa ttaaaaatac ccccaaatct tcgatataga tacacgagac 60

agtgatgcag aaaaaacaac agctgagcac cgccctgatt atg gga ttg gca tta    115
                                            Met Gly Leu Ala Leu
                                            1               5

ttg tca gcc agc tcc gcg cta gcg act gat atg tat ttg ccg gca atg    163
Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala Met
                10                  15                  20

cct ggt att gcg gaa gat ttg ggg aca act gca ccg atg gtg cag tta    211
Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln Leu
            25                  30                  35

act ctt tct tcc ttt atg gct gga atg gcg att ggc caa ttg atc att    259
Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile Ile
        40                  45                  50

ggt cct ttg tcg gat caa ttg gga agg aaa ggc ctg ctc gtt gca ggt    307
Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala Gly
    55                  60                  65

gcg gtg gct gcg ctg gtc gct agt gtg gtg tgc gcg ctg gcg ccg tcg    355
Ala Val Ala Ala Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro Ser
70                  75                  80                  85

ata agc gta tta gtg atc gca cgc ctg gtg cag ggg ctt ggc ggc ggt    403
Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly Gly
                90                  95                  100

gcg tgc gtg gta ttg cgc gcg cga tcg tgc cag acc ttg aac gcg gac    451
Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala Asp
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105 110 115

aaa agg ctg cgc acg cct ttg cac tgc tgatgattat tcagggaatt 498
Lys Arg Leu Arg Thr Pro Leu His Cys
120 125

gct 501

<210> 132
<211> 126
<212> PRT
<213> Corynebacterium glutamicum

<400> 132
Met Gly Leu Ala Leu Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met
1 5 10 15

Tyr Leu Pro Ala Met Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala
20 25 30

Pro Met Val Gln Leu Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile
35 40 45

Gly Gln Leu Ile Ile Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly
50 55 60

Leu Leu Val Ala Gly Ala Val Ala Ala Leu Val Ala Ser Val Val Cys
65 70 75 80

Ala Leu Ala Pro Ser Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln
85 90 95

Gly Leu Gly Gly Gly Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln
100 105 110

Thr Leu Asn Ala Asp Lys Arg Leu Arg Thr Pro Leu His Cys
115 120 125

<210> 133
<211> 1299
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1276)
<223> RXA00289

<400> 133
cctccccata agttcactca agcaagttct cccgaacaga ttcacccgag aagtcgacag 60

accccattaa acagcccgat tcaagaaagg cttcgcagcc atg agc acc acc acc 115
Met Ser Thr Thr Thr
1 5

gcg ccc gaa gca cgg ttt cct gtc gtc cct ttg acc gcc atg agt ttc 163
Ala Pro Glu Ala Arg Phe Pro Val Val Pro Leu Thr Ala Met Ser Phe
10 15 20

gcg gca ttt gtt tat gtc acg ttc gag atg ttt gca gtt ggc ctc atc 211
Ala Ala Phe Val Tyr Val Thr Phe Glu Met Phe Ala Val Gly Leu Ile
25 30 35

aag ccg atg gcc agc gat ctt gga gtg tca gaa tcc agc atc ggc ctg 259
Lys Pro Met Ala Ser Asp Leu Gly Val Ser Glu Ser Ser Ile Gly Leu
40 45 50

ttg atg act gtg tat gcg act gtc gtt gcc gtg gtg acg atc cct gcc 307
Leu Met Thr Val Tyr Ala Thr Val Val Ala Val Val Thr Ile Pro Ala
55 60 65

atg ttg tgg gtt tct cga ttt aac aag cgc aca gtt ttc ctg att act 355
Met Leu Trp Val Ser Arg Phe Asn Lys Arg Thr Val Phe Leu Ile Thr
70 75 80 85

ctg gca ttt ttg gcc acg ggc att gtt gtt cag gca ctg acc gtt aat 403
Leu Ala Phe Leu Ala Thr Gly Ile Val Val Gln Ala Leu Thr Val Asn
90 95 100

tat gga atg cta gcc atc ggc cgc act atc gca gca ttg act cac ggg 451
Tyr Gly Met Leu Ala Ile Gly Arg Thr Ile Ala Ala Leu Thr His Gly
105 110 115

gtg ttt tgg gca ctt gtt ggg cca atg gca gcg cgt atg tcc cca ggt 499
Val Phe Trp Ala Leu Val Gly Pro Met Ala Ala Arg Met Ser Pro Gly
120 125 130

cac act ggt cgt gca gta ggc gtt gtg tcg att gga tca acc atg gcg 547
His Thr Gly Arg Ala Val Gly Val Val Ser Ile Gly Ser Thr Met Ala
135 140 145

ctg gtc gtt ggt tct ccg ctg gca aca tgg atc ggt gaa ctc atc gga 595
Leu Val Val Gly Ser Pro Leu Ala Thr Trp Ile Gly Glu Leu Ile Gly
150 155 160 165

tgg cgt cct gcc acc tgg att ctt ggt gcg ctg acc att gcg gcc gtg 643
Trp Arg Pro Ala Thr Trp Ile Leu Gly Ala Leu Thr Ile Ala Ala Val
170 175 180

gct gta ctc att cca acc gtt cca tca ctg cca cca ctt cca gac acg 691
Ala Val Leu Ile Pro Thr Val Pro Ser Leu Pro Pro Leu Pro Asp Thr
185 190 195

gaa tca gag tcc aaa gaa aag aaa tcc ctt cca tgg ggt ctc att tcc 739
Glu Ser Glu Ser Lys Glu Lys Lys Ser Leu Pro Trp Gly Leu Ile Ser
200 205 210

ctg gtc att ttc ctt ctc ctt gcc gtc acc ggt gtt ttt gct gcc tac 787
Leu Val Ile Phe Leu Leu Leu Ala Val Thr Gly Val Phe Ala Ala Tyr
215 220 225

acc tac ctt ggc ctc atc atc gct gaa aca gca ggg gac agc ttc gtg 835

Thr Tyr Leu Gly Leu Ile Ile Ala Glu Thr Ala Gly Asp Ser Phe Val
230 235 240 245

tcc att ggc ttg ttc gcc ttc ggt gca ctc gga ctc att ggc gtg aca 883
Ser Ile Gly Leu Phe Ala Phe Gly Ala Leu Gly Leu Ile Gly Val Thr
250 255 260

gtg gca acc cga act gtg gat caa cgc atg ctg cgt gga agt gtt cac 931
Val Ala Thr Arg Thr Val Asp Gln Arg Met Leu Arg Gly Ser Val His
265 270 275

acc acc act ttg ttt gtc att gct gca att ctc gga cag atc gca ttc 979
Thr Thr Thr Leu Phe Val Ile Ala Ala Ile Leu Gly Gln Ile Ala Phe
280 285 290

gga tta gag ggc aca cta gcc gta gta gct atc ttc ctt gca gtc acc 1027
Gly Leu Glu Gly Thr Leu Ala Val Val Ala Ile Phe Leu Ala Val Thr
295 300 305

gtg ttt ggt gga gca tac ggc gct ctc cca acc ctg gga acc acc atc 1075
Val Phe Gly Gly Ala Tyr Gly Ala Leu Pro Thr Leu Gly Thr Thr Ile
310 315 320 325

ttc ctc cat gcg ggt cgc gac cac cca gat act gca tcc tcc att tat 1123
Phe Leu His Ala Gly Arg Asp His Pro Asp Thr Ala Ser Ser Ile Tyr
330 335 340

gtg gtc act tac caa gtg ggt atc gcg tct ggc gcg gca ctt ggc gcg 1171
Val Val Thr Tyr Gln Val Gly Ile Ala Ser Gly Ala Ala Leu Gly Ala
345 350 355

atg gct gtg gat gcc gat tgg gtt gct ggc act ttg tgg atc atg gct 1219
Met Ala Val Asp Ala Asp Trp Val Ala Gly Thr Leu Trp Ile Met Ala
360 365 370

gga ctg tca ttg gct tcc acg ttg gcc ttg gcg ctg tgg tcc cgc ccg 1267
Gly Leu Ser Leu Ala Ser Thr Leu Ala Leu Ala Leu Trp Ser Arg Pro
375 380 385

cta ctg aag tagcagccca aattcagccc act 1299
Leu Leu Lys
390

<210> 134
<211> 392
<212> PRT
<213> Corynebacterium glutamicum

<400> 134
Met Ser Thr Thr Thr Ala Pro Glu Ala Arg Phe Pro Val Val Pro Leu
1 5 10 15

Thr Ala Met Ser Phe Ala Ala Phe Val Tyr Val Thr Phe Glu Met Phe
20 25 30

Ala Val Gly Leu Ile Lys Pro Met Ala Ser Asp Leu Gly Val Ser Glu

35 40 45

Ser Ser Ile Gly Leu Leu Met Thr Val Tyr Ala Thr Val Val Ala Val
50 55 60

Val Thr Ile Pro Ala Met Leu Trp Val Ser Arg Phe Asn Lys Arg Thr
65 70 75 80

Val Phe Leu Ile Thr Leu Ala Phe Leu Ala Thr Gly Ile Val Val Gln
85 90 95

Ala Leu Thr Val Asn Tyr Gly Met Leu Ala Ile Gly Arg Thr Ile Ala
100 105 110

Ala Leu Thr His Gly Val Phe Trp Ala Leu Val Gly Pro Met Ala Ala
115 120 125

Arg Met Ser Pro Gly His Thr Gly Arg Ala Val Gly Val Val Ser Ile
130 135 140

Gly Ser Thr Met Ala Leu Val Val Gly Ser Pro Leu Ala Thr Trp Ile
145 150 155 160

Gly Glu Leu Ile Gly Trp Arg Pro Ala Thr Trp Ile Leu Gly Ala Leu
165 170 175

Thr Ile Ala Ala Val Ala Val Leu Ile Pro Thr Val Pro Ser Leu Pro
180 185 190

Pro Leu Pro Asp Thr Glu Ser Glu Ser Lys Glu Lys Lys Ser Leu Pro
195 200 205

Trp Gly Leu Ile Ser Leu Val Ile Phe Leu Leu Leu Ala Val Thr Gly
210 215 220

Val Phe Ala Ala Tyr Thr Tyr Leu Gly Leu Ile Ile Ala Glu Thr Ala
225 230 235 240

Gly Asp Ser Phe Val Ser Ile Gly Leu Phe Ala Phe Gly Ala Leu Gly
245 250 255

Leu Ile Gly Val Thr Val Ala Thr Arg Thr Val Asp Gln Arg Met Leu
260 265 270

Arg Gly Ser Val His Thr Thr Thr Leu Phe Val Ile Ala Ala Ile Leu
275 280 285

Gly Gln Ile Ala Phe Gly Leu Glu Gly Thr Leu Ala Val Val Ala Ile
290 295 300

Phe Leu Ala Val Thr Val Phe Gly Gly Ala Tyr Gly Ala Leu Pro Thr
305 310 315 320

Leu Gly Thr Thr Ile Phe Leu His Ala Gly Arg Asp His Pro Asp Thr
325 330 335

Ala Ser Ser Ile Tyr Val Val Thr Tyr Gln Val Gly Ile Ala Ser Gly

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        340                 345                 350

Ala Ala Leu Gly Ala Met Ala Val Asp Ala Asp Trp Val Ala Gly Thr
        355                 360                 365

Leu Trp Ile Met Ala Gly Leu Ser Leu Ala Ser Thr Leu Ala Leu Ala
    370                 375                 380

Leu Trp Ser Arg Pro Leu Leu Lys
385                 390


<210> 135
<211> 420
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(397)
<223> RXN01984

<400> 135
aggaaatgtc tcacgtcaca accttttgaa aggtggctaa gtacgcacat ttgttgtctg 60

caatagtgcc ggtgagggag ctgtccgata ttgtgcttac atg cac gaa tct gga    115
                                            Met His Glu Ser Gly
                                            1               5

aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt    163
Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly
                10                  15                  20

ggg cat atc ggc gga cat atc aaa cgc cgc ccg att cct agg caa acg    211
Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr
            25                  30                  35

gaa att tcc gag gtt cgt cga tat atc gtc atg act gcc ctc gca ctc    259
Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu
        40                  45                  50

ggt ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc    307
Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu
    55                  60                  65

agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac    355
Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His
70                  75                  80                  85

atc atc acc atc tac gcc ctc gcg tgg ttg tgg gtg ccc cgc            397
Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp Val Pro Arg
                90                  95

tgatcacagc gtttaccggc aaa                                          420


<210> 136
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<211> 99
<212> PRT
<213> Corynebacterium glutamicum

<400> 136
Met His Glu Ser Gly Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala
1   5   10   15

Pro Gln Gly Arg Gly Gly His Ile Gly Gly His Ile Lys Arg Arg Pro
            20   25   30

Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
        35   40   45

Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
    50   55   60

Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
65   70   75   80

Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp
                85   90   95

Val Pro Arg

<210> 137
<211> 379
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(379)
<223> FRXA01984

<400> 137
aggaaatgtc tcacgtcaca acctttgaa aggtggctaa gtacgcacat ttgttgtctg 60

caatagtgcc ggtgagggag ctgtccgata ttgtgcttac atg cac gaa tct gga 115
Met His Glu Ser Gly
1   5

aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt 163
Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly
            10   15   20

ggg cat atc ggc gga cat atc aaa cgc cgc ccg att cct agg caa acg 211
Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr
            25   30   35

gaa att tcc gag gtt cgt cga tat atc gtc atg act gcc ctc gca ctc 259
Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu
        40   45   50

ggt ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc 307

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Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu
    55                  60                  65

agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac     355
Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His
 70                 75                  80                  85

atc atc acc atc tac gcc ctc gcg                                     379
Ile Ile Thr Ile Tyr Ala Leu Ala
                90


<210> 138
<211> 93
<212> PRT
<213> Corynebacterium glutamicum

<400> 138
Met His Glu Ser Gly Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala
  1               5                  10                  15

Pro Gln Gly Arg Gly Gly His Ile Gly Gly His Ile Lys Arg Arg Pro
             20                  25                  30

Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
        35                  40                  45

Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
    50                  55                  60

Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
 65                  70                  75                  80

Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala
                85                  90


<210> 139
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> RXA00109

<400> 139
aagtggggga agatttcgac aactaaccgg gcgcaaagat gaaactaatg cgtccgacca 60

cggcgaaaag gaagtttcgc ccatctatga gaggttgaat gtg gct tca gag aag    115
                                           Val Ala Ser Glu Lys
                                             1               5

aat cta aaa ttg cgt acc ttg gcg gca gct gct ggg gtg ttg ggc gtt    163
Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala Gly Val Leu Gly Val
                10                  15                  20
```

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ggc gcg atg tcg atg ctc gtg gct ccg cag gct gct gcc cat gat gtg     211
Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala Ala Ala His Asp Val
            25                  30                  35

gtg gtg gat tct aat cct gaa aat ggc agt gtc gtt gat gag ttc ccg     259
Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val Val Asp Glu Phe Pro
        40                  45                  50

gag acc att gag ttg gag ttt tcc ggt att cct cag gat ctg ttc aca     307
Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro Gln Asp Leu Phe Thr
    55                  60                  65

aca gtt gca ttg agc aat gcg gat tcc gga gag gtg tta act tct gga     355
Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu Val Leu Thr Ser Gly
70                  75                  80                  85

act cct cag ctt gag ggg cag cac ttg agc tat gaa gtg cca tct gat     403
Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr Glu Val Pro Ser Asp
                90                  95                  100

gtg cag acg gga gct ggt aac tac att ttg ggt ttc cag atc act tct     451
Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly Phe Gln Ile Thr Ser
            105                 110                 115

tct gat ggt cac gct act aaa ggt tca atc tct ttt gag gtg aca ggc     499
Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser Phe Glu Val Thr Gly
        120                 125                 130

tct gct gaa acg aca aca gag aca aca gca gag acg aca act gag tca     547
Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu Thr Thr Thr Glu Ser
    135                 140                 145

gca gca acc act gac acc tca gag acc acc gaa gca gag aca act gaa     595
Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu Ala Glu Thr Thr Glu
150                 155                 160                 165

act gct gat gaa act tct gga att cct gcg ccg tgg aat tgg gtt ttg     643
Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro Trp Asn Trp Val Leu
                170                 175                 180

agc atc gtg gcg gtg ctt gtt gtt gca agt gcc atc gtc atg atg att     691
Ser Ile Val Ala Val Leu Val Val Ala Ser Ala Ile Val Met Met Ile
            185                 190                 195

gca aag aat cgt aac cag aaa taagagggtt tattcaccat gaa               735
Ala Lys Asn Arg Asn Gln Lys
        200
```

<210> 140
<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 140
Val Ala Ser Glu Lys Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala

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 1               5                   10                  15

Gly Val Leu Gly Val Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala
            20                  25                  30

Ala Ala His Asp Val Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val
        35                  40                  45

Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro
    50                  55                  60

Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu
65                  70                  75                  80

Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr
                85                  90                  95

Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly
            100                 105                 110

Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser
        115                 120                 125

Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu
    130                 135                 140

Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu
145                 150                 155                 160

Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro
                165                 170                 175

Trp Asn Trp Val Leu Ser Ile Val Ala Val Leu Val Val Ala Ser Ala
            180                 185                 190

Ile Val Met Met Ile Ala Lys Asn Arg Asn Gln Lys
        195                 200
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<210> 141
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> RXA00109

<400> 141

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aagtggggga agatttcgac aactaaccgg gcgcaaagat gaaactaatg cgtccgacca 60

cggcgaaaag gaagtttcgc ccatctatga gaggttgaat gtg gct tca gag aag   115
                                           Val Ala Ser Glu Lys
                                           1               5

aat cta aaa ttg cgt acc ttg gcg gca gct gct ggg gtg ttg ggc gtt   163
```

```
Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala Gly Val Leu Gly Val
                10                  15                  20

ggc gcg atg tcg atg ctc gtg gct ccg cag gct gct gcc cat gat gtg      211
Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala Ala Ala His Asp Val
            25                  30                  35

gtg gtg gat tct aat cct gaa aat ggc agt gtc gtt gat gag ttc ccg      259
Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val Val Asp Glu Phe Pro
        40                  45                  50

gag acc att gag ttg gag ttt tcc ggt att cct cag gat ctg ttc aca      307
Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro Gln Asp Leu Phe Thr
    55                  60                  65

aca gtt gca ttg agc aat gcg gat tcc gga gag gtg tta act tct gga      355
Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu Val Leu Thr Ser Gly
70                  75                  80                  85

act cct cag ctt gag ggg cag cac ttg agc tat gaa gtg cca tct gat      403
Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr Glu Val Pro Ser Asp
                90                  95                  100

gtg cag acg gga gct ggt aac tac att ttg ggt ttc cag atc act tct      451
Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly Phe Gln Ile Thr Ser
            105                 110                 115

tct gat ggt cac gct act aaa ggt tca atc tct ttt gag gtg aca ggc      499
Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser Phe Glu Val Thr Gly
        120                 125                 130

tct gct gaa acg aca aca gag aca aca gca gag acg aca act gag tca      547
Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu Thr Thr Thr Glu Ser
    135                 140                 145

gca gca acc act gac acc tca gag acc acc gaa gca gag aca act gaa      595
Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu Ala Glu Thr Thr Glu
150                 155                 160                 165

act gct gat gaa act tct gga att cct gcg ccg tgg aat tgg gtt ttg      643
Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro Trp Asn Trp Val Leu
                170                 175                 180

agc atc gtg gcg gtg ctt gtt gtt gca agt gcc atc gtc atg atg att      691
Ser Ile Val Ala Val Leu Val Val Ala Ser Ala Ile Val Met Met Ile
            185                 190                 195

gca aag aat cgt aac cag aaa taagagggtt tattcaccat gaa                735
Ala Lys Asn Arg Asn Gln Lys
        200
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<210> 142
<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 142
Val Ala Ser Glu Lys Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala
1 5 10 15

Gly Val Leu Gly Val Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala
20 25 30

Ala Ala His Asp Val Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val
35 40 45

Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro
50 55 60

Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu
65 70 75 80

Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr
85 90 95

Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly
100 105 110

Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser
115 120 125

Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu
130 135 140

Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu
145 150 155 160

Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro
165 170 175

Trp Asn Trp Val Leu Ser Ile Val Ala Val Leu Val Val Ala Ser Ala
180 185 190

Ile Val Met Met Ile Ala Lys Asn Arg Asn Gln Lys
195 200

<210> 143
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXA00996

<400> 143
atcttaagcc ttttgtccaa ggctctgagt tcttagtggc ggtatttacc aagaagtaac 60

acctctatct tgcacctgat ctggcgtaga ctcataagtt atg agc acc gta acg 115
Met Ser Thr Val Thr
1 5

```
gca gtg cag gtc aac ggc cta aaa gtt tcc ata tcg tcc ggt ttt tca     163
Ala Val Gln Val Asn Gly Leu Lys Val Ser Ile Ser Ser Gly Phe Ser
                10                  15                  20

cgc aag aaa aca aaa acg atc ttg cat gat ctc gat ttc acc gta gag     211
Arg Lys Lys Thr Lys Thr Ile Leu His Asp Leu Asp Phe Thr Val Glu
            25                  30                  35

acc gga aag atc acg gga ttg ctg ggg cca tcg ggc agc ggc aag aca     259
Thr Gly Lys Ile Thr Gly Leu Leu Gly Pro Ser Gly Ser Gly Lys Thr
        40                  45                  50

act ttg atg cgc gcg att gtg gga gtg caa aac ttc gac ggc acc ctt     307
Thr Leu Met Arg Ala Ile Val Gly Val Gln Asn Phe Asp Gly Thr Leu
    55                  60                  65

gag gtg ttt gat cag ccc gca ggt gct gcc tct ctg cgc ggg aaa atc     355
Glu Val Phe Asp Gln Pro Ala Gly Ala Ala Ser Leu Arg Gly Lys Ile
70                  75                  80                  85

ggc tat gtc acc caa aac gcc agc gta tat cac gat ctg tcg gtg ata     403
Gly Tyr Val Thr Gln Asn Ala Ser Val Tyr His Asp Leu Ser Val Ile
                90                  95                  100

gaa aac ctc aag tat ttc ggg gct ctg gct aaa gga acc tcc act cca     451
Glu Asn Leu Lys Tyr Phe Gly Ala Leu Ala Lys Gly Thr Ser Thr Pro
            105                 110                 115

cgc acc ccg gaa aag att ctg gag gtc tta gac atc gca gat ctt gct     499
Arg Thr Pro Glu Lys Ile Leu Glu Val Leu Asp Ile Ala Asp Leu Ala
        120                 125                 130

caa cgc caa gta tca aca cta tct ggt ggg cag cgc ggc cga gtc tcc     547
Gln Arg Gln Val Ser Thr Leu Ser Gly Gly Gln Arg Gly Arg Val Ser
    135                 140                 145

ctt gga tgt gcg ctt att gcc tca cca gaa ctc ttg gtg atg gat gag     595
Leu Gly Cys Ala Leu Ile Ala Ser Pro Glu Leu Leu Val Met Asp Glu
150                 155                 160                 165

cca acc gtg ggt ttg gat ccc att acc cgg caa gca ctg tgg gaa gag     643
Pro Thr Val Gly Leu Asp Pro Ile Thr Arg Gln Ala Leu Trp Glu Glu
                170                 175                 180

ttc acc acc atc gca aaa gca ggt gct gga gtg gtt atc tcc agt cac     691
Phe Thr Thr Ile Ala Lys Ala Gly Ala Gly Val Val Ile Ser Ser His
            185                 190                 195

gtg ttg gag gaa gcc gcg cgg tgc gac aac ctc att ttg ttg cgt gat     739
Val Leu Glu Glu Ala Ala Arg Cys Asp Asn Leu Ile Leu Leu Arg Asp
        200                 205                 210

ggt cgg atc atc tgg agg gga aca ccc aca cgc ctt cta gaa gat aca     787
Gly Arg Ile Ile Trp Arg Gly Thr Pro Thr Arg Leu Leu Glu Asp Thr
    215                 220                 225
```

```
ggc aaa agc tca tac gaa gat gct ttc ttg gct gcc att gac ggg gta      835
Gly Lys Ser Ser Tyr Glu Asp Ala Phe Leu Ala Ala Ile Asp Gly Val
230                 235                 240                 245

agg tca tgaaccctca ctatctgctt gcc                                    864
Arg Ser



<210> 144
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 144
Met Ser Thr Val Thr Ala Val Gln Val Asn Gly Leu Lys Val Ser Ile
  1               5                  10                  15

Ser Ser Gly Phe Ser Arg Lys Lys Thr Lys Thr Ile Leu His Asp Leu
             20                  25                  30

Asp Phe Thr Val Glu Thr Gly Lys Ile Thr Gly Leu Leu Gly Pro Ser
         35                  40                  45

Gly Ser Gly Lys Thr Thr Leu Met Arg Ala Ile Val Gly Val Gln Asn
     50                  55                  60

Phe Asp Gly Thr Leu Glu Val Phe Asp Gln Pro Ala Gly Ala Ala Ser
 65                  70                  75                  80

Leu Arg Gly Lys Ile Gly Tyr Val Thr Gln Asn Ala Ser Val Tyr His
                 85                  90                  95

Asp Leu Ser Val Ile Glu Asn Leu Lys Tyr Phe Gly Ala Leu Ala Lys
            100                 105                 110

Gly Thr Ser Thr Pro Arg Thr Pro Glu Lys Ile Leu Glu Val Leu Asp
        115                 120                 125

Ile Ala Asp Leu Ala Gln Arg Gln Val Ser Thr Leu Ser Gly Gly Gln
    130                 135                 140

Arg Gly Arg Val Ser Leu Gly Cys Ala Leu Ile Ala Ser Pro Glu Leu
145                 150                 155                 160

Leu Val Met Asp Glu Pro Thr Val Gly Leu Asp Pro Ile Thr Arg Gln
                165                 170                 175

Ala Leu Trp Glu Glu Phe Thr Thr Ile Ala Lys Ala Gly Ala Gly Val
            180                 185                 190

Val Ile Ser Ser His Val Leu Glu Glu Ala Ala Arg Cys Asp Asn Leu
        195                 200                 205

Ile Leu Leu Arg Asp Gly Arg Ile Ile Trp Arg Gly Thr Pro Thr Arg
    210                 215                 220
```

```
Leu Leu Glu Asp Thr Gly Lys Ser Ser Tyr Glu Asp Ala Phe Leu Ala
225                 230                 235                 240

Ala Ile Asp Gly Val Arg Ser
                245


<210> 145
<211> 2463
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2440)
<223> RXN00829

<400> 145
tgttttagcc atggacccca tactagggag agttttgttt tggtgctaga aaaggttcac 60

caagcgcgaa caggcctatg caaacggtac gatatgacac atg caa aaa gct gat    115
                                          Met Gln Lys Ala Asp
                                          1               5

tcc cat gat tgg att tcg gtc cac ggt gcg aat gaa aac aac ctc aaa    163
Ser His Asp Trp Ile Ser Val His Gly Ala Asn Glu Asn Asn Leu Lys
                10                  15                  20

aat gtg tcg gtg cgc atc cct aaa agg cgt ctc acc gtg ttc acg ggt    211
Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu Thr Val Phe Thr Gly
            25                  30                  35

gtg tcg gga tct ggc aag tcc tcg ctg gtg ttc ggc aca att gct gcg    259
Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe Gly Thr Ile Ala Ala
        40                  45                  50

gaa tca cgc cgg ttg atc aac gaa acc tat agc act ttt gtg caa ggt    307
Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser Thr Phe Val Gln Gly
    55                  60                  65

ttc atg ccg tcg atg gca agg ccc gat gtt gac cat ttg gaa ggc atc    355
Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp His Leu Glu Gly Ile
70                  75                  80                  85

acc acg gcg atc atc gtc gat cag gag cag atg ggc gca aac cca cgg    403
Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met Gly Ala Asn Pro Arg
                90                  95                  100

tct acg gtg ggt acc gca act gat gcc acc gcg atg ttg cgc att ttg    451
Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala Met Leu Arg Ile Leu
            105                 110                 115

ttt tcc cga atc gcg gaa cct aac gcg ggt ggc ccg gga gct tat tcc    499
Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly Pro Gly Ala Tyr Ser
        120                 125                 130

ttc aac gtc ccc tct gtt tcc gca tcc ggc gcc atc acg gtg gaa aag    547
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```
Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala Ile Thr Val Glu Lys
    135                 140                 145

ggc gga aac acc aag cgg gag aaa gct acc ttc aaa cgc acg ggt ggc      595
Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe Lys Arg Thr Gly Gly
150                 155                 160                 165

atg tgc cca gcg tgc gag ggc atg ggc agg gcc tca gac atc gac ctc      643
Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala Ser Asp Ile Asp Leu
                170                 175                 180

aaa gag ctt ttc gac gcc tcc ctc tcc ctc aac gac ggc gcc ctg acc      691
Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn Asp Gly Ala Leu Thr
            185                 190                 195

atc ccc ggt tac acc cca ggt gga tgg agt tat cgg atg tat tca gaa      739
Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr Arg Met Tyr Ser Glu
        200                 205                 210

tcg ggc ctt ttt gat gct gcc aag ccg att aag gat ttc acc gag gaa      787
Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys Asp Phe Thr Glu Glu
    215                 220                 225

gaa cgc cac aac ttc ctt tat ctt gag ccc acc aag atg aag atc gct      835
Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr Lys Met Lys Ile Ala
230                 235                 240                 245

ggc atc aac atg acc tat gag ggt ctt atc ccc cgc att cag aaa tcc      883
Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro Arg Ile Gln Lys Ser
                250                 255                 260

atg ttg tct aag gat cgc gaa ggc atg cag aag cat att cgt gcg ttc      931
Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys His Ile Arg Ala Phe
            265                 270                 275

gtg gat cga gcg gtt acc ttc att cct tgc cct gcg tgt ggt gga act      979
Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro Ala Cys Gly Gly Thr
        280                 285                 290

cga tta gcg cca cat gcc ttg gag tcc aag atc aat ggc aaa aac atc      1027
Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile Asn Gly Lys Asn Ile
    295                 300                 305

gct gag ttg tgc gcg atg gag gtc cgt gat ttg gcc aag tgg atc aaa      1075
Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu Ala Lys Trp Ile Lys
310                 315                 320                 325

acg gtg gaa gcc ccc tcg gtt gct ccc ctg ctc acc gca ctg act gaa      1123
Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu Thr Ala Leu Thr Glu
                330                 335                 340

acc ctg gat aac ttc gtg gag atc ggt ttg ggc tat atc caa ctc gat      1171
Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly Tyr Ile Gln Leu Asp
            345                 350                 355

cgc ccc gct ggc acg ttg tct ggt ggt gag gca cag cgc acc aag atg      1219
Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala Gln Arg Thr Lys Met
```

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        360                 365                 370

atc cgc cat ttg ggc tct gca ttg act gac gtc acc tat gtt ttt gat    1267
Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val Thr Tyr Val Phe Asp
    375                 380                 385

gaa ccc acc gcc ggt ttg cac gcc tac gac att gaa cgc atg aac aag    1315
Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile Glu Arg Met Asn Lys
390                 395                 400                 405

ttg ctg ctc gat ctt cgc gat aaa ggc aat acc gtt tta gtc gtg gag    1363
Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr Val Leu Val Val Glu
                410                 415                 420

cac aag ccg gaa acc atc gcc att gca gat cat gtg gtg gac ctt ggg    1411
His Lys Pro Glu Thr Ile Ala Ile Ala Asp His Val Val Asp Leu Gly
            425                 430                 435

cca ggt gca ggc gcg ggt gga ggt gaa att cgg ttt gag ggg agc gtc    1459
Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg Phe Glu Gly Ser Val
        440                 445                 450

gac aag ctt aaa gac agc gac acc gtg act ggc ctc cat ttt aat gac    1507
Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp
    455                 460                 465

cgg gcg tca ttg aag gaa tcc gtg cgt gcg ccg cat ggc gcc ctg gag    1555
Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro His Gly Ala Leu Glu
470                 475                 480                 485

atc cgc ggg gcc gat cga aat aat ttg aac aat gtg gat gtc gat att    1603
Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn Val Asp Val Asp Ile
                490                 495                 500

ccg ctc ggc gtg ttc acg gcg att tcc ggc gtt gca ggt tcg ggt aag    1651
Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val Ala Gly Ser Gly Lys
            505                 510                 515

tcc tcg ttg att cat gag att ccg cgt gat gag tcg gtt gtg ttt gtc    1699
Ser Ser Leu Ile His Glu Ile Pro Arg Asp Glu Ser Val Val Phe Val
        520                 525                 530

gat caa acc gca atc cac ggt tct aat cgt tcc aat cct gcg aca tat    1747
Asp Gln Thr Ala Ile His Gly Ser Asn Arg Ser Asn Pro Ala Thr Tyr
    535                 540                 545

aca ggc atg ctg gat tcg att cgc aag gct ttt gcc aag gcc aat gat    1795
Thr Gly Met Leu Asp Ser Ile Arg Lys Ala Phe Ala Lys Ala Asn Asp
550                 555                 560                 565

gtg aaa ccg gcg ctg ttc tcc ccc aat tct gaa ggc gcg tgc cca aac    1843
Val Lys Pro Ala Leu Phe Ser Pro Asn Ser Glu Gly Ala Cys Pro Asn
                570                 575                 580

tgt aag ggc gcc ggc tcg gtc tat gtc gat ttg ggc atg atg gct ggg    1891
Cys Lys Gly Ala Gly Ser Val Tyr Val Asp Leu Gly Met Met Ala Gly
            585                 590                 595
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gta tct tcg ccg tgt gag gtg tgc gag ggc aag cgt ttt gat gag tcc    1939
Val Ser Ser Pro Cys Glu Val Cys Glu Gly Lys Arg Phe Asp Glu Ser
        600                 605                 610

gtg ttg gac tac cac ttt ggt ggc aag gac atc gca gac gtg ttg ggg    1987
Val Leu Asp Tyr His Phe Gly Gly Lys Asp Ile Ala Asp Val Leu Gly
    615                 620                 625

ctg tcg gct gcc aat gcg tat gag ttt ttc gcg gcg aaa gat tca aag    2035
Leu Ser Ala Ala Asn Ala Tyr Glu Phe Phe Ala Ala Lys Asp Ser Lys
630                 635                 640                 645

att ttg cct gcg gca aag atc gca aag agg ctt gtc gac gtc ggc ctc    2083
Ile Leu Pro Ala Ala Lys Ile Ala Lys Arg Leu Val Asp Val Gly Leu
                650                 655                 660

ggc tac atc acc ctc ggc cag ccg ctc acc acg ttg tcc ggc ggt gaa    2131
Gly Tyr Ile Thr Leu Gly Gln Pro Leu Thr Thr Leu Ser Gly Gly Glu
            665                 670                 675

cgc cag cgt ttg aag ctc gcc acc cac atg gca gac aag gcc acc acc    2179
Arg Gln Arg Leu Lys Leu Ala Thr His Met Ala Asp Lys Ala Thr Thr
        680                 685                 690

ttt att ttg gat gag ccc acc aca ggc ctg cac ctc gct gat gtg aaa    2227
Phe Ile Leu Asp Glu Pro Thr Thr Gly Leu His Leu Ala Asp Val Lys
    695                 700                 705

acc ttg ctg gat ctt ttt gat caa ctg gtt gat gac ggc aag tct gtc    2275
Thr Leu Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val
710                 715                 720                 725

atc gtc atc gaa cac cac ctc ggc gtg ctc gct cac gct gac cac atc    2323
Ile Val Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile
                730                 735                 740

att gat gtc ggc cct ggt gca ggt tct gat ggt ggc tcg att gta ttc    2371
Ile Asp Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe
            745                 750                 755

gag ggc agc ccc gcg gaa ctc atc aaa act gat act cca aca gga cgc    2419
Glu Gly Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg
        760                 765                 770

cac ctt aaa gct tat gta gat tagtttctta tggaaaaccc tgg              2463
His Leu Lys Ala Tyr Val Asp
    775                 780
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<210> 146
<211> 780
<212> PRT
<213> Corynebacterium glutamicum

<400> 146
Met Gln Lys Ala Asp Ser His Asp Trp Ile Ser Val His Gly Ala Asn

1 5 10 15

Glu Asn Asn Leu Lys Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu
20 25 30

Thr Val Phe Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe
35 40 45

Gly Thr Ile Ala Ala Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser
50 55 60

Thr Phe Val Gln Gly Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp
65 70 75 80

His Leu Glu Gly Ile Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met
85 90 95

Gly Ala Asn Pro Arg Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala
100 105 110

Met Leu Arg Ile Leu Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly
115 120 125

Pro Gly Ala Tyr Ser Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala
130 135 140

Ile Thr Val Glu Lys Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe
145 150 155 160

Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala
165 170 175

Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn
180 185 190

Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr
195 200 205

Arg Met Tyr Ser Glu Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys
210 215 220

Asp Phe Thr Glu Glu Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr
225 230 235 240

Lys Met Lys Ile Ala Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro
245 250 255

Arg Ile Gln Lys Ser Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys
260 265 270

His Ile Arg Ala Phe Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro
275 280 285

Ala Cys Gly Gly Thr Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile
290 295 300

Asn Gly Lys Asn Ile Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu

305 310 315 320

Ala Lys Trp Ile Lys Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu
325 330 335

Thr Ala Leu Thr Glu Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly
340 345 350

Tyr Ile Gln Leu Asp Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala
355 360 365

Gln Arg Thr Lys Met Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val
370 375 380

Thr Tyr Val Phe Asp Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile
385 390 395 400

Glu Arg Met Asn Lys Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr
405 410 415

Val Leu Val Val Glu His Lys Pro Glu Thr Ile Ala Ile Ala Asp His
420 425 430

Val Val Asp Leu Gly Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg
435 440 445

Phe Glu Gly Ser Val Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly
450 455 460

Leu His Phe Asn Asp Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro
465 470 475 480

His Gly Ala Leu Glu Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn
485 490 495

Val Asp Val Asp Ile Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val
500 505 510

Ala Gly Ser Gly Lys Ser Ser Leu Ile His Glu Ile Pro Arg Asp Glu
515 520 525

Ser Val Val Phe Val Asp Gln Thr Ala Ile His Gly Ser Asn Arg Ser
530 535 540

Asn Pro Ala Thr Tyr Thr Gly Met Leu Asp Ser Ile Arg Lys Ala Phe
545 550 555 560

Ala Lys Ala Asn Asp Val Lys Pro Ala Leu Phe Ser Pro Asn Ser Glu
565 570 575

Gly Ala Cys Pro Asn Cys Lys Gly Ala Gly Ser Val Tyr Val Asp Leu
580 585 590

Gly Met Met Ala Gly Val Ser Ser Pro Cys Glu Val Cys Glu Gly Lys
595 600 605

Arg Phe Asp Glu Ser Val Leu Asp Tyr His Phe Gly Gly Lys Asp Ile

610 615 620

Ala Asp Val Leu Gly Leu Ser Ala Ala Asn Ala Tyr Glu Phe Phe Ala
625 630 635 640

Ala Lys Asp Ser Lys Ile Leu Pro Ala Ala Lys Ile Ala Lys Arg Leu
645 650 655

Val Asp Val Gly Leu Gly Tyr Ile Thr Leu Gly Gln Pro Leu Thr Thr
660 665 670

Leu Ser Gly Gly Glu Arg Gln Arg Leu Lys Leu Ala Thr His Met Ala
675 680 685

Asp Lys Ala Thr Thr Phe Ile Leu Asp Glu Pro Thr Thr Gly Leu His
690 695 700

Leu Ala Asp Val Lys Thr Leu Leu Asp Leu Phe Asp Gln Leu Val Asp
705 710 715 720

Asp Gly Lys Ser Val Ile Val Ile Glu His His Leu Gly Val Leu Ala
725 730 735

His Ala Asp His Ile Ile Asp Val Gly Pro Gly Ala Gly Ser Asp Gly
740 745 750

Gly Ser Ile Val Phe Glu Gly Ser Pro Ala Glu Leu Ile Lys Thr Asp
755 760 765

Thr Pro Thr Gly Arg His Leu Lys Ala Tyr Val Asp
770 775 780

<210> 147
<211> 278
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(255)
<223> FRXA00829

<400> 147
ttg gat gag ccc acc aca ggc ctg cac ctc gct gat gtg aaa acc ttg 48
Leu Asp Glu Pro Thr Thr Gly Leu His Leu Ala Asp Val Lys Thr Leu
1 5 10 15

ctg gat ctt ttt gat caa ctg gtt gat gac ggc aag tct gtc atc gtc 96
Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val Ile Val
20 25 30

atc gaa cac cac ctc ggc gtg ctc gct cac gct gac cac atc att gat 144
Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp
35 40 45

gtc ggc cct ggt gca ggt tct gat ggt ggc tcg att gta ttc gag ggc 192

Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
50 55 60

agc ccc gcg gaa ctc atc aaa act gat act cca aca gga cgc cac ctt 240
Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg His Leu
65 70 75 80

aaa gct tat gta gat tagtttctta tggaaaaccc tgg 278
Lys Ala Tyr Val Asp
85

<210> 148
<211> 85
<212> PRT
<213> Corynebacterium glutamicum

<400> 148
Leu Asp Glu Pro Thr Thr Gly Leu His Leu Ala Asp Val Lys Thr Leu
1 5 10 15

Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val Ile Val
20 25 30

Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp
35 40 45

Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
50 55 60

Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg His Leu
65 70 75 80

Lys Ala Tyr Val Asp
85

<210> 149
<211> 1663
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1663)
<223> FRXA00834

<400> 149
tgttttagcc atggacccca tactagggag agttttgttt tggtgctaga aaaggttcac 60

caagcgcgaa caggcctatg caaacggtac gatatgacac atg caa aaa gct gat 115
Met Gln Lys Ala Asp
1 5

tcc cat gat tgg att tcg gtc cac ggt gcg aat gaa aac aac ctc aaa 163
Ser His Asp Trp Ile Ser Val His Gly Ala Asn Glu Asn Asn Leu Lys
10 15 20

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aat gtg tcg gtg cgc atc cct aaa agg cgt ctc acc gtg ttc acg ggt    211
Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu Thr Val Phe Thr Gly
            25                  30                  35

gtg tcg gga tct ggc aag tcc tcg ctg gtg ttc ggc aca att gct gcg    259
Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe Gly Thr Ile Ala Ala
        40                  45                  50

gaa tca cgc cgg ttg atc aac gaa acc tat agc act ttt gtg caa ggt    307
Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser Thr Phe Val Gln Gly
    55                  60                  65

ttc atg ccg tcg atg gca agg ccc gat gtt gac cat ttg gaa ggc atc    355
Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp His Leu Glu Gly Ile
70                  75                  80                  85

acc acg gcg atc atc gtc gat cag gag cag atg ggc gca aac cca cgg    403
Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met Gly Ala Asn Pro Arg
                90                  95                  100

tct acg gtg ggt acc gca act gat gcc acc gcg atg ttg cgc att ttg    451
Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala Met Leu Arg Ile Leu
            105                 110                 115

ttt tcc cga atc gcg gaa cct aac gcg ggt ggc ccg gga gct tat tcc    499
Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly Pro Gly Ala Tyr Ser
        120                 125                 130

ttc aac gtc ccc tct gtt tcc gca tcc ggc gcc atc acg gtg gaa aag    547
Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala Ile Thr Val Glu Lys
    135                 140                 145

ggc gga aac acc aag cgg gag aaa gct acc ttc aaa cgc acg ggt ggc    595
Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe Lys Arg Thr Gly Gly
150                 155                 160                 165

atg tgc cca gcg tgc gag ggc atg ggc agg gcc tca gac atc gac ctc    643
Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala Ser Asp Ile Asp Leu
                170                 175                 180

aaa gag ctt ttc gac gcc tcc ctc tcc ctc aac gac ggc gcc ctg acc    691
Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn Asp Gly Ala Leu Thr
            185                 190                 195

atc ccc ggt tac acc cca ggt gga tgg agt tat cgg atg tat tca gaa    739
Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr Arg Met Tyr Ser Glu
        200                 205                 210

tcg ggc ctt ttt gat gct gcc aag ccg att aag gat ttc acc gag gaa    787
Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys Asp Phe Thr Glu Glu
    215                 220                 225

gaa cgc cac aac ttc ctt tat ctt gag ccc acc aag atg aag atc gct    835
Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr Lys Met Lys Ile Ala
230                 235                 240                 245
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ggc atc aac atg acc tat gag ggt ctt atc ccc cgc att cag aaa tcc 883
Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro Arg Ile Gln Lys Ser
250 255 260

atg ttg tct aag gat cgc gaa ggc atg cag aag cat att cgt gcg ttc 931
Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys His Ile Arg Ala Phe
265 270 275

gtg gat cga gcg gtt acc ttc att cct tgc cct gcg tgt ggt gga act 979
Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro Ala Cys Gly Gly Thr
280 285 290

cga tta gcg cca cat gcc ttg gag tcc aag atc aat ggc aaa aac atc 1027
Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile Asn Gly Lys Asn Ile
295 300 305

gct gag ttg tgc gcg atg gag gtc cgt gat ttg gcc aag tgg atc aaa 1075
Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu Ala Lys Trp Ile Lys
310 315 320 325

acg gtg gaa gcc ccc tcg gtt gct ccc ctg ctc acc gca ctg act gaa 1123
Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu Thr Ala Leu Thr Glu
330 335 340

acc ctg gat aac ttc gtg gag atc ggt ttg ggc tat atc caa ctc gat 1171
Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly Tyr Ile Gln Leu Asp
345 350 355

cgc ccc gct ggc acg ttg tct ggt ggt gag gca cag cgc acc aag atg 1219
Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala Gln Arg Thr Lys Met
360 365 370

atc cgc cat ttg ggc tct gca ttg act gac gtc acc tat gtt ttt gat 1267
Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val Thr Tyr Val Phe Asp
375 380 385

gaa ccc acc gcc ggt ttg cac gcc tac gac att gaa cgc atg aac aag 1315
Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile Glu Arg Met Asn Lys
390 395 400 405

ttg ctg ctc gat ctt cgc gat aaa ggc aat acc gtt tta gtc gtg gag 1363
Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr Val Leu Val Val Glu
410 415 420

cac aag ccg gaa acc atc gcc att gca gat cat gtg gtg gac ctt ggg 1411
His Lys Pro Glu Thr Ile Ala Ile Ala Asp His Val Val Asp Leu Gly
425 430 435

cca ggt gca ggc gcg ggt gga ggt gaa att cgg ttt gag ggg agc gtc 1459
Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg Phe Glu Gly Ser Val
440 445 450

gac aag ctt aaa gac agc gac acc gtg act ggc ctc cat ttt aat gac 1507
Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp
455 460 465

cgg gcg tca ttg aag gaa tcc gtg cgt gcg ccg cat ggc gcc ctg gag 1555

Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro His Gly Ala Leu Glu
470 475 480 485

atc cgc ggg gcc gat cga aat aat ttg aac aat gtg gat gtc gat att 1603
Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn Val Asp Val Asp Ile
490 495 500

ccg ctc ggc gtg ttc acg gcg att tcc ggc gtt gca ggt tcg ggt aag 1651
Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val Ala Gly Ser Gly Lys
505 510 515

tcc tcg ttg att 1663
Ser Ser Leu Ile
520

<210> 150
<211> 521
<212> PRT
<213> Corynebacterium glutamicum

<400> 150
Met Gln Lys Ala Asp Ser His Asp Trp Ile Ser Val His Gly Ala Asn
1 5 10 15

Glu Asn Asn Leu Lys Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu
20 25 30

Thr Val Phe Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe
35 40 45

Gly Thr Ile Ala Ala Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser
50 55 60

Thr Phe Val Gln Gly Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp
65 70 75 80

His Leu Glu Gly Ile Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met
85 90 95

Gly Ala Asn Pro Arg Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala
100 105 110

Met Leu Arg Ile Leu Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly
115 120 125

Pro Gly Ala Tyr Ser Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala
130 135 140

Ile Thr Val Glu Lys Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe
145 150 155 160

Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala
165 170 175

Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn
180 185 190

Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr
195 200 205

Arg Met Tyr Ser Glu Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys
210 215 220

Asp Phe Thr Glu Glu Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr
225 230 235 240

Lys Met Lys Ile Ala Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro
245 250 255

Arg Ile Gln Lys Ser Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys
260 265 270

His Ile Arg Ala Phe Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro
275 280 285

Ala Cys Gly Gly Thr Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile
290 295 300

Asn Gly Lys Asn Ile Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu
305 310 315 320

Ala Lys Trp Ile Lys Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu
325 330 335

Thr Ala Leu Thr Glu Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly
340 345 350

Tyr Ile Gln Leu Asp Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala
355 360 365

Gln Arg Thr Lys Met Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val
370 375 380

Thr Tyr Val Phe Asp Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile
385 390 395 400

Glu Arg Met Asn Lys Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr
405 410 415

Val Leu Val Val Glu His Lys Pro Glu Thr Ile Ala Ile Ala Asp His
420 425 430

Val Val Asp Leu Gly Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg
435 440 445

Phe Glu Gly Ser Val Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly
450 455 460

Leu His Phe Asn Asp Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro
465 470 475 480

His Gly Ala Leu Glu Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn
485 490 495

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Val Asp Val Asp Ile Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val
            500                 505                 510

Ala Gly Ser Gly Lys Ser Ser Leu Ile
        515                 520


<210> 151
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXA00995

<400> 151
gtcggatcat ctggagggga acacccacac gccttctaga agatacaggc aaaagctcat 60

acgaagatgc tttcttggct gccattgacg ggtaaggtc atg aac cct cac tat    115
                                           Met Asn Pro His Tyr
                                           1               5

ctg ctt gcc acg gtc aaa cga gtc ctg ctg cag ctg aaa gcc gat aaa    163
Leu Leu Ala Thr Val Lys Arg Val Leu Leu Gln Leu Lys Ala Asp Lys
                10                  15                  20

cgt tcc atc gcg ctg att ctt cta gca ccc gtg gcg ttg atg tcg ctg    211
Arg Ser Ile Ala Leu Ile Leu Leu Ala Pro Val Ala Leu Met Ser Leu
            25                  30                  35

ttt tat tac atg tat tcc tcc aca ccg gca ggc acc cag ctg ttt aag    259
Phe Tyr Tyr Met Tyr Ser Ser Thr Pro Ala Gly Thr Gln Leu Phe Lys
        40                  45                  50

acc att tcc acg gtc atg atc gca gtg ttc ccc ttg atg ctc atg ttt    307
Thr Ile Ser Thr Val Met Ile Ala Val Phe Pro Leu Met Leu Met Phe
    55                  60                  65

ttg atg acg tcg gtg acg atg caa aga gaa cgc aac gct gga acg ctc    355
Leu Met Thr Ser Val Thr Met Gln Arg Glu Arg Asn Ala Gly Thr Leu
70                  75                  80                  85

gag cgc ttg tgg acc acg aac att cac cgc gtt gat ttg atc ggt ggc    403
Glu Arg Leu Trp Thr Thr Asn Ile His Arg Val Asp Leu Ile Gly Gly
                90                  95                  100

tac ggg gtg gcc ttc ggc atc atg gcg gtg gcg caa tct ttg ctc atg    451
Tyr Gly Val Ala Phe Gly Ile Met Ala Val Ala Gln Ser Leu Leu Met
            105                 110                 115

gtg ctc acc ctt cgg tat ctc ctg ggt gtg gaa acc gaa tcg gag tgg    499
Val Leu Thr Leu Arg Tyr Leu Leu Gly Val Glu Thr Glu Ser Glu Trp
        120                 125                 130
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tgg att tct acg ctc att gct gcg atc acc ggt ctt atc gga gtg tct      547
Trp Ile Ser Thr Leu Ile Ala Ala Ile Thr Gly Leu Ile Gly Val Ser
    135                 140                 145

ctt ggc ctg ttg agc tct gcg ttt gcc agc act gag ttc caa gct atc      595
Leu Gly Leu Leu Ser Ser Ala Phe Ala Ser Thr Glu Phe Gln Ala Ile
150                 155                 160                 165

caa acg ctg ccg ttg ctt att ttg ccc cag ttc cta ttg tgc ggt ttg      643
Gln Thr Leu Pro Leu Leu Ile Leu Pro Gln Phe Leu Leu Cys Gly Leu
                170                 175                 180

ctg atc cca cgg gat gat ctg ccg gat gtg ttg cgc tgg gtt tct aat      691
Leu Ile Pro Arg Asp Asp Leu Pro Asp Val Leu Arg Trp Val Ser Asn
            185                 190                 195

gtg ttg ccg ctg tcc tat gca gtt gat gca gcg ctt gag gcc tca cgg      739
Val Leu Pro Leu Ser Tyr Ala Val Asp Ala Ala Leu Glu Ala Ser Arg
        200                 205                 210

acg gga atc gga cag caa gta gtg gtc aac att gcc atc tgc gcc gcg      787
Thr Gly Ile Gly Gln Gln Val Val Val Asn Ile Ala Ile Cys Ala Ala
    215                 220                 225

ttt gcc gtg agc ttc ctg ctg gtg gcg gcg cta tcg atg ccg aga atg      835
Phe Ala Val Ser Phe Leu Leu Val Ala Ala Leu Ser Met Pro Arg Met
230                 235                 240                 245

acc cgc tagattactc ttccagcgag gtg                                    864
Thr Arg


<210> 152
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 152
Met Asn Pro His Tyr Leu Leu Ala Thr Val Lys Arg Val Leu Leu Gln
  1               5                  10                  15

Leu Lys Ala Asp Lys Arg Ser Ile Ala Leu Ile Leu Leu Ala Pro Val
            20                  25                  30

Ala Leu Met Ser Leu Phe Tyr Tyr Met Tyr Ser Ser Thr Pro Ala Gly
        35                  40                  45

Thr Gln Leu Phe Lys Thr Ile Ser Thr Val Met Ile Ala Val Phe Pro
    50                  55                  60

Leu Met Leu Met Phe Leu Met Thr Ser Val Thr Met Gln Arg Glu Arg
65                  70                  75                  80

Asn Ala Gly Thr Leu Glu Arg Leu Trp Thr Thr Asn Ile His Arg Val
                85                  90                  95
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Asp Leu Ile Gly Gly Tyr Gly Val Ala Phe Gly Ile Met Ala Val Ala
            100                 105                 110

Gln Ser Leu Leu Met Val Leu Thr Leu Arg Tyr Leu Leu Gly Val Glu
        115                 120                 125

Thr Glu Ser Glu Trp Trp Ile Ser Thr Leu Ile Ala Ala Ile Thr Gly
    130                 135                 140

Leu Ile Gly Val Ser Leu Gly Leu Leu Ser Ser Ala Phe Ala Ser Thr
145                 150                 155                 160

Glu Phe Gln Ala Ile Gln Thr Leu Pro Leu Leu Ile Leu Pro Gln Phe
                165                 170                 175

Leu Leu Cys Gly Leu Leu Ile Pro Arg Asp Asp Leu Pro Asp Val Leu
            180                 185                 190

Arg Trp Val Ser Asn Val Leu Pro Leu Ser Tyr Ala Val Asp Ala Ala
        195                 200                 205

Leu Glu Ala Ser Arg Thr Gly Ile Gly Gln Gln Val Val Val Asn Ile
    210                 215                 220

Ala Ile Cys Ala Ala Phe Ala Val Ser Phe Leu Leu Val Ala Ala Leu
225                 230                 235                 240

Ser Met Pro Arg Met Thr Arg
                245


<210> 153
<211> 1353
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1330)
<223> RXN00803

<400> 153
tcatccttcc ttagctcgcg tgagcttccc aagcgtaagc acccccgtgt gagggcataa 60

cggccgttct gttaaagatt ggtctggcca tttcctccat atg ggg gtg tcc gcg   115
                                          Met Gly Val Ser Ala
                                          1               5

ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc   163
Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
                10                  15                  20

tgg cta gcg gta gct tta tcg gtc ttt acg gtc gcg tgg ggt ggc aat   211
Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
            25                  30                  35

gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc   259
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```
Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser
        40                  45                  50

aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg      307
Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr Ala Ile Gly Val Ala
    55                  60                  65

gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt      355
Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg
70                  75                  80                  85

gcc gtc atg ttg cct gcg cca ttg atc gcg atc ttg ggt tcc gcg ttg      403
Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile Leu Gly Ser Ala Leu
                90                  95                  100

att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg      451
Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val
            105                 110                 115

ctg tcg gga att tcg gtg ggc atg gtg atg aca gcg gga ggt tcc tgg      499
Leu Ser Gly Ile Ser Val Gly Met Val Met Thr Ala Gly Gly Ser Trp
        120                 125                 130

att aag gag ctt tca tcg tcg cgg ttt gag cca ggg gtg aaa acc agt      547
Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro Gly Val Lys Thr Ser
    135                 140                 145

gct ggt gca aaa cgc gca tcg atg tct ttg acc ggt ggt ttt gcg ctc      595
Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr Gly Gly Phe Ala Leu
150                 155                 160                 165

ggc cca gcg ctt gct ggt gtg atg gca cag tgg ctg cca cta cct gga      643
Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp Leu Pro Leu Pro Gly
                170                 175                 180

cag ttg gca tat gtt ttg cac att att ctc act ctg att ttg ttc ccg      691
Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr Leu Ile Leu Phe Pro
            185                 190                 195

ttg ctt att aca gcg ccg gaa act cgt caa tca gcg cac ctg aaa act      739
Leu Leu Ile Thr Ala Pro Glu Thr Arg Gln Ser Ala His Leu Lys Thr
        200                 205                 210

aag gga tca ttc tgg tca gat gtg ctt gtg cca tct gca cta gac aag      787
Lys Gly Ser Phe Trp Ser Asp Val Leu Val Pro Ser Ala Leu Asp Lys
    215                 220                 225

cga ttc ttg ttt gtg gtt gct cca att gga ccg tgg gtt ttc ggt gcg      835
Arg Phe Leu Phe Val Val Ala Pro Ile Gly Pro Trp Val Phe Gly Ala
230                 235                 240                 245

gcc ttc act gcc tac gca gtt ttg ccg tcg cag ctg cgt gac atg gtt      883
Ala Phe Thr Ala Tyr Ala Val Leu Pro Ser Gln Leu Arg Asp Met Val
                250                 255                 260

tct gca ccc gtt gcg tat tct gcg ctg atc gct ttg gtt acc tta ggt      931
Ser Ala Pro Val Ala Tyr Ser Ala Leu Ile Ala Leu Val Thr Leu Gly
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265 270 275

tct gga ttt ggt atc caa caa ttc ggt cct caa atc atg ggc acc tct 979
Ser Gly Phe Gly Ile Gln Gln Phe Gly Pro Gln Ile Met Gly Thr Ser
280 285 290

aaa act cgc ggg ccg att ttg gcc atg ttc gtc aca gtc atc ggc atg 1027
Lys Thr Arg Gly Pro Ile Leu Ala Met Phe Val Thr Val Ile Gly Met
295 300 305

atc ggc gcg gtg atc gtg gtg atg aac cct cat cca tgg tgg gcg cta 1075
Ile Gly Ala Val Ile Val Val Met Asn Pro His Pro Trp Trp Ala Leu
310 315 320 325

gtt ggc tgc atg gcc ctc ggc ctg tct tat ggc ctg tgt atg ttc atg 1123
Val Gly Cys Met Ala Leu Gly Leu Ser Tyr Gly Leu Cys Met Phe Met
330 335 340

ggg ttg gcg gaa act caa aac att gct cca cct att gat atg gca ggc 1171
Gly Leu Ala Glu Thr Gln Asn Ile Ala Pro Pro Ile Asp Met Ala Gly
345 350 355

ctg acg ggt att ttc tac tgc ctg acg tac gta ggt atg gtc ttt cca 1219
Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val Gly Met Val Phe Pro
360 365 370

gcc ttg atg acc tgg ttg aat caa tgg ctc agt tac ccg ttc atg ctg 1267
Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser Tyr Pro Phe Met Leu
375 380 385

ggc ttt ggt gcg gtg atg gca act att tgt ctg atc att gtg agt ttt 1315
Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu Ile Ile Val Ser Phe
390 395 400 405

agt gca cgc cga ttc tgagaaacaa ctaaagtgag cca 1353
Ser Ala Arg Arg Phe
410

<210> 154
<211> 410
<212> PRT
<213> Corynebacterium glutamicum

<400> 154
Met Gly Val Ser Ala Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg
1 5 10 15

Ala Gln Arg Lys Val Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val
20 25 30

Ala Trp Gly Gly Asn Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly
35 40 45

Glu Gly Phe Phe Ser Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr
50 55 60

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Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp
 65                  70                  75                  80

Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile
                85                  90                  95

Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile
            100                 105                 110

Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr
        115                 120                 125

Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro
    130                 135                 140

Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr
145                 150                 155                 160

Gly Gly Phe Ala Leu Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp
                165                 170                 175

Leu Pro Leu Pro Gly Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr
            180                 185                 190

Leu Ile Leu Phe Pro Leu Leu Ile Thr Ala Pro Glu Thr Arg Gln Ser
        195                 200                 205

Ala His Leu Lys Thr Lys Gly Ser Phe Trp Ser Asp Val Leu Val Pro
    210                 215                 220

Ser Ala Leu Asp Lys Arg Phe Leu Phe Val Val Ala Pro Ile Gly Pro
225                 230                 235                 240

Trp Val Phe Gly Ala Ala Phe Thr Ala Tyr Ala Val Leu Pro Ser Gln
                245                 250                 255

Leu Arg Asp Met Val Ser Ala Pro Val Ala Tyr Ser Ala Leu Ile Ala
            260                 265                 270

Leu Val Thr Leu Gly Ser Gly Phe Gly Ile Gln Gln Phe Gly Pro Gln
        275                 280                 285

Ile Met Gly Thr Ser Lys Thr Arg Gly Pro Ile Leu Ala Met Phe Val
    290                 295                 300

Thr Val Ile Gly Met Ile Gly Ala Val Ile Val Val Met Asn Pro His
305                 310                 315                 320

Pro Trp Trp Ala Leu Val Gly Cys Met Ala Leu Gly Leu Ser Tyr Gly
                325                 330                 335

Leu Cys Met Phe Met Gly Leu Ala Glu Thr Gln Asn Ile Ala Pro Pro
            340                 345                 350

Ile Asp Met Ala Gly Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val
        355                 360                 365
```

Gly Met Val Phe Pro Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser
    370   375   380

Tyr Pro Phe Met Leu Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu
385   390   395   400

Ile Ile Val Ser Phe Ser Ala Arg Arg Phe
                405   410

<210> 155
<211> 703
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> FRXA00803

<400> 155
tcatccttcc ttagctcgcg tgagcttccc aagcgtaagc acccccgtgt gagggcataa 60

cggccgttct gttaaagatt ggtctggcca tttcctccat atg ggg gtg tcc gcg 115
Met Gly Val Ser Ala
1   5

ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc 163
Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
                10   15   20

tgg cta gcg gta gct tta tcg gtc ttt acg gtc gcg tgg ggt ggc aat 211
Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
            25   30   35

gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc 259
Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser
        40   45   50

aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg 307
Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr Ala Ile Gly Val Ala
    55   60   65

gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt 355
Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg
70   75   80   85

gcc gtc atg ttg cct gcg cca ttg atc gcg atc ttg ggt tcc gcg ttg 403
Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile Leu Gly Ser Ala Leu
                90   95   100

att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg 451
Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val
            105   110   115

ctg tcg gga att tcg gtg ggc atg gtg atg aca gcg gga ggt tcc tgg 499
Leu Ser Gly Ile Ser Val Gly Met Val Met Thr Ala Gly Gly Ser Trp

```
        120                     125                     130

att aag gag ctt tca tcg tcg cgg ttt gag cca ggg gtg aaa acc agt     547
Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro Gly Val Lys Thr Ser
    135                     140                     145

gct ggt gca aaa cgc gca tcg atg tct ttg acc ggt ggt ttt gcg ctc     595
Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr Gly Gly Phe Ala Leu
150                 155                     160                 165

ggc cca gcg ctt gct ggt gtg atg gca cag tgg ctg cca caa cct gga     643
Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp Leu Pro Gln Pro Gly
                170                     175                 180

cag ttg gca tat gtt ttg cac att att ctc act ctg att ttg ttc ccg     691
Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr Leu Ile Leu Phe Pro
            185                     190                 195

ttg ctt att aca                                                     703
Leu Leu Ile Thr
        200


<210> 156
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<400> 156
Met Gly Val Ser Ala Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg
  1               5                  10                  15

Ala Gln Arg Lys Val Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val
             20                  25                  30

Ala Trp Gly Gly Asn Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly
         35                  40                  45

Glu Gly Phe Phe Ser Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr
     50                  55                  60

Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp
 65                  70                  75                  80

Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile
                 85                  90                  95

Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile
            100                 105                 110

Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr
        115                 120                 125

Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro
    130                 135                 140

Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr
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145                 150                 155                 160

Gly Gly Phe Ala Leu Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp
                165                 170                 175

Leu Pro Gln Pro Gly Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr
            180                 185                 190

Leu Ile Leu Phe Pro Leu Leu Ile Thr
        195                 200


<210> 157
<211> 1014
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(991)
<223> RXA01407

<400> 157
atccggggaa cggatcccaa agatctcctt gatgccatcg cgtttttaac ctggccagct 60

ctggttgccc cagtgatcgc cccacttctg ggaggtcttc ttg caa gat acc att    115
                                            Leu Gln Asp Thr Ile
                                             1               5

ggt tgc cga tgg atc ttc ctc ctc aac gtg ccc tta gga atc atc gcg    163
Gly Cys Arg Trp Ile Phe Leu Leu Asn Val Pro Leu Gly Ile Ile Ala
                10                  15                  20

atc atg gct gga cta ttc atc cag ccc aag aac acg gcc gtg aat gtg    211
Ile Met Ala Gly Leu Phe Ile Gln Pro Lys Asn Thr Ala Val Asn Val
            25                  30                  35

aag cga ttt gat cgg cca ggt ttc ctc ggc gca atg ctg gtg atg gtg    259
Lys Arg Phe Asp Arg Pro Gly Phe Leu Gly Ala Met Leu Val Met Val
        40                  45                  50

gcg caa gcc gtg att gcg gag tta att tgc agc aga agt ccg gcc gca    307
Ala Gln Ala Val Ile Ala Glu Leu Ile Cys Ser Arg Ser Pro Ala Ala
    55                  60                  65

ctt act atc tgt gca tgc ctc gtc tta agt gct gcg gtg gta tgc ggt    355
Leu Thr Ile Cys Ala Cys Leu Val Leu Ser Ala Ala Val Val Cys Gly
70                  75                  80                  85

ttt gta gtg cgc tgg ctg cga gtt cca ggc cga ctt ttt gat ctc agc    403
Phe Val Val Arg Trp Leu Arg Val Pro Gly Arg Leu Phe Asp Leu Ser
                90                  95                  100

atc atg cgc atc cca ggt ttc cga gtg ggt aat tcc tcc gga agt atc    451
Ile Met Arg Ile Pro Gly Phe Arg Val Gly Asn Ser Ser Gly Ser Ile
            105                 110                 115
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tac cgc ttg gta atc acc gca gca cca ttc atg ttc act ttg ctc ttc    499
Tyr Arg Leu Val Ile Thr Ala Ala Pro Phe Met Phe Thr Leu Leu Phe
        120                 125                 130

caa gtg gcg ttt ggg tgg tct gca aca tta gcg ggt gcc atg gtg gtc    547
Gln Val Ala Phe Gly Trp Ser Ala Thr Leu Ala Gly Ala Met Val Val
    135                 140                 145

gca cta ttc gca ggc aac gtg gca atc aaa cct ttc acc acg ccg atc    595
Ala Leu Phe Ala Gly Asn Val Ala Ile Lys Pro Phe Thr Thr Pro Ile
150                 155                 160                 165

att aaa cgc tgg aat ttc aaa cca gta ctg gtc ttt tct aac gct gct    643
Ile Lys Arg Trp Asn Phe Lys Pro Val Leu Val Phe Ser Asn Ala Ala
                170                 175                 180

ggc gcc ttg gta ttg gca act ttt ttg ttc gtt cgt gca gat acc cca    691
Gly Ala Leu Val Leu Ala Thr Phe Leu Phe Val Arg Ala Asp Thr Pro
            185                 190                 195

ctg gtt ctc atc gtg ctg ctg ctc ttt gtt tcg ggc gca tta agg tcc    739
Leu Val Leu Ile Val Leu Leu Leu Phe Val Ser Gly Ala Leu Arg Ser
        200                 205                 210

ctc ggt ttc agc gcc tac aac acc ttg cag ttt gtc gat atc tca cca    787
Leu Gly Phe Ser Ala Tyr Asn Thr Leu Gln Phe Val Asp Ile Ser Pro
    215                 220                 225

gaa caa acc agc aac gcc aac gtg tta tca gca acc ctg cac caa cta    835
Glu Gln Thr Ser Asn Ala Asn Val Leu Ser Ala Thr Leu His Gln Leu
230                 235                 240                 245

ggc atg tct ttg ggt att gcg gta gca gtc atc gcc atg tcc ctt gca    883
Gly Met Ser Leu Gly Ile Ala Val Ala Val Ile Ala Met Ser Leu Ala
                250                 255                 260

ccc acc gcc aac tgg gca ttc cca ctg gca gca gcg ttg ttc ctc att    931
Pro Thr Ala Asn Trp Ala Phe Pro Leu Ala Ala Ala Leu Phe Leu Ile
            265                 270                 275

cct cta atc ggc gca cta tct ttg cct cgc gac ggc ggt gcc cga gcc    979
Pro Leu Ile Gly Ala Leu Ser Leu Pro Arg Asp Gly Gly Ala Arg Ala
        280                 285                 290

ttt tcc tcc tct tagaaaccca cttctgaaag gta                          1014
Phe Ser Ser Ser
    295
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<210> 158
<211> 297
<212> PRT
<213> Corynebacterium glutamicum

<400> 158

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Leu Gln Asp Thr Ile Gly Cys Arg Trp Ile Phe Leu Leu Asn Val Pro
  1               5                  10                  15
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Leu Gly Ile Ile Ala Ile Met Ala Gly Leu Phe Ile Gln Pro Lys Asn
            20                  25                  30

Thr Ala Val Asn Val Lys Arg Phe Asp Arg Pro Gly Phe Leu Gly Ala
        35                  40                  45

Met Leu Val Met Val Ala Gln Ala Val Ile Ala Glu Leu Ile Cys Ser
    50                  55                  60

Arg Ser Pro Ala Ala Leu Thr Ile Cys Ala Cys Leu Val Leu Ser Ala
65                  70                  75                  80

Ala Val Val Cys Gly Phe Val Val Arg Trp Leu Arg Val Pro Gly Arg
                85                  90                  95

Leu Phe Asp Leu Ser Ile Met Arg Ile Pro Gly Phe Arg Val Gly Asn
            100                 105                 110

Ser Ser Gly Ser Ile Tyr Arg Leu Val Ile Thr Ala Ala Pro Phe Met
        115                 120                 125

Phe Thr Leu Leu Phe Gln Val Ala Phe Gly Trp Ser Ala Thr Leu Ala
    130                 135                 140

Gly Ala Met Val Val Ala Leu Phe Ala Gly Asn Val Ala Ile Lys Pro
145                 150                 155                 160

Phe Thr Thr Pro Ile Ile Lys Arg Trp Asn Phe Lys Pro Val Leu Val
                165                 170                 175

Phe Ser Asn Ala Ala Gly Ala Leu Val Leu Ala Thr Phe Leu Phe Val
            180                 185                 190

Arg Ala Asp Thr Pro Leu Val Leu Ile Val Leu Leu Leu Phe Val Ser
        195                 200                 205

Gly Ala Leu Arg Ser Leu Gly Phe Ser Ala Tyr Asn Thr Leu Gln Phe
    210                 215                 220

Val Asp Ile Ser Pro Glu Gln Thr Ser Asn Ala Asn Val Leu Ser Ala
225                 230                 235                 240

Thr Leu His Gln Leu Gly Met Ser Leu Gly Ile Ala Val Ala Val Ile
                245                 250                 255

Ala Met Ser Leu Ala Pro Thr Ala Asn Trp Ala Phe Pro Leu Ala Ala
            260                 265                 270

Ala Leu Phe Leu Ile Pro Leu Ile Gly Ala Leu Ser Leu Pro Arg Asp
        275                 280                 285

Gly Gly Ala Arg Ala Phe Ser Ser Ser
    290                 295
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<210> 159

<211> 324
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(301)
<223> RXA01408

<400> 159
cgcatagagt tatctcgaaa ctaccaagac ggtttctttt ctttagatct aaggaggaga 60

gaccgtcttt caccctttca tctgattgga catcgacgcc atg cgc aat gat cgg 115
Met Arg Asn Asp Arg
1 5

tcc ttt agc gtt ccc att gcg cta ctt gcc gcg gga gca ctg ttt cta 163
Ser Phe Ser Val Pro Ile Ala Leu Leu Ala Ala Gly Ala Leu Phe Leu
10 15 20

gaa atc ctc gac ggc acc atc ctg aca acc gca gtg cca gct att gct 211
Glu Ile Leu Asp Gly Thr Ile Leu Thr Thr Ala Val Pro Ala Ile Ala
25 30 35

cgt gac ttc ggt att gac gcc gtg gat gtc agc att gca ctg gtt gct 259
Arg Asp Phe Gly Ile Asp Ala Val Asp Val Ser Ile Ala Leu Val Ala
40 45 50

tac ttg gca gcc gca gca gct ggc att ccg ctg cag ggt ggc 301
Tyr Leu Ala Ala Ala Ala Ala Gly Ile Pro Leu Gln Gly Gly
55 60 65

tagcggatcg atttggtgtg cgc 324

<210> 160
<211> 67
<212> PRT
<213> Corynebacterium glutamicum

<400> 160
Met Arg Asn Asp Arg Ser Phe Ser Val Pro Ile Ala Leu Leu Ala Ala
1 5 10 15

Gly Ala Leu Phe Leu Glu Ile Leu Asp Gly Thr Ile Leu Thr Thr Ala
20 25 30

Val Pro Ala Ile Ala Arg Asp Phe Gly Ile Asp Ala Val Asp Val Ser
35 40 45

Ile Ala Leu Val Ala Tyr Leu Ala Ala Ala Ala Ala Gly Ile Pro Leu
50 55 60

Gln Gly Gly
65

<210> 161
<211> 1275
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1252)
<223> RXN01922

<400> 161
acactccttt ggtcacctgg tttggttgag ggaaacagac cgcccaagaa cccaagaaat 60

cccaagaaaa catgctgctt atgaattaaa gtgagcaccc atg aga tca gga aac 115
Met Arg Ser Gly Asn
1 5

gcc aat cgc gtc ttc ata ggt gtt acc atc ctg ctg ttt act gca gga 163
Ala Asn Arg Val Phe Ile Gly Val Thr Ile Leu Leu Phe Thr Ala Gly
10 15 20

tgg gca gcc aat cat ttc gcg tca gtg ttg gtg ttg atc cgt gaa caa 211
Trp Ala Ala Asn His Phe Ala Ser Val Leu Val Leu Ile Arg Glu Gln
25 30 35

tta gac gta tca agc gtg ctg gtc aac ggc gct ttt ggt att tat gca 259
Leu Asp Val Ser Ser Val Leu Val Asn Gly Ala Phe Gly Ile Tyr Ala
40 45 50

ctg gga ctt ctt cca agt ttg ctc gca ggc ggt gtg ctt gcc gac cgt 307
Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Gly Val Leu Ala Asp Arg
55 60 65

ttt ggt gcc cgc atg gtg gta ctc acc gga ggt gta ctt tct gcg ctt 355
Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly Val Leu Ser Ala Leu
70 75 80 85

gga aac ctt tct ctt tta gcg ttt cat gat ggt cct tcc ctc ctg gta 403
Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly Pro Ser Leu Leu Val
90 95 100

gga cga ttc atc gtt ggt ctg ggc gtt gga tta gtc gtc agc gcg ggc 451
Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu Val Val Ser Ala Gly
105 110 115

acc gca tgg gcg ggc aga ttg cgc gga gca agc ggc gtg aca ttg gcc 499
Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser Gly Val Thr Leu Ala
120 125 130

ggc att att ctg acc gcc ggt ttc atg atg ggg ccg att gtg aca agt 547
Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly Pro Ile Val Thr Ser
135 140 145

ggg ttg ggg atg gcg tcg aca agc att att acg ccc ttt gcc ata agc 595
Gly Leu Gly Met Ala Ser Thr Ser Ile Ile Thr Pro Phe Ala Ile Ser
150 155 160 165

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gtt gcc ctc tcg ctg atc gcg gtg gtt gtg gga ttt gcg ctt ggc gat    643
Val Ala Leu Ser Leu Ile Ala Val Val Val Gly Phe Ala Leu Gly Asp
                170                 175                 180

gcc cgc agc acc ccg agc gca ctt ggc gca tcc agc gga atc aaa cac    691
Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala Ser Ser Gly Ile Lys His
            185                 190                 195

gaa cga agc atg aaa aag gcc ctc gcg gtg tcc ttg ccg atg gca att    739
Glu Arg Ser Met Lys Lys Ala Leu Ala Val Ser Leu Pro Met Ala Ile
        200                 205                 210

tgg gtg ttc agc tgc atc acc acc tcc ctg atc gtg atg tcc gcg cgc    787
Trp Val Phe Ser Cys Ile Thr Thr Ser Leu Ile Val Met Ser Ala Arg
    215                 220                 225

atc gac tcc acc ttc ggc aac gcc att ctt ctc ccc gga atc ggc gcg    835
Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu Leu Pro Gly Ile Gly Ala
230                 235                 240                 245

gcg atc gcc ttc agc gca ggc ctg atc gca caa ttt tta ggt agg aaa    883
Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala Gln Phe Leu Gly Arg Lys
                250                 255                 260

ttc gcg tgg ggt cgt ggc tcc gga atc gtg ggc gcg ctg tgt gcc ctc    931
Phe Ala Trp Gly Arg Gly Ser Gly Ile Val Gly Ala Leu Cys Ala Leu
            265                 270                 275

gcg ggt ttt gcg ctg gca gct ttt ggt ggc gac tcc att cca gtg tgg    979
Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly Asp Ser Ile Pro Val Trp
        280                 285                 290

ctt ttc gtt atc gcc tcg atc ctg ttc ggc acc gca tat ggc ctc tgc    1027
Leu Phe Val Ile Ala Ser Ile Leu Phe Gly Thr Ala Tyr Gly Leu Cys
    295                 300                 305

ctg cgc gaa ggc ctc ctc agc atc gaa act tac acg cca ctc aac cga    1075
Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr Tyr Thr Pro Leu Asn Arg
310                 315                 320                 325

cgt ggc acc ggc atc ggc atc tat tat gtg ttc acg tat ttg gga ttc    1123
Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val Phe Thr Tyr Leu Gly Phe
                330                 335                 340

ggg ctg cca gtg ctt ctc gac gcc ctc ctc ccg cac ctt ggc gcc tcc    1171
Gly Leu Pro Val Leu Leu Asp Ala Leu Leu Pro His Leu Gly Ala Ser
            345                 350                 355

att ccg ctg tac gcg ctg gcg gcg ctc gcc ctt ggc tcc gca gta atc    1219
Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala Leu Gly Ser Ala Val Ile
        360                 365                 370

cgc ggc gta caa atc aag cgc ggg tat gtg gtt tagatttcta cctacgacct 1272
Arg Gly Val Gln Ile Lys Arg Gly Tyr Val Val
    375                 380

gaa                                                                1275
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<210> 162
<211> 384
<212> PRT
<213> Corynebacterium glutamicum

<400> 162
Met Arg Ser Gly Asn Ala Asn Arg Val Phe Ile Gly Val Thr Ile Leu
1 5 10 15

Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu Val
20 25 30

Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly Ala
35 40 45

Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Gly
50 55 60

Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly
65 70 75 80

Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly
85 90 95

Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu
100 105 110

Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser
115 120 125

Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly
130 135 140

Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile Thr
145 150 155 160

Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val Gly
165 170 175

Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala Ser
180 185 190

Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val Ser
195 200 205

Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu Ile
210 215 220

Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu Leu
225 230 235 240

Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala Gln
245 250 255

Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val Gly

260 265 270

Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly Asp
275 280 285

Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly Thr
290 295 300

Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr Tyr
305 310 315 320

Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val Phe
325 330 335

Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu Pro
340 345 350

His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala Leu
355 360 365

Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val Val
370 375 380

<210> 163
<211> 1130
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1107)
<223> FRXA01922

<400> 163
ctg ctg ttt act gca gga tgg gca gcc aat cat ttc gcg tca gtg ttg 48
Leu Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu
1 5 10 15

gtg ttg atc cgt gaa caa tta gac gta tca agc gtg ctg gtc aac ggc 96
Val Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly
20 25 30

gct ttt ggt att tat gca ctg gga ctt ctt cca agt ttg ctc gca ggc 144
Ala Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly
35 40 45

ggt gtg ctt gcc gac cgt ttt ggt gcc cgc atg gtg gta ctc acc gga 192
Gly Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly
50 55 60

ggt gta ctt tct gcg ctt gga aac ctt tct ctt tta gcg ttt cat gat 240
Gly Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp
65 70 75 80

ggt cct tcc ctc ctg gta gga cga ttc atc gtt ggt ctg ggc gtt gga 288
Gly Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly
85 90 95

tta gtc gtc agc gcg ggc acc gca tgg gcg ggc aga ttg cgc gga gca 336
Leu Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala
100 105 110

agc ggc gtg aca ttg gcc ggc att att ctg acc gcc ggt ttc atg atg 384
Ser Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met
115 120 125

ggg ccg att gtg aca agt ggg ttg ggg atg gcg tcg aca agc att att 432
Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile
130 135 140

acg ccc ttt gcc ata agc gtt gcc ctc tcg ctg atc gcg gtg gtt gtg 480
Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val
145 150 155 160

gga ttt gcg ctt ggc gat gcc cgc agc acc ccg agc gca ctt ggc gca 528
Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala
165 170 175

tcc agc gga atc aaa cac gaa cga agc atg aaa aag gcc ctc gcg gtg 576
Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val
180 185 190

tcc ttg ccg atg gca att tgg gtg ttc agc tgc atc acc acc tcc ctg 624
Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu
195 200 205

atc gtg atg tcc gcg cgc atc gac tcc acc ttc ggc aac gcc att ctt 672
Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu
210 215 220

ctc ccc gga atc ggc gcg gcg atc gcc ttc agc gca ggc ctg atc gca 720
Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala
225 230 235 240

caa ttt tta ggt agg aaa ttc gcg tgg ggt cgt ggc tcc gga atc gtg 768
Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val
245 250 255

ggc gcg ctg tgt gcc ctc gcg ggt ttt gcg ctg gca gct ttt ggt ggc 816
Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly
260 265 270

gac tcc att cca gtg tgg ctt ttc gtt atc gcc tcg atc ctg ttc ggc 864
Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly
275 280 285

acc gca tat ggc ctc tgc ctg cgc gaa ggc ctc ctc agc atc gaa act 912
Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr
290 295 300

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tac acg cca ctc aac cga cgt ggc acc ggc atc ggc atc tat tat gtg    960
Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val
305                 310                 315                 320

ttc acg tat ttg gga ttc ggg ctg cca gtg ctt ctc gac gcc ctc ctc    1008
Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu
                325                 330                 335

ccg cac ctt ggc gcc tcc att ccg ctg tac gcg ctg gcg gcg ctc gcc    1056
Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala
            340                 345                 350

ctt ggc tcc gca gta atc cgc ggc gta caa atc aag cgc ggg tat gtg    1104
Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val
        355                 360                 365

gtt tagatttcta cctacgacct gaa                                      1130
Val


<210> 164
<211> 369
<212> PRT
<213> Corynebacterium glutamicum

<400> 164
Leu Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu
  1               5                  10                  15

Val Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly
             20                  25                  30

Ala Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly
         35                  40                  45

Gly Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly
     50                  55                  60

Gly Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp
 65                  70                  75                  80

Gly Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly
                 85                  90                  95

Leu Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala
            100                 105                 110

Ser Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met
        115                 120                 125

Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile
    130                 135                 140

Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val
145                 150                 155                 160
```

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Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala
                165                 170                 175

Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val
            180                 185                 190

Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu
        195                 200                 205

Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu
    210                 215                 220

Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala
225                 230                 235                 240

Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val
                245                 250                 255

Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly
            260                 265                 270

Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly
        275                 280                 285

Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr
    290                 295                 300

Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val
305                 310                 315                 320

Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu
                325                 330                 335

Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala
            340                 345                 350

Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val
        355                 360                 365

Val


<210> 165
<211> 362
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(339)
<223> RXA02060

<400> 165
gaa ttt gcc cgc att ttg aag cca aag gga cag gtc atc gtg ctt acc      48
Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
  1               5                  10                  15
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gca gat acc ggc cac ttg gct gag ctt cgt gaa cca ctg ggc atc att 96
Ala Asp Thr Gly His Leu Ala Glu Leu Arg Glu Pro Leu Gly Ile Ile
20 25 30

gat gtg gag gcc ggc aaa gtt gat cgc atg atc gaa caa gcg gca ggc 144
Asp Val Glu Ala Gly Lys Val Asp Arg Met Ile Glu Gln Ala Ala Gly
35 40 45

cac ctc aag cca gtt ggc gaa aga gac ttg gtg gaa ttt gaa atg ctg 192
His Leu Lys Pro Val Gly Glu Arg Asp Leu Val Glu Phe Glu Met Leu
50 55 60

ctg gat caa aaa tcc att gca tct cag atc ggt atg agc cct tct gca 240
Leu Asp Gln Lys Ser Ile Ala Ser Gln Ile Gly Met Ser Pro Ser Ala
65 70 75 80

cgc cac att aag cct gag gct ttg gcg gaa cgc atc gcc gct cta cca 288
Arg His Ile Lys Pro Glu Ala Leu Ala Glu Arg Ile Ala Ala Leu Pro
85 90 95

gaa caa atg aag gtt aca gcc cgg gcc aag atc acc agg ctg gaa cgc 336
Glu Gln Met Lys Val Thr Ala Arg Ala Lys Ile Thr Arg Leu Glu Arg
100 105 110

atc taactcttat ctcactgggc ctt 362
Ile

<210> 166
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 166
Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
1 5 10 15

Ala Asp Thr Gly His Leu Ala Glu Leu Arg Glu Pro Leu Gly Ile Ile
20 25 30

Asp Val Glu Ala Gly Lys Val Asp Arg Met Ile Glu Gln Ala Ala Gly
35 40 45

His Leu Lys Pro Val Gly Glu Arg Asp Leu Val Glu Phe Glu Met Leu
50 55 60

Leu Asp Gln Lys Ser Ile Ala Ser Gln Ile Gly Met Ser Pro Ser Ala
65 70 75 80

Arg His Ile Lys Pro Glu Ala Leu Ala Glu Arg Ile Ala Ala Leu Pro
85 90 95

Glu Gln Met Lys Val Thr Ala Arg Ala Lys Ile Thr Arg Leu Glu Arg
100 105 110

Ile

<210> 167
<211> 1395
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1372)
<223> RXN01936

<400> 167
gcgcggtgac accacagccg ttgtcagcgg cgcttggtct gtggaggatc gccgaggtta 60

ctaacaaata ggcccaacaa agaggtctaa gctctacctg gtg agt ttc cga gat 115
Val Ser Phe Arg Asp
1 5

att ttc gct gac acc aga ccg ctg aaa gaa ccg gcc ttc aaa cgc ctc 163
Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro Ala Phe Lys Arg Leu
10 15 20

tgg ctt ggc aat gtt gcc acc gtc att ggt gcc caa tta act gtt gtt 211
Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala Gln Leu Thr Val Val
25 30 35

gcc gtt ccg gtg cag att tac caa atg act ggg tcc tcc ggc tat gtg 259
Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly Ser Ser Gly Tyr Val
40 45 50

ggc ttg acc ggg ctt ttt ggc ctt att cct ttg gtt att ttt ggc ctt 307
Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu Val Ile Phe Gly Leu
55 60 65

tat ggt gga tcc att gcg gat gct ttt gat aaa cgc atc gtg ctg atc 355
Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys Arg Ile Val Leu Ile
70 75 80 85

tgc acc acg atc ggc atg tgt gtc acc act gcc ggt ttt tgg gtg ctg 403
Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala Gly Phe Trp Val Leu
90 95 100

acc att tta ggc aat gag aat att tgg ctc ctg tta ata aac ttt tct 451
Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu Leu Ile Asn Phe Ser
105 110 115

tta cag cag gca ttt ttc gcg gtg aat caa ccc acc cga acg gcg atc 499
Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro Thr Arg Thr Ala Ile
120 125 130

ctt cga agt att ttg ccg att gat caa tta gcg tcg gca aca tca ctg 547
Leu Arg Ser Ile Leu Pro Ile Asp Gln Leu Ala Ser Ala Thr Ser Leu
135 140 145

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aat atg ctg ctc atg cag acc ggc gca atc gtt ggc ccg ctg atc gca    595
Asn Met Leu Leu Met Gln Thr Gly Ala Ile Val Gly Pro Leu Ile Ala
150                 155                 160                 165

ggt gcg ttg att ccg ctg atc ggt ttc ggg tgg ctg tat ttc ctt gat    643
Gly Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp
                170                 175                 180

gtt gtc tcc atc atc ccc aca ctg tgg gct gta tgg tca ctg cct tcg    691
Val Val Ser Ile Ile Pro Thr Leu Trp Ala Val Trp Ser Leu Pro Ser
            185                 190                 195

atc aag cca tcc ggc aag gtg atg aag gct ggt ttc gcc agt gtg gtg    739
Ile Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val
        200                 205                 210

gat ggc ctg aag tat ttg gct ggc caa ccc gtg ttg ttg atg gtg atg    787
Asp Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met
    215                 220                 225

gtg ctg gat ctt atc gcc atg att ttc ggc atg cca cgt gcg ctt tac    835
Val Leu Asp Leu Ile Ala Met Ile Phe Gly Met Pro Arg Ala Leu Tyr
230                 235                 240                 245

ccc gag atc gca gaa gtg aac ttc ggt ggg ggt gac gcc ggt gca acg    883
Pro Glu Ile Ala Glu Val Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr
                250                 255                 260

atg ctg gcg ttc atg tac tca tcc atg gct gtt ggc gca gtt ctt ggc    931
Met Leu Ala Phe Met Tyr Ser Ser Met Ala Val Gly Ala Val Leu Gly
            265                 270                 275

ggc gtg ctg tct ggt tgg gtg gcc cgg att agc cgc cag ggt gtt gca    979
Gly Val Leu Ser Gly Trp Val Ala Arg Ile Ser Arg Gln Gly Val Ala
        280                 285                 290

gtt tat tgg tgc atc atc gcc tgg ggc gca gcc gtt gct ttg ggt ggt    1027
Val Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala Val Ala Leu Gly Gly
    295                 300                 305

gtg gca att gtt gtc agc ccc ggc gcg gtg act gcg tgg gcg tgg atg    1075
Val Ala Ile Val Val Ser Pro Gly Ala Val Thr Ala Trp Ala Trp Met
310                 315                 320                 325

ttc atc atc atg atg gtc att ggt ggc atg gct gac atg ttc agc tcg    1123
Phe Ile Ile Met Met Val Ile Gly Gly Met Ala Asp Met Phe Ser Ser
                330                 335                 340

gca gtt cga aac gct att ttg cag cag tct gct gcg gaa cat gtg cag    1171
Ala Val Arg Asn Ala Ile Leu Gln Gln Ser Ala Ala Glu His Val Gln
            345                 350                 355

ggc cga atc caa ggt gtg tgg atc atc gtc gtg gtg ggt gga cct cgt    1219
Gly Arg Ile Gln Gly Val Trp Ile Ile Val Val Val Gly Gly Pro Arg
        360                 365                 370

tta gct gac gtc ctt cac ggt tgg gcc gct gag ccc ctc ggc gca ggt    1267
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Leu Ala Asp Val Leu His Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly
    375                 380                 385

tgg acg gta tta tgg ggc gga gta gcg gtg gtt gta ctc act gca att    1315
Trp Thr Val Leu Trp Gly Gly Val Ala Val Val Val Leu Thr Ala Ile
390                 395                 400                 405

tgt atg gtg gcg gtg cct aaa ttc tgg aaa tac gag aaa cca aaa att    1363
Cys Met Val Ala Val Pro Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile
                410                 415                 420

acc ggc atc taaatactta tccatgccca ttt                              1395
Thr Gly Ile



<210> 168
<211> 424
<212> PRT
<213> Corynebacterium glutamicum

<400> 168
Val Ser Phe Arg Asp Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
1               5                   10                  15

Ala Phe Lys Arg Leu Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala
            20                  25                  30

Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
        35                  40                  45

Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
    50                  55                  60

Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
65                  70                  75                  80

Arg Ile Val Leu Ile Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala
                85                  90                  95

Gly Phe Trp Val Leu Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu
            100                 105                 110

Leu Ile Asn Phe Ser Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro
        115                 120                 125

Thr Arg Thr Ala Ile Leu Arg Ser Ile Leu Pro Ile Asp Gln Leu Ala
    130                 135                 140

Ser Ala Thr Ser Leu Asn Met Leu Leu Met Gln Thr Gly Ala Ile Val
145                 150                 155                 160

Gly Pro Leu Ile Ala Gly Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp
                165                 170                 175

Leu Tyr Phe Leu Asp Val Val Ser Ile Ile Pro Thr Leu Trp Ala Val
            180                 185                 190
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```
Trp Ser Leu Pro Ser Ile Lys Pro Ser Gly Lys Val Met Lys Ala Gly
        195                 200                 205

Phe Ala Ser Val Val Asp Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val
    210                 215                 220

Leu Leu Met Val Met Val Leu Asp Leu Ile Ala Met Ile Phe Gly Met
225                 230                 235                 240

Pro Arg Ala Leu Tyr Pro Glu Ile Ala Glu Val Asn Phe Gly Gly Gly
                245                 250                 255

Asp Ala Gly Ala Thr Met Leu Ala Phe Met Tyr Ser Ser Met Ala Val
            260                 265                 270

Gly Ala Val Leu Gly Gly Val Leu Ser Gly Trp Val Ala Arg Ile Ser
        275                 280                 285

Arg Gln Gly Val Ala Val Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala
    290                 295                 300

Val Ala Leu Gly Gly Val Ala Ile Val Val Ser Pro Gly Ala Val Thr
305                 310                 315                 320

Ala Trp Ala Trp Met Phe Ile Ile Met Met Val Ile Gly Gly Met Ala
                325                 330                 335

Asp Met Phe Ser Ser Ala Val Arg Asn Ala Ile Leu Gln Gln Ser Ala
            340                 345                 350

Ala Glu His Val Gln Gly Arg Ile Gln Gly Val Trp Ile Ile Val Val
        355                 360                 365

Val Gly Gly Pro Arg Leu Ala Asp Val Leu His Gly Trp Ala Ala Glu
    370                 375                 380

Pro Leu Gly Ala Gly Trp Thr Val Leu Trp Gly Gly Val Ala Val Val
385                 390                 395                 400

Val Leu Thr Ala Ile Cys Met Val Ala Val Pro Lys Phe Trp Lys Tyr
                405                 410                 415

Glu Lys Pro Lys Ile Thr Gly Ile
            420
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<210> 169
<211> 945
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(922)
<223> FRXA01936

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<400> 169
tttacagcag gcatttttcg cggtgaatca acccacccga acggcgatcc ttcgaagtat 60

tttgccgatt gatcaataag cgtcggcaac atcactgaat atg ctg ctc atg cag   115
                                            Met Leu Leu Met Gln
                                             1               5

acc ggc gca atc gtt ggc ccg ctg atc gca ggt gcg ttg att ccg ctg   163
Thr Gly Ala Ile Val Gly Pro Leu Ile Ala Gly Ala Leu Ile Pro Leu
                10                  15                  20

atc ggt ttc ggg tgg ctg tat ttc ctt gat gtt gtc tcc atc atc ccc   211
Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp Val Val Ser Ile Ile Pro
            25                  30                  35

aca ctg tgg gct gta tgg tca ctg cct tcg atc aag cca tcc ggc aag   259
Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile Lys Pro Ser Gly Lys
        40                  45                  50

gtg atg aag gct ggt ttc gcc agt gtg gtg gat ggc ctg aag tat ttg   307
Val Met Lys Ala Gly Phe Ala Ser Val Val Asp Gly Leu Lys Tyr Leu
    55                  60                  65

gct ggc caa ccc gtg ttg ttg atg gtg atg gtg ctg gat ctt atc gcc   355
Ala Gly Gln Pro Val Leu Leu Met Val Met Val Leu Asp Leu Ile Ala
70                  75                  80                  85

atg att ttc ggc atg cca cgt gcg ctt tac ccc gag atc gca gaa gtg   403
Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro Glu Ile Ala Glu Val
                90                  95                  100

aac ttc ggt ggg ggt gac gcc ggt gca acg atg ctg gcg ttc atg tac   451
Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr Met Leu Ala Phe Met Tyr
            105                 110                 115

tca tcc atg gct gtt ggc gca gtt ctt ggc ggc gtg ctg tct ggt tgg   499
Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly Val Leu Ser Gly Trp
        120                 125                 130

gtg gcc cgg att agc cgc cag ggt gtt gca gtt tat tgg tgc atc atc   547
Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val Tyr Trp Cys Ile Ile
    135                 140                 145

gcc tgg ggc gca gcc gtt gct ttg ggt ggt gtg gca att gtt gtc agc   595
Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val Ala Ile Val Val Ser
150                 155                 160                 165

ccc ggc gcg gtg act gcg tgg gcg tgg atg ttc atc atc atg atg gtc   643
Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe Ile Ile Met Met Val
                170                 175                 180

att ggt ggc atg gct gac atg ttc agc tcg gca gtt cga aac gct att   691
Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala Val Arg Asn Ala Ile
            185                 190                 195

ttg cag cag tct gct gcg gaa cat gtg cag ggc cga atc caa ggt gtg   739
Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly Arg Ile Gln Gly Val
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200 205 210

tgg atc atc gtc gtg gtg ggt gga cct cgt tta gct gac gtc ctt cac 787
Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu Ala Asp Val Leu His
215 220 225

ggt tgg gcc gct gag ccc ctc ggc gca ggt tgg acg gta tta tgg ggc 835
Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp Thr Val Leu Trp Gly
230 235 240 245

gga gta gcg gtg gtt gta ctc act gca att tgt atg gtg gcg gtg cct 883
Gly Val Ala Val Val Val Leu Thr Ala Ile Cys Met Val Ala Val Pro
250 255 260

aaa ttc tgg aaa tac gag aaa cca aaa att acc ggc atc taaatactta 932
Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr Gly Ile
265 270

tccatgccca ttt 945

<210> 170
<211> 274
<212> PRT
<213> Corynebacterium glutamicum

<400> 170
Met Leu Leu Met Gln Thr Gly Ala Ile Val Gly Pro Leu Ile Ala Gly
1 5 10 15

Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp Val
20 25 30

Val Ser Ile Ile Pro Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile
35 40 45

Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val Asp
50 55 60

Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met Val
65 70 75 80

Leu Asp Leu Ile Ala Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro
85 90 95

Glu Ile Ala Glu Val Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr Met
100 105 110

Leu Ala Phe Met Tyr Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly
115 120 125

Val Leu Ser Gly Trp Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val
130 135 140

Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val
145 150 155 160

```
Ala Ile Val Val Ser Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe
                165                 170                 175

Ile Ile Met Met Val Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala
            180                 185                 190

Val Arg Asn Ala Ile Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly
        195                 200                 205

Arg Ile Gln Gly Val Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu
    210                 215                 220

Ala Asp Val Leu His Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp
225                 230                 235                 240

Thr Val Leu Trp Gly Gly Val Ala Val Val Val Leu Thr Ala Ile Cys
                245                 250                 255

Met Val Ala Val Pro Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr
            260                 265                 270

Gly Ile


&lt;210&gt; 171
&lt;211&gt; 549
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(526)
&lt;223&gt; FRXA01937

&lt;400&gt; 171
gcgcggtgac accacagccg ttgtcagcgg cgcttggtct gtggaggatc gccgaggtta 60

ctaacaaata ggcccaacaa agaggtctaa gctctacctg gtg agt ttc cga gat    115
                                            Val Ser Phe Arg Asp
                                            1               5

att ttc gct gac acc aga ccg ctg aaa gaa ccg gcc ttc aaa cgc ctc    163
Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro Ala Phe Lys Arg Leu
                10                  15                  20

tgg ctt ggc aat gtt gcc acc gtc att ggt gcc caa tta act gtt gtt    211
Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala Gln Leu Thr Val Val
            25                  30                  35

gcc gtt ccg gtg cag att tac caa atg act ggg tcc tcc ggc tat gtg    259
Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly Ser Ser Gly Tyr Val
        40                  45                  50

ggc ttg acc ggg ctt ttt ggc ctt att cct ttg gtt att ttt ggc ctt    307
Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu Val Ile Phe Gly Leu
    55                  60                  65
```

```
tat ggt gga tcc att gcg gat gct ttt gat aaa cgc atc gtg ctg atc      355
Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys Arg Ile Val Leu Ile
 70                  75                  80                  85

tgc acc acg atc ggc atg tgt gtc acc act gcc ggt ttt tgg gtg ctg      403
Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala Gly Phe Trp Val Leu
                 90                  95                 100

acc att tta ggc aat gag aat att tgg ctc ctg tta ata aac ttt tct      451
Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu Leu Ile Asn Phe Ser
            105                 110                 115

tta cag cag gca ttt ttc gcg gtg aat caa ccc acc cga acg gcg atc      499
Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro Thr Arg Thr Ala Ile
        120                 125                 130

ctt cga agt att ttg ccg att gat caa taagcgtcgg caacatcact            546
Leu Arg Ser Ile Leu Pro Ile Asp Gln
    135                 140

gaa                                                                  549


<210> 172
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 172
Val Ser Phe Arg Asp Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
  1               5                  10                  15

Ala Phe Lys Arg Leu Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala
             20                  25                  30

Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
         35                  40                  45

Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
     50                  55                  60

Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
 65                  70                  75                  80

Arg Ile Val Leu Ile Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala
                 85                  90                  95

Gly Phe Trp Val Leu Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu
            100                 105                 110

Leu Ile Asn Phe Ser Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro
        115                 120                 125

Thr Arg Thr Ala Ile Leu Arg Ser Ile Leu Pro Ile Asp Gln
    130                 135                 140
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<210> 173
<211> 1242
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1219)
<223> RXN01010

<400> 173
gtgccaaagc gtttcctgta aaacgcataa ccccgaatac cccctgtttc cagatccaaa 60

aaaagatctg gcagggggtt taggcataga ttaggaactt atg aag aaa ctg caa 115
Met Lys Lys Leu Gln
1 5

atg ccg gcc att ttg gtc gga ggc ttt gtg ggg ccg ttt act ggc caa 163
Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly Pro Phe Thr Gly Gln
10 15 20

gct cta tca gtg gtc ttg ccg gaa ttt gca gac acc ttt gat atc agt 211
Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp Thr Phe Asp Ile Ser
25 30 35

gtc agc cag gca gcg ctg acc atg acc gca tac ttg ttg ccc ttt gcc 259
Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr Leu Leu Pro Phe Ala
40 45 50

acc atg atg ttg ttt tcg ggg cgc atc acc aga aag atc cat ccg cat 307
Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg Lys Ile His Pro His
55 60 65

aag gtg gtg cag gcg gct tat att gtc aca ctg cca ctt gcg ctg ttg 355
Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu Pro Leu Ala Leu Leu
70 75 80 85

ctc cta gtt aca cca tcg tgg ggg ctg ttt atg gct gcg tat gcc acg 403
Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met Ala Ala Tyr Ala Thr
90 95 100

att ggt atc gct aat gca ttt acc act ccg gtg ctg caa att atg ttg 451
Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val Leu Gln Ile Met Leu
105 110 115

cgt gag ctt gtt ccg ccg cgt tct ttg ggt aag gca ttg ggc acc tat 499
Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys Ala Leu Gly Thr Tyr
120 125 130

gct gcg atg caa tca ctc ggc atg ttg tcg gcg cca ctg atc gca ggt 547
Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala Pro Leu Ile Ala Gly
135 140 145

gtg tct tcg gtg gtg tcg tgg agg ttg acc ttc ctg gtc act gca gca 595
Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe Leu Val Thr Ala Ala
150 155 160 165

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gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca    643
Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro
                170                 175                 180

tca gca tcg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc    691
Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr
            185                 190                 195

atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc    739
Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly
        200                 205                 210

att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt gat    787
Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asp
    215                 220                 225

gct gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc ctg gct gcg ttc    835
Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Leu Ala Ala Phe
230                 235                 240                 245

ttt gcc tcc cgc aag att ggc gat ttg gca gac aaa ttt ggt gtg cgc    883
Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp Lys Phe Gly Val Arg
                250                 255                 260

gcg gtg ctc att gtc agt gct gtc atc ggt acc atc gca ctc gca ctg    931
Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr Ile Ala Leu Ala Leu
            265                 270                 275

ctg ccg atc gca ccg tgg atc att gtg gtg gcc gta ctg tgg gcc ttc    979
Leu Pro Ile Ala Pro Trp Ile Ile Val Val Ala Val Leu Trp Ala Phe
        280                 285                 290

gca gta gca gca gca caa gga atc caa gca acc gtc aac ttg gct gtc    1027
Ala Val Ala Ala Ala Gln Gly Ile Gln Ala Thr Val Asn Leu Ala Val
    295                 300                 305

atc gga agc ccc ggt gga tca tcg ctg ctt tct acc gtg cag gct ttc    1075
Ile Gly Ser Pro Gly Gly Ser Ser Leu Leu Ser Thr Val Gln Ala Phe
310                 315                 320                 325

cga ttc ttc gga tca gcg gca gca cca gtg aca ttc ctt cct atc tat    1123
Arg Phe Phe Gly Ser Ala Ala Ala Pro Val Thr Phe Leu Pro Ile Tyr
                330                 335                 340

atg ggc atc ggc tcg ggg gcg ttt tgg gtc agc gcg gta gcg ctg ttc    1171
Met Gly Ile Gly Ser Gly Ala Phe Trp Val Ser Ala Val Ala Leu Phe
            345                 350                 355

ttc gtt gcc atc gcc cag tgg ctc aac ccg cag cgg gtg gag cgg ggc    1219
Phe Val Ala Ile Ala Gln Trp Leu Asn Pro Gln Arg Val Glu Arg Gly
        360                 365                 370

tgagggagac gtcgagaagc gtc                                          1242
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<210> 174

<211> 373
<212> PRT
<213> Corynebacterium glutamicum

<400> 174
Met Lys Lys Leu Gln Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly
1 5 10 15

Pro Phe Thr Gly Gln Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp
20 25 30

Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
35 40 45

Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
50 55 60

Lys Ile His Pro His Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu
65 70 75 80

Pro Leu Ala Leu Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
85 90 95

Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
100 105 110

Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
115 120 125

Ala Leu Gly Thr Tyr Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala
130 135 140

Pro Leu Ile Ala Gly Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe
145 150 155 160

Leu Val Thr Ala Ala Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro
165 170 175

Val Val Pro Pro Pro Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val
180 185 190

Gln Trp Gly Pro Thr Ile Ile His Met Val Ser Gly Phe Val Val Gly
195 200 205

Ile Gly Ile Ile Gly Ile Gly Phe Met Thr Ser Leu His Val Gly Glu
210 215 220

Gln Phe Gly Leu Asp Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly
225 230 235 240

Gly Leu Ala Ala Phe Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp
245 250 255

Lys Phe Gly Val Arg Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr
260 265 270

Ile Ala Leu Ala Leu Leu Pro Ile Ala Pro Trp Ile Ile Val Val Ala

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        275                 280                 285

Val Leu Trp Ala Phe Ala Val Ala Ala Ala Gln Gly Ile Gln Ala Thr
    290                 295                 300

Val Asn Leu Ala Val Ile Gly Ser Pro Gly Gly Ser Ser Leu Leu Ser
305                 310                 315                 320

Thr Val Gln Ala Phe Arg Phe Phe Gly Ser Ala Ala Ala Pro Val Thr
                325                 330                 335

Phe Leu Pro Ile Tyr Met Gly Ile Gly Ser Gly Ala Phe Trp Val Ser
            340                 345                 350

Ala Val Ala Leu Phe Phe Val Ala Ile Ala Gln Trp Leu Asn Pro Gln
        355                 360                 365

Arg Val Glu Arg Gly
    370


<210> 175
<211> 871
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(871)
<223> FRXA01010

<400> 175
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aaaagatctg gcagggggtt taggcataga ttaggaactt atg aag aaa ctg caa   115
                                          Met Lys Lys Leu Gln
                                          1               5

atg ccg gcc att ttg gtc gga ggc ttt gtg ggg ccg ttt act ggc caa   163
Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly Pro Phe Thr Gly Gln
                10                  15                  20

gct cta tca gtg gtc ttg ccg gaa ttt gca gac acc ttt gat atc agt   211
Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp Thr Phe Asp Ile Ser
            25                  30                  35

gtc agc cag gca gcg ctg acc atg acc gca tac ttg ttg ccc ttt gcc   259
Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr Leu Leu Pro Phe Ala
        40                  45                  50

acc atg atg ttg ttt tcg ggg cgc atc acc aga aag atc cat ccg cat   307
Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg Lys Ile His Pro His
    55                  60                  65

aag gtg gtg cag gcg gct tat att gtc aca ctg cca ctt gcg ctg ttg   355
Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu Pro Leu Ala Leu Leu
70                  75                  80                  85
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ctc cta gtt aca cca tcg tgg ggg ctg ttt atg gct gcg tat gcc acg 403
Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met Ala Ala Tyr Ala Thr
90 95 100

att ggt atc gct aat gca ttt acc act ccg gtg ctg caa att atg ttg 451
Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val Leu Gln Ile Met Leu
105 110 115

cgt gag ctt gtt ccg ccg cgt tct ttg ggt aag gca ttg ggc acc tat 499
Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys Ala Leu Gly Thr Tyr
120 125 130

gct gcg atg caa tca ctc ggc atg ttg tcg gcg cca ctg atc gca ggt 547
Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala Pro Leu Ile Ala Gly
135 140 145

gtg tct tcg gtg gtg tcg tgg agg ttg acc ttc ctg gtc act gca gca 595
Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe Leu Val Thr Ala Ala
150 155 160 165

gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca 643
Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro
170 175 180

tca gca ttg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc 691
Ser Ala Leu Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr
185 190 195

atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc 739
Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly
200 205 210

att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt aat 787
Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asn
215 220 225

act gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc cgg gct gcg ttc 835
Thr Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Arg Ala Ala Phe
230 235 240 245

ttt gcc tcc cgc aag ata ggc gat ttg gca gac aaa 871
Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp Lys
250 255

<210> 176
<211> 257
<212> PRT
<213> Corynebacterium glutamicum

<400> 176
Met Lys Lys Leu Gln Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly
1 5 10 15

Pro Phe Thr Gly Gln Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp
20 25 30

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Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
        35                  40                  45

Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
    50                  55                  60

Lys Ile His Pro His Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu
65                  70                  75                  80

Pro Leu Ala Leu Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
                85                  90                  95

Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
            100                 105                 110

Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
        115                 120                 125

Ala Leu Gly Thr Tyr Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala
    130                 135                 140

Pro Leu Ile Ala Gly Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe
145                 150                 155                 160

Leu Val Thr Ala Ala Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro
                165                 170                 175

Val Val Pro Pro Pro Ser Ala Leu Lys Gln Asn Val Ser Gly Lys Val
            180                 185                 190

Gln Trp Gly Pro Thr Ile Ile His Met Val Ser Gly Phe Val Val Gly
        195                 200                 205

Ile Gly Ile Ile Gly Ile Gly Phe Met Thr Ser Leu His Val Gly Glu
    210                 215                 220

Gln Phe Gly Leu Asn Thr Ala Ala Arg Gly Leu Val Val Met Cys Gly
225                 230                 235                 240

Gly Arg Ala Ala Phe Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp
                245                 250                 255

Lys
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<210> 177
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1243)
<223> RXN03142

<400> 177
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aaaaccacac ccatcgcaac caacggcact gttcactcca gtg ttt att ttg ggc 115
Val Phe Ile Leu Gly
1 5

tgg ctc gtc aac ttg acc cag tac ttg agc ttc tac ttc ctg atc aca 163
Trp Leu Val Asn Leu Thr Gln Tyr Leu Ser Phe Tyr Phe Leu Ile Thr
10 15 20

gtc atg gcg ctg tat gcg atg gaa agc ttc gcc gtt tca gag gcc gct 211
Val Met Ala Leu Tyr Ala Met Glu Ser Phe Ala Val Ser Glu Ala Ala
25 30 35

gtc gga ttt gcg gcc agc tcc ttt gtt atc ggc gca acc gtg gct cgt 259
Val Gly Phe Ala Ala Ser Ser Phe Val Ile Gly Ala Thr Val Ala Arg
40 45 50

gtg ttc gcg gga tgg acg tcc gac cgt ttt ggt aaa aaa cag atc ctg 307
Val Phe Ala Gly Trp Thr Ser Asp Arg Phe Gly Lys Lys Gln Ile Leu
55 60 65

ctc atc ttt gtc ggc ttg gaa gcg gta gca tca cta ttc tat att cca 355
Leu Ile Phe Val Gly Leu Glu Ala Val Ala Ser Leu Phe Tyr Ile Pro
70 75 80 85

gct gcc tca cta cca gcg ctg gtt gct gtg cgt ttt gtt cac ggt ttt 403
Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly Phe
90 95 100

tct tat tct ctt gct tcc acc gct gtg atg gca ctt gtg cag tcc gtg 451
Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser Val
105 110 115

att cct gca agc cgt agg gca gag ggc acc ggc tac ttc gcg ctc gga 499
Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu Gly
120 125 130

tcc aca ctg gct aca gct ttc ggc cca gca att gcg ctg ttt gtt atc 547
Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val Ile
135 140 145

gat gac ttc aac tac aac acc ctg ttc tgg att acc act gcg acc agt 595
Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr Ser
150 155 160 165

gtt ttc ggc ctg atc ctc acc gtt ttg atc cgc aag ccg gag ttc att 643
Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe Ile
170 175 180

aag aat gcg gaa cac ggc aga gta aag cca gtc tgg tct atc aag act 691
Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys Thr
185 190 195

gtt gtg cac cca tcg gtc atg ctc att gga ttc ttc atg ctc gct gtc 739
Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala Val

200 205 210

gga ctg gct tac gca ggc gtg atc acc ttc ctc aac ggc ttc gcg caa 787
Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala Gln
215 220 225

gac act ggc ctc acc gcc gga gcg ggt ctt ttc ttt atc gct tat gcg 835
Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala
230 235 240 245

gtt gcg atg ctg gtc atg cgt ttc ttc ctt gga cgc att cag gac aaa 883
Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp Lys
250 255 260

cat ggt gac aac ccg gtt att tac ttc ggt ttg atc agc ttc gcc ctc 931
His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala Leu
265 270 275

gcg ctg ggg ctt atg gct ttg gcg act gaa gac tgg cac att gtt ctc 979
Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val Leu
280 285 290

gct ggc gca ctc acc ggt ttg ggc tat ggc acc atc atg ccg gcc gca 1027
Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala Ala
295 300 305

caa gcc att gct gtc gat tca gtt cca agc act cag gtt ggt tcc ggt 1075
Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser Gly
310 315 320 325

att tct acg ctt ttc ctg ttc acc gac atc ggc att ggc tta ggc cca 1123
Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly Pro
330 335 340

atc ctg ctg ggt gga ttg gtt gca gcg acc gga tac aac gtc atg tac 1171
Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met Tyr
345 350 355

gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg gtt 1219
Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu Val
360 365 370

gct ttg ggt agg aaa gct agc cac taagttagag cattttattg agc 1266
Ala Leu Gly Arg Lys Ala Ser His
375 380

<210> 178
<211> 381
<212> PRT
<213> Corynebacterium glutamicum

<400> 178
Val Phe Ile Leu Gly Trp Leu Val Asn Leu Thr Gln Tyr Leu Ser Phe
1 5 10 15

Tyr Phe Leu Ile Thr Val Met Ala Leu Tyr Ala Met Glu Ser Phe Ala

20 25 30

Val Ser Glu Ala Ala Val Gly Phe Ala Ala Ser Ser Phe Val Ile Gly
35 40 45

Ala Thr Val Ala Arg Val Phe Ala Gly Trp Thr Ser Asp Arg Phe Gly
50 55 60

Lys Lys Gln Ile Leu Leu Ile Phe Val Gly Leu Glu Ala Val Ala Ser
65 70 75 80

Leu Phe Tyr Ile Pro Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg
85 90 95

Phe Val His Gly Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala
100 105 110

Leu Val Gln Ser Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly
115 120 125

Tyr Phe Ala Leu Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile
130 135 140

Ala Leu Phe Val Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile
145 150 155 160

Thr Thr Ala Thr Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg
165 170 175

Lys Pro Glu Phe Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val
180 185 190

Trp Ser Ile Lys Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe
195 200 205

Phe Met Leu Ala Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu
210 215 220

Asn Gly Phe Ala Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe
225 230 235 240

Phe Ile Ala Tyr Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly
245 250 255

Arg Ile Gln Asp Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu
260 265 270

Ile Ser Phe Ala Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp
275 280 285

Trp His Ile Val Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr
290 295 300

Ile Met Pro Ala Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr
305 310 315 320

Gln Val Gly Ser Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly

325 330 335

Ile Gly Leu Gly Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly
340 345 350

Tyr Asn Val Met Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly
355 360 365

Val Leu Tyr Leu Val Ala Leu Gly Arg Lys Ala Ser His
370 375 380

<210> 179
<211> 914
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(891)
<223> FRXA01150

<400> 179
cca gct gcc tca cta cca gcg ctg gtt gct gtg cgt ttt gtt cac ggt 48
Pro Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly
1 5 10 15

ttt tct tat tct ctt gct tcc acc gct gtg atg gca ctt gtg cag tcc 96
Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser
20 25 30

gtg att cct gca agc cgt agg gca gag ggc acc ggc tac ttc gcg ctc 144
Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu
35 40 45

gga tcc aca ctg gct aca gct ttc ggc cca gca att gcg ctg ttt gtt 192
Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val
50 55 60

atc gat gac ttc aac tac aac acc ctg ttc tgg att acc act gcg acc 240
Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr
65 70 75 80

agt gtt ttc ggc ctg atc ctc acc gtt ttg atc cgc aag ccg gag ttc 288
Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe
85 90 95

att aag aat gcg gaa cac ggc aga gta aag cca gtc tgg tct atc aag 336
Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys
100 105 110

act gtt gtg cac cca tcg gtc atg ctc att gga ttc ttc atg ctc gct 384
Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala
115 120 125

gtc gga ctg gct tac gca ggc gtg atc acc ttc ctc aac ggc ttc gcg 432
Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala

130 135 140

caa gac act ggc ctc acc gcc gga gcg ggt ctt ttc ttt atc gct tat 480
Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr
145 150 155 160

gcg gtt gcg atg ctg gtc atg cgt ttc ttc ctt gga cgc att cag gac 528
Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp
165 170 175

aaa cat ggt gac aac ccg gtt att tac ttc ggt ttg atc agc ttc gcc 576
Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala
180 185 190

ctc gcg ctg ggg ctt atg gct ttg gcg act gaa gac tgg cac att gtt 624
Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val
195 200 205

ctc gct ggc gca ctc acc ggt ttg ggc tat ggc acc atc atg ccg gcc 672
Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala
210 215 220

gca caa gcc att gct gtc gat tca gtt cca agc act cag gtt ggt tcc 720
Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser
225 230 235 240

ggt att tct acg ctt ttc ctg ttc acc gac atc ggc att ggc tta ggc 768
Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly
245 250 255

cca atc ctg ctg ggt gga ttg gtt gca gcg acc gga tac aac gtc atg 816
Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met
260 265 270

tac gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg 864
Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu
275 280 285

gtt gct ttg ggt agg aaa gct agc cac taagttagag cattttattg 911
Val Ala Leu Gly Arg Lys Ala Ser His
290 295

agc 914

<210> 180
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<213> Corynebacterium glutamicum

<400> 180
Pro Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly
1 5 10 15

Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser
20 25 30

Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu
35 40 45

Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val
50 55 60

Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr
65 70 75 80

Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe
85 90 95

Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys
100 105 110

Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala
115 120 125

Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala
130 135 140

Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr
145 150 155 160

Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp
165 170 175

Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala
180 185 190

Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val
195 200 205

Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala
210 215 220

Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser
225 230 235 240

Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly
245 250 255

Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met
260 265 270

Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu
275 280 285

Val Ala Leu Gly Arg Lys Ala Ser His
290 295

<210> 181
<211> 1341
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1318)
<223> RXN02964

<400> 181
ttttatatcc tagcaagggt gttgcatgat gcaataaacg tggtagtttg tgttcataac 60

aaaattgcat gatgcaataa tttcgattta aaggagaaca gtg tcc gta gct gaa   115
                                           Val Ser Val Ala Glu
                                           1               5

gaa ggg aaa ctt ttt aca cca acg ttt gtc atg gga tgg ttt gcc aac   163
Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met Gly Trp Phe Ala Asn
                10                  15                  20

ctt ttc cag ttc ctg gtg ttc tac ttc ctc atc acc acc atg gct ttg   211
Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile Thr Thr Met Ala Leu
            25                  30                  35

tac gcc atc aag gaa ttt caa gcc tct gaa gta gaa gct ggc ttc gca   259
Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val Glu Ala Gly Phe Ala
        40                  45                  50

tcc agc tca att gtt atc ggc gca gtc ttt tcc agg ttt ttc tcc ggc   307
Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser Arg Phe Phe Ser Gly
    55                  60                  65

tat att att gac cgt ttt ggt cga cgc aag att gtg ctc atc tca gtc   355
Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile Val Leu Ile Ser Val
70                  75                  80                  85

cta gtc act acc att gcg tgt gcc ttg tac ctt ccc atc gaa tca ttg   403
Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu Pro Ile Glu Ser Leu
                90                  95                  100

cca ttg cta tac gca aac agg ttc ctc cac ggt gtt gga tac gct ttt   451
Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly Val Gly Tyr Ala Phe
            105                 110                 115

gct gcc acc gcg atc atg gca atg gtc cag gag ctc att cca gcg tca   499
Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu Leu Ile Pro Ala Ser
        120                 125                 130

cga cgt tcc gaa ggt act ggt tac ctg gca ttg ggc act acc gtt tct   547
Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu Gly Thr Thr Val Ser
    135                 140                 145

gca gca ctt gga cca gcc cta gca ctt ttt gtc cta gga aca ttt gat   595
Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val Leu Gly Thr Phe Asp
150                 155                 160                 165

tac gac atg ctg ttt atc gtg gtc ttg gca acc tcg gtc atc tct ttg   643
Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr Ser Val Ile Ser Leu
                170                 175                 180

atc gcc gtc gtg ttc atg tac ttt aag acc agc gac cct gag cct tct   691
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```
Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser Asp Pro Glu Pro Ser
        185                 190                 195

ggg gaa cca gcc aag ttc agc ttc aaa tct att atg aac cca aag atc     739
Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile Met Asn Pro Lys Ile
    200                 205                 210

atc ccc atc ggc atc ttt atc ttg ctt att tgc ttt gct tac tct ggc     787
Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys Phe Ala Tyr Ser Gly
215                 220                 225

gtc att gcc tac atc aac gca ttt gct gaa gaa cgc gat ctg att acg     835
Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu Arg Asp Leu Ile Thr
230                 235                 240                 245

ggt gct gga ttg ttc ttc att gcc tac gca gta tca atg ttt gtg atg     883
Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val Ser Met Phe Val Met
                250                 255                 260

cgc agc ttc ctt ggc aaa ctg cag gac cgt cgc gga gac aac gtc gtt     931
Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg Gly Asp Asn Val Val
            265                 270                 275

att tac ttt gga ttg ttc ttc ttc gtt att tcc ttg acg att ttg tcc     979
Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser Leu Thr Ile Leu Ser
        280                 285                 290

ttt gcc act tcc aac tgg cac gtt gtg ttg tcc gga gtc att gca ggt     1027
Phe Ala Thr Ser Asn Trp His Val Val Leu Ser Gly Val Ile Ala Gly
    295                 300                 305

ctg gga tac ggc act ttg atg cca gca gtg cag tcc atc gct gtt ggt     1075
Leu Gly Tyr Gly Thr Leu Met Pro Ala Val Gln Ser Ile Ala Val Gly
310                 315                 320                 325

gta gta gac aaa acc gaa ttc ggt acg gcc ttc tcc act ttg ttc ctg     1123
Val Val Asp Lys Thr Glu Phe Gly Thr Ala Phe Ser Thr Leu Phe Leu
                330                 335                 340

ttt gtg gac tta ggt ttt ggc ttt gga cct att atc ctg gga gca gtt     1171
Phe Val Asp Leu Gly Phe Gly Phe Gly Pro Ile Ile Leu Gly Ala Val
            345                 350                 355

tct gcg gca att ggt ttc gga cct atg tat gca gca ctg gca ggt gtg     1219
Ser Ala Ala Ile Gly Phe Gly Pro Met Tyr Ala Ala Leu Ala Gly Val
        360                 365                 370

ggt gtg att gcc gga atc ttc tac ctg ttc aca cac gct cgc acc gat     1267
Gly Val Ile Ala Gly Ile Phe Tyr Leu Phe Thr His Ala Arg Thr Asp
    375                 380                 385

cga gct aag aat ggc ttt gtt aaa cac cca gag cct gtc gct tta gtt     1315
Arg Ala Lys Asn Gly Phe Val Lys His Pro Glu Pro Val Ala Leu Val
390                 395                 400                 405

agc tagttctttc agctttccct ccc                                      1341
Ser
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<210> 182
<211> 406
<212> PRT
<213> Corynebacterium glutamicum

<400> 182
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Val Ser Val Ala Glu Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met
1               5                   10                  15

Gly Trp Phe Ala Asn Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile
            20                  25                  30

Thr Thr Met Ala Leu Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val
        35                  40                  45

Glu Ala Gly Phe Ala Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser
    50                  55                  60

Arg Phe Phe Ser Gly Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile
65                  70                  75                  80

Val Leu Ile Ser Val Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu
                85                  90                  95

Pro Ile Glu Ser Leu Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly
            100                 105                 110

Val Gly Tyr Ala Phe Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu
        115                 120                 125

Leu Ile Pro Ala Ser Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu
    130                 135                 140

Gly Thr Thr Val Ser Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val
145                 150                 155                 160

Leu Gly Thr Phe Asp Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr
                165                 170                 175

Ser Val Ile Ser Leu Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser
            180                 185                 190

Asp Pro Glu Pro Ser Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile
        195                 200                 205

Met Asn Pro Lys Ile Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys
    210                 215                 220

Phe Ala Tyr Ser Gly Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu
225                 230                 235                 240

Arg Asp Leu Ile Thr Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val
                245                 250                 255
```

```
Ser Met Phe Val Met Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg
            260                 265                 270

Gly Asp Asn Val Val Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser
        275                 280                 285

Leu Thr Ile Leu Ser Phe Ala Thr Ser Asn Trp His Val Val Leu Ser
    290                 295                 300

Gly Val Ile Ala Gly Leu Gly Tyr Gly Thr Leu Met Pro Ala Val Gln
305                 310                 315                 320

Ser Ile Ala Val Gly Val Val Asp Lys Thr Glu Phe Gly Thr Ala Phe
                325                 330                 335

Ser Thr Leu Phe Leu Phe Val Asp Leu Gly Phe Gly Phe Gly Pro Ile
            340                 345                 350

Ile Leu Gly Ala Val Ser Ala Ala Ile Gly Phe Gly Pro Met Tyr Ala
        355                 360                 365

Ala Leu Ala Gly Val Gly Val Ile Ala Gly Ile Phe Tyr Leu Phe Thr
    370                 375                 380

His Ala Arg Thr Asp Arg Ala Lys Asn Gly Phe Val Lys His Pro Glu
385                 390                 395                 400

Pro Val Ala Leu Val Ser
                405


&lt;210&gt; 183
&lt;211&gt; 1006
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(1006)
&lt;223&gt; FRXA02116

&lt;400&gt; 183
ttttatatcc tagcaagggt gttgcatgat gcaataaacg tggtagtttg tgttcataac 60

aaaattgcat gatgcaataa tttcgattta aaggagaaca gtg tcc gta gct gaa    115
                                           Val Ser Val Ala Glu
                                           1               5

gaa ggg aaa ctt ttt aca cca acg ttt gtc atg gga tgg ttt gcc aac    163
Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met Gly Trp Phe Ala Asn
                10                  15                  20

ctt ttc cag ttc ctg gtg ttc tac ttc ctc atc acc acc atg gct ttg    211
Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile Thr Thr Met Ala Leu
            25                  30                  35

tac gcc atc aag gaa ttt caa gcc tct gaa gta gaa gct ggc ttc gca    259
```

```
Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val Glu Ala Gly Phe Ala
        40                  45                  50

tcc agc tca att gtt atc ggc gca gtc ttt tcc agg ttt ttc tcc ggc     307
Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser Arg Phe Phe Ser Gly
    55                  60                  65

tat att att gac cgt ttt ggt cga cgc aag att gtg ctc atc tca gtc     355
Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile Val Leu Ile Ser Val
70                  75                  80                  85

cta gtc act acc att gcg tgt gcc ttg tac ctt ccc atc gaa tca ttg     403
Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu Pro Ile Glu Ser Leu
                90                  95                  100

cca ttg cta tac gca aac agg ttc ctc cac ggt gtt gga tac gct ttt     451
Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly Val Gly Tyr Ala Phe
            105                 110                 115

gct gcc acc gcg atc atg gca atg gtc cag gag ctc att cca gcg tca     499
Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu Leu Ile Pro Ala Ser
        120                 125                 130

cga cgt tcc gaa ggt act ggt tac ctg gca ttg ggc act acc gtt tct     547
Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu Gly Thr Thr Val Ser
    135                 140                 145

gca gca ctt gga cca gcc cta gca ctt ttt gtc cta gga aca ttt gat     595
Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val Leu Gly Thr Phe Asp
150                 155                 160                 165

tac gac atg ctg ttt atc gtg gtc ttg gca acc tcg gtc atc tct ttg     643
Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr Ser Val Ile Ser Leu
                170                 175                 180

atc gcc gtc gtg ttc atg tac ttt aag acc agc gac cct gag cct tct     691
Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser Asp Pro Glu Pro Ser
            185                 190                 195

ggg gaa cca gcc aag ttc agc ttc aaa tct att atg aac cca aag atc     739
Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile Met Asn Pro Lys Ile
        200                 205                 210

atc ccc atc ggc atc ttt atc ttg ctt att tgc ttt gct tac tct ggc     787
Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys Phe Ala Tyr Ser Gly
    215                 220                 225

gtc att gcc tac atc aac gca ttt gct gaa gaa cgc gat ctg att acg     835
Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu Arg Asp Leu Ile Thr
230                 235                 240                 245

ggt gct gga ttg ttc ttc att gcc tac gca gta tca atg ttt gtg atg     883
Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val Ser Met Phe Val Met
                250                 255                 260

cgc agc ttc ctt ggc aaa ctg cag gac cgt cgc gga gac aac gtc gtt     931
Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg Gly Asp Asn Val Val
```

265 270 275

att tac ttt gga ttg ttc ttc ttc gtt att tcc ttg acg att ttg tcc 979
Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser Leu Thr Ile Leu Ser
280 285 290

ttt gcc act tcc aac tgg cac gtt gtg 1006
Phe Ala Thr Ser Asn Trp His Val Val
295 300

<210> 184
<211> 302
<212> PRT
<213> Corynebacterium glutamicum

<400> 184
Val Ser Val Ala Glu Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met
1 5 10 15

Gly Trp Phe Ala Asn Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile
20 25 30

Thr Thr Met Ala Leu Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val
35 40 45

Glu Ala Gly Phe Ala Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser
50 55 60

Arg Phe Phe Ser Gly Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile
65 70 75 80

Val Leu Ile Ser Val Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu
85 90 95

Pro Ile Glu Ser Leu Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly
100 105 110

Val Gly Tyr Ala Phe Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu
115 120 125

Leu Ile Pro Ala Ser Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu
130 135 140

Gly Thr Thr Val Ser Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val
145 150 155 160

Leu Gly Thr Phe Asp Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr
165 170 175

Ser Val Ile Ser Leu Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser
180 185 190

Asp Pro Glu Pro Ser Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile
195 200 205

Met Asn Pro Lys Ile Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys

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    210                 215                 220

Phe Ala Tyr Ser Gly Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu
225                 230                 235                 240

Arg Asp Leu Ile Thr Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val
                245                 250                 255

Ser Met Phe Val Met Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg
            260                 265                 270

Gly Asp Asn Val Val Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser
        275                 280                 285

Leu Thr Ile Leu Ser Phe Ala Thr Ser Asn Trp His Val Val
    290                 295                 300


<210> 185
<211> 568
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(568)
<223> RXA00858

<400> 185
ttttgttttt cagatgcatg ttagatgcgt tgagggacaa gggtgggga gacctccggt 60

tcttaaattg tctaaccaag aaccggaggt tctttttgtc atg gaa gta aac tta   115
                                            Met Glu Val Asn Leu
                                             1               5

gcc aca tgg cta atc act atc gca gtg att gct ggc ttc ttc att ttc   163
Ala Thr Trp Leu Ile Thr Ile Ala Val Ile Ala Gly Phe Phe Ile Phe
                10                  15                  20

gat ttc tat tcc cac gtc cgc acc cca cac gag ccc act atc aaa gaa   211
Asp Phe Tyr Ser His Val Arg Thr Pro His Glu Pro Thr Ile Lys Glu
            25                  30                  35

tcc gca tgg tgg agc ctc ttc tac gta gcc ctc gcc tgt gtt ttc ggc   259
Ser Ala Trp Trp Ser Leu Phe Tyr Val Ala Leu Ala Cys Val Phe Gly
        40                  45                  50

gtg ttc ctc tgg ttt gct tgg ggc gag cca ggt aac cca cac cag cac   307
Val Phe Leu Trp Phe Ala Trp Gly Glu Pro Gly Asn Pro His Gln His
    55                  60                  65

ggc att gag ttc ttc acc ggt tac gtg aca gag aag gcg ttg agt gtt   355
Gly Ile Glu Phe Phe Thr Gly Tyr Val Thr Glu Lys Ala Leu Ser Val
70                  75                  80                  85

gat aac ctc ttc atc ttc gcg ctg atc atg ggt tct ttc aag att cct   403
Asp Asn Leu Phe Ile Phe Ala Leu Ile Met Gly Ser Phe Lys Ile Pro
```

```
                 90                  95                  100

cgc aag tac cag cag aag gtt ctg ctc atc ggt atc gcg ctg gca ctg    451
Arg Lys Tyr Gln Gln Lys Val Leu Leu Ile Gly Ile Ala Leu Ala Leu
            105                 110                 115

gtc ttc cgc ctg gca ttc atc ctc gca ggt gct gca gtt atc gaa gcc    499
Val Phe Arg Leu Ala Phe Ile Leu Ala Gly Ala Ala Val Ile Glu Ala
        120                 125                 130

tgg tcc gat gtc ttc tac atc ttc tcc atc tgg ctg atc tac acc gct    547
Trp Ser Asp Val Phe Tyr Ile Phe Ser Ile Trp Leu Ile Tyr Thr Ala
    135                 140                 145

gtg aag gct cct gtg cac gag                                        568
Val Lys Ala Pro Val His Glu
150                 155


&lt;210&gt; 186
&lt;211&gt; 156
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 186
Met Glu Val Asn Leu Ala Thr Trp Leu Ile Thr Ile Ala Val Ile Ala
  1               5                  10                  15

Gly Phe Phe Ile Phe Asp Phe Tyr Ser His Val Arg Thr Pro His Glu
            20                  25                  30

Pro Thr Ile Lys Glu Ser Ala Trp Trp Ser Leu Phe Tyr Val Ala Leu
        35                  40                  45

Ala Cys Val Phe Gly Val Phe Leu Trp Phe Ala Trp Gly Glu Pro Gly
    50                  55                  60

Asn Pro His Gln His Gly Ile Glu Phe Phe Thr Gly Tyr Val Thr Glu
 65                  70                  75                  80

Lys Ala Leu Ser Val Asp Asn Leu Phe Ile Phe Ala Leu Ile Met Gly
                85                  90                  95

Ser Phe Lys Ile Pro Arg Lys Tyr Gln Gln Lys Val Leu Leu Ile Gly
            100                 105                 110

Ile Ala Leu Ala Leu Val Phe Arg Leu Ala Phe Ile Leu Ala Gly Ala
        115                 120                 125

Ala Val Ile Glu Ala Trp Ser Asp Val Phe Tyr Ile Phe Ser Ile Trp
    130                 135                 140

Leu Ile Tyr Thr Ala Val Lys Ala Pro Val His Glu
145                 150                 155


&lt;210&gt; 187
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<211> 975
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(952)
<223> RXA02305

<400> 187
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tatgcgcgca ggtgtctact ggtgacgcag ccgacgacga ttattttgac gaagccaccg 60

caaacgatga cttcgatccc gaaaagtgga ggaacatgta atg cca gcc ttt gag   115
                                           Met Pro Ala Phe Glu
                                           1               5

gca atg cca gga atg ccg tat tgg atc gac ctg tcc acc tcg gac att   163
Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu Ser Thr Ser Asp Ile
                10                  15                  20

gca aaa tct gca cac ttc tac gaa aac gtt ctc ggc tgg gaa att gaa   211
Ala Lys Ser Ala His Phe Tyr Glu Asn Val Leu Gly Trp Glu Ile Glu
            25                  30                  35

gaa gtc aac gat ggc tac cgc atg gct cgt ctg cag gga cta ccc gtg   259
Glu Val Asn Asp Gly Tyr Arg Met Ala Arg Leu Gln Gly Leu Pro Val
        40                  45                  50

gca ggg ctg atc gat cag cgc ggt gaa tca agc atc ccg gat acc tgg   307
Ala Gly Leu Ile Asp Gln Arg Gly Glu Ser Ser Ile Pro Asp Thr Trp
    55                  60                  65

att acc tac ttc ctc tcc tac gat ctg gat gcc act gca aag aag atc   355
Ile Thr Tyr Phe Leu Ser Tyr Asp Leu Asp Ala Thr Ala Lys Lys Ile
70                  75                  80                  85

gca gaa ctg ggt gga cga att ctg gcc gag cca act gac gtg cac ttg   403
Ala Glu Leu Gly Gly Arg Ile Leu Ala Glu Pro Thr Asp Val His Leu
                90                  95                  100

gga cgc atg atc cta gct gtt gat act gcc ggc gca ctg ttc ggc gtt   451
Gly Arg Met Ile Leu Ala Val Asp Thr Ala Gly Ala Leu Phe Gly Val
            105                 110                 115

att gag cca ggc agc gag gaa tca ttc gtc gct gct ggt gaa cca ggc   499
Ile Glu Pro Gly Ser Glu Glu Ser Phe Val Ala Ala Gly Glu Pro Gly
        120                 125                 130

aca tcc gtg tgg cat gaa ctc acc act gtc tcc aaa tat tcc gaa gct   547
Thr Ser Val Trp His Glu Leu Thr Thr Val Ser Lys Tyr Ser Glu Ala
    135                 140                 145

atc gat ttc tac ggt gag ctg ttc act tgg aca acc tct gaa atg gct   595
Ile Asp Phe Tyr Gly Glu Leu Phe Thr Trp Thr Thr Ser Glu Met Ala
150                 155                 160                 165

agt gct gaa gac gat agt ttc cgc tac acc acc gca ttg gct gac ggt   643
```

Ser Ala Glu Asp Asp Ser Phe Arg Tyr Thr Thr Ala Leu Ala Asp Gly
170 175 180

tcc gcc ttt gct gga att ttt gat gcc aaa ggc cac ttc cca cct cag 691
Ser Ala Phe Ala Gly Ile Phe Asp Ala Lys Gly His Phe Pro Pro Gln
185 190 195

gtt cca agc ttc tgg cag tcc tac ctt ggc gtg ctc aac gcc gat gat 739
Val Pro Ser Phe Trp Gln Ser Tyr Leu Gly Val Leu Asn Ala Asp Asp
200 205 210

gct gca gcg aag gcc aag gaa ttt ggt ggc gat gtt att cgt aag cca 787
Ala Ala Ala Lys Ala Lys Glu Phe Gly Gly Asp Val Ile Arg Lys Pro
215 220 225

tgg gac tca gaa ttt ggc cgc atg gtt ctc atc tct gat tcc act ggt 835
Trp Asp Ser Glu Phe Gly Arg Met Val Leu Ile Ser Asp Ser Thr Gly
230 235 240 245

gcc aca att acc ttg tgt gaa gta gag gaa tac gtc gag gaa gca gca 883
Ala Thr Ile Thr Leu Cys Glu Val Glu Glu Tyr Val Glu Glu Ala Ala
250 255 260

gaa ggc gat gat ctc ttc gac atc gat ctc agt gct ttc gaa gag cag 931
Glu Gly Asp Asp Leu Phe Asp Ile Asp Leu Ser Ala Phe Glu Glu Gln
265 270 275

ttc cgc aag caa gaa gga cag taatcctaca gcgccatgga gga 975
Phe Arg Lys Gln Glu Gly Gln
280

<210> 188
<211> 284
<212> PRT
<213> Corynebacterium glutamicum

<400> 188
Met Pro Ala Phe Glu Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu
1 5 10 15

Ser Thr Ser Asp Ile Ala Lys Ser Ala His Phe Tyr Glu Asn Val Leu
20 25 30

Gly Trp Glu Ile Glu Glu Val Asn Asp Gly Tyr Arg Met Ala Arg Leu
35 40 45

Gln Gly Leu Pro Val Ala Gly Leu Ile Asp Gln Arg Gly Glu Ser Ser
50 55 60

Ile Pro Asp Thr Trp Ile Thr Tyr Phe Leu Ser Tyr Asp Leu Asp Ala
65 70 75 80

Thr Ala Lys Lys Ile Ala Glu Leu Gly Gly Arg Ile Leu Ala Glu Pro
85 90 95

Thr Asp Val His Leu Gly Arg Met Ile Leu Ala Val Asp Thr Ala Gly

```
            100                 105                 110

Ala Leu Phe Gly Val Ile Glu Pro Gly Ser Glu Glu Ser Phe Val Ala
        115                 120                 125

Ala Gly Glu Pro Gly Thr Ser Val Trp His Glu Leu Thr Thr Val Ser
    130                 135                 140

Lys Tyr Ser Glu Ala Ile Asp Phe Tyr Gly Glu Leu Phe Thr Trp Thr
145                 150                 155                 160

Thr Ser Glu Met Ala Ser Ala Glu Asp Asp Ser Phe Arg Tyr Thr Thr
                165                 170                 175

Ala Leu Ala Asp Gly Ser Ala Phe Ala Gly Ile Phe Asp Ala Lys Gly
            180                 185                 190

His Phe Pro Pro Gln Val Pro Ser Phe Trp Gln Ser Tyr Leu Gly Val
        195                 200                 205

Leu Asn Ala Asp Asp Ala Ala Ala Lys Ala Lys Glu Phe Gly Gly Asp
    210                 215                 220

Val Ile Arg Lys Pro Trp Asp Ser Glu Phe Gly Arg Met Val Leu Ile
225                 230                 235                 240

Ser Asp Ser Thr Gly Ala Thr Ile Thr Leu Cys Glu Val Glu Glu Tyr
                245                 250                 255

Val Glu Glu Ala Ala Glu Gly Asp Asp Leu Phe Asp Ile Asp Leu Ser
            260                 265                 270

Ala Phe Glu Glu Gln Phe Arg Lys Gln Glu Gly Gln
        275                 280
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<210> 189
<211> 948
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(925)
<223> RXA00084

<400> 189

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tcacccttgt cgataccagc tactgggtat ctggcgtcgg tccacttggc ggcagcaaag 60

tcttggaaga catcgatgcc ttcctcgacg cacagcaata atg tcc aca gct ctc    115
                                           Met Ser Thr Ala Leu
                                           1               5

ccc gat cag ctc aag tgg gaa tac agt gcc ttc ccc gtg cag atc tcg    163
Pro Asp Gln Leu Lys Trp Glu Tyr Ser Ala Phe Pro Val Gln Ile Ser
                10                  15                  20
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cag aag caa cgg ctt agt ccc ggc ttc atg cgg atc acc gtc act ggt    211
Gln Lys Gln Arg Leu Ser Pro Gly Phe Met Arg Ile Thr Val Thr Gly
            25                  30                  35

gac aag ctc cga ttc ttt ggc cag tgg ggt ttg gac caa cgc atc aaa    259
Asp Lys Leu Arg Phe Phe Gly Gln Trp Gly Leu Asp Gln Arg Ile Lys
        40                  45                  50

ctg atc att cca agc ccg gct ggg aac atc cca gat ttc gga att ctc    307
Leu Ile Ile Pro Ser Pro Ala Gly Asn Ile Pro Asp Phe Gly Ile Leu
    55                  60                  65

gac gaa ccc act ccc cca ccg aca acg tgg ctt cct cgt gct aag tct    355
Asp Glu Pro Thr Pro Pro Pro Thr Thr Trp Leu Pro Arg Ala Lys Ser
70                  75                  80                  85

ttt cca gcg gac caa cga ccg atc ttg cgc acc tac acc cca tct gcg    403
Phe Pro Ala Asp Gln Arg Pro Ile Leu Arg Thr Tyr Thr Pro Ser Ala
                90                  95                  100

gtc cga ccc gaa cta tgc gaa gta gac att gat atc tat ctt cac aac    451
Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp Ile Tyr Leu His Asn
            105                 110                 115

cct tcg gga cca gta tcc aga tgg gca aag aac tgc agt gtt gac gat    499
Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn Cys Ser Val Asp Asp
        120                 125                 130

gaa cta atc atc acc ggc cct gac gta cgc gca gga gaa acc ggc tac    547
Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala Gly Glu Thr Gly Tyr
    135                 140                 145

gga atc acc tat cat ccg act tct gcg atc gat cgc ctc tgt ctc atc    595
Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp Arg Leu Cys Leu Ile
150                 155                 160                 165

ggc gat tgt gca tca gct ccc gcg atc gca aat atc gtc aat caa tca    643
Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn Ile Val Asn Gln Ser
                170                 175                 180

aaa gta cct act acg gtt ttc ctc cac gta gac agc cta gaa gat gat    691
Lys Val Pro Thr Thr Val Phe Leu His Val Asp Ser Leu Glu Asp Asp
            185                 190                 195

gta ttg atc gcc gat agc tcc acc aag ctc act ttc gaa gac atc gac    739
Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr Phe Glu Asp Ile Asp
        200                 205                 210

gct tac aaa gca aag gtc ttc caa tgg gct tca gcc aat gca gca gat    787
Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser Ala Asn Ala Ala Asp
    215                 220                 225

cct tca gta cac ttc tgg atc gcc ggt gaa act agc atg gtg cgc ttc    835
Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr Ser Met Val Arg Phe
230                 235                 240                 245

att cgc aaa gaa cta atc aac agc tac cga gtt gat tcc tca cga atc    883
```

Ile Arg Lys Glu Leu Ile Asn Ser Tyr Arg Val Asp Ser Ser Arg Ile
250 255 260

act ttc ctc ggc tac tgg aaa tac ggc cga cga acc gta gac 925
Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg Thr Val Asp
265 270 275

tagctttcag attcagaccc cag 948

<210> 190
<211> 275
<212> PRT
<213> Corynebacterium glutamicum

<400> 190
Met Ser Thr Ala Leu Pro Asp Gln Leu Lys Trp Glu Tyr Ser Ala Phe
1 5 10 15

Pro Val Gln Ile Ser Gln Lys Gln Arg Leu Ser Pro Gly Phe Met Arg
20 25 30

Ile Thr Val Thr Gly Asp Lys Leu Arg Phe Phe Gly Gln Trp Gly Leu
35 40 45

Asp Gln Arg Ile Lys Leu Ile Ile Pro Ser Pro Ala Gly Asn Ile Pro
50 55 60

Asp Phe Gly Ile Leu Asp Glu Pro Thr Pro Pro Pro Thr Thr Trp Leu
65 70 75 80

Pro Arg Ala Lys Ser Phe Pro Ala Asp Gln Arg Pro Ile Leu Arg Thr
85 90 95

Tyr Thr Pro Ser Ala Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp
100 105 110

Ile Tyr Leu His Asn Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn
115 120 125

Cys Ser Val Asp Asp Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala
130 135 140

Gly Glu Thr Gly Tyr Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp
145 150 155 160

Arg Leu Cys Leu Ile Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn
165 170 175

Ile Val Asn Gln Ser Lys Val Pro Thr Thr Val Phe Leu His Val Asp
180 185 190

Ser Leu Glu Asp Asp Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr
195 200 205

Phe Glu Asp Ile Asp Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser
210 215 220

```
Ala Asn Ala Ala Asp Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr
225                 230                 235                 240

Ser Met Val Arg Phe Ile Arg Lys Glu Leu Ile Asn Ser Tyr Arg Val
                245                 250                 255

Asp Ser Ser Arg Ile Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg
            260                 265                 270

Thr Val Asp
        275


<210> 191
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> RXA00843

<400> 191
gccctgatgc gaaaccggcg ccaacaatga tgccgacgaa ggcaaatgcc actcttagga 60

tttgaataat catggaacaa accttagtag gctcaacgtt atg aaa gtc acg att   115
                                            Met Lys Val Thr Ile
                                            1               5

ttc cat aat ccg cgt tgt tcc aca tcc aga aat acc ctc gct tac ctc   163
Phe His Asn Pro Arg Cys Ser Thr Ser Arg Asn Thr Leu Ala Tyr Leu
                10                  15                  20

cgc gac aag gac att gag cct gaa att gtt cag tat ctc aaa gac acg   211
Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln Tyr Leu Lys Asp Thr
            25                  30                  35

ccc acc gct tcc gag ctc aaa gaa cta ttc aat acg ctg gga att cca   259
Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn Thr Leu Gly Ile Pro
        40                  45                  50

gtc cac gac ggc atc aga acc cgc gaa gct gag tac aca gaa ctg ggc   307
Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu Tyr Thr Glu Leu Gly
    55                  60                  65

ctg tca cca gaa aca cct gaa act gag ctt atc gac gcc atc gtt gcc   355
Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile Asp Ala Ile Val Ala
70                  75                  80                  85

cat ccc agg ctc ctt cag cgt ccg atc gtg gtg acg gcc aaa ggc gcg   403
His Pro Arg Leu Leu Gln Arg Pro Ile Val Val Thr Ala Lys Gly Ala
                90                  95                  100

cgc att gcg cgc ccc aaa atc gac gtc att gac agc atc ttg           445
Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp Ser Ile Leu
```

```
            105                 110                 115

tgacaacatt ttgtagagca acc                                        468


<210> 192
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 192
Met Lys Val Thr Ile Phe His Asn Pro Arg Cys Ser Thr Ser Arg Asn
  1               5                  10                  15

Thr Leu Ala Tyr Leu Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln
             20                  25                  30

Tyr Leu Lys Asp Thr Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn
         35                  40                  45

Thr Leu Gly Ile Pro Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu
     50                  55                  60

Tyr Thr Glu Leu Gly Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile
 65                  70                  75                  80

Asp Ala Ile Val Ala His Pro Arg Leu Leu Gln Arg Pro Ile Val Val
                 85                  90                  95

Thr Ala Lys Gly Ala Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp
            100                 105                 110

Ser Ile Leu
        115


<210> 193
<211> 432
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> RXA01052

<400> 193
tatggccaac cctaggggga tggcctgtgt gttcactgtt aggtttcctc aaaatcttta 60

acgaacaacg aagagcttgc ccgagagtat cttgggtcgc atg gac aca aaa tta    115
                                           Met Asp Thr Lys Leu
                                             1               5

ggc gct gaa ttg ggt act gaa ttt gat ctc att gtt gtt ggt ttc ggc    163
Gly Ala Glu Leu Gly Thr Glu Phe Asp Leu Ile Val Val Gly Phe Gly
                 10                  15                  20
```

```
aaa gca ggc aag act atc gcg atg aaa cgc tcg gca gcg ggg gat aag      211
Lys Ala Gly Lys Thr Ile Ala Met Lys Arg Ser Ala Ala Gly Asp Lys
            25                  30                  35

gtc gca ctg atc gag cag agt cca cag atg tat ggc ggt acc tgc atc      259
Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr Gly Gly Thr Cys Ile
        40                  45                  50

aat gta ggt tgc atc ccc acg aag aag ttg ttg ttt gag act gca acg      307
Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu Phe Glu Thr Ala Thr
    55                  60                  65

ggc aag gat ttc ccg gat gcg gtt gtg gcg cgt gat cag ttg att ggc      355
Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg Asp Gln Leu Ile Gly
70                  75                  80                  85

aag ctg aat gcc aag aat ctt gcg atg gcc aca gac aag ggt gtc acc      403
Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr Asp Lys Gly Val Thr
                90                  95                  100

cgt cat tgatggaaaa gctacgttta cag                                    432
Arg His


<210> 194
<211> 103
<212> PRT
<213> Corynebacterium glutamicum

<400> 194
Met Asp Thr Lys Leu Gly Ala Glu Leu Gly Thr Glu Phe Asp Leu Ile
 1               5                  10                  15

Val Val Gly Phe Gly Lys Ala Gly Lys Thr Ile Ala Met Lys Arg Ser
            20                  25                  30

Ala Ala Gly Asp Lys Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr
        35                  40                  45

Gly Gly Thr Cys Ile Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu
    50                  55                  60

Phe Glu Thr Ala Thr Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg
65                  70                  75                  80

Asp Gln Leu Ile Gly Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr
                85                  90                  95

Asp Lys Gly Val Thr Arg His
            100


<210> 195
<211> 543
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(520)
<223> RXA01053

<400> 195
ttgcgatggc cacagacaag ggtgtcaccc gtcattgatg gaaaagctac gtttacagct 60

agccacgaaa tcacaagtaa cttcaggtag tgacactctt gtg ctg tat gcg cca   115
                                          Val Leu Tyr Ala Pro
                                          1               5

acg att gtg atc aac acg ggc tcc acg ccg gtc atc ccc aat gtc cca   163
Thr Ile Val Ile Asn Thr Gly Ser Thr Pro Val Ile Pro Asn Val Pro
                10                  15                  20

ggc acc gac aat ccg cat gtt ttt gat tcc act ggc att cag cac att   211
Gly Thr Asp Asn Pro His Val Phe Asp Ser Thr Gly Ile Gln His Ile
            25                  30                  35

tcg ccc ctg ccg aag cac ctc gcg atc atc ggc ggt ggc ccc atc ggt   259
Ser Pro Leu Pro Lys His Leu Ala Ile Ile Gly Gly Gly Pro Ile Gly
        40                  45                  50

ttg gaa ttt gcc acg ctt ttc agt gga caa ggc tcc aaa gtc acc atc   307
Leu Glu Phe Ala Thr Leu Phe Ser Gly Gln Gly Ser Lys Val Thr Ile
    55                  60                  65

atc gac cgt ggt gaa ttg ccg ctg aaa aat ttc gac agg gaa gta gcg   355
Ile Asp Arg Gly Glu Leu Pro Leu Lys Asn Phe Asp Arg Glu Val Ala
70                  75                  80                  85

gag ctg gcc aaa acc gac ctg gag gcc cgc gga atc acc ttc ctc aac   403
Glu Leu Ala Lys Thr Asp Leu Glu Ala Arg Gly Ile Thr Phe Leu Asn
                90                  95                  100

aac gct gaa ctc acc gga ttc agc ggt gac ctc acc atc gcg ctc aaa   451
Asn Ala Glu Leu Thr Gly Phe Ser Gly Asp Leu Thr Ile Ala Leu Lys
            105                 110                 115

gac cac gac ctc ctc gcc gac gcc gca ctt ttt gca tcg gcc gac gcc   499
Asp His Asp Leu Leu Ala Asp Ala Ala Leu Phe Ala Ser Ala Asp Ala
        120                 125                 130

cgg cac cga cgg gct cgg cct tgaacaggcg ggcatcaaaa cag             543
Arg His Arg Arg Ala Arg Pro
    135                 140


<210> 196
<211> 140
<212> PRT
<213> Corynebacterium glutamicum

<400> 196
Val Leu Tyr Ala Pro Thr Ile Val Ile Asn Thr Gly Ser Thr Pro Val
```

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1               5                   10                  15

Ile Pro Asn Val Pro Gly Thr Asp Asn Pro His Val Phe Asp Ser Thr
            20                  25                  30

Gly Ile Gln His Ile Ser Pro Leu Pro Lys His Leu Ala Ile Ile Gly
        35                  40                  45

Gly Gly Pro Ile Gly Leu Glu Phe Ala Thr Leu Phe Ser Gly Gln Gly
    50                  55                  60

Ser Lys Val Thr Ile Ile Asp Arg Gly Glu Leu Pro Leu Lys Asn Phe
65                  70                  75                  80

Asp Arg Glu Val Ala Glu Leu Ala Lys Thr Asp Leu Glu Ala Arg Gly
                85                  90                  95

Ile Thr Phe Leu Asn Asn Ala Glu Leu Thr Gly Phe Ser Gly Asp Leu
            100                 105                 110

Thr Ile Ala Leu Lys Asp His Asp Leu Leu Ala Asp Ala Ala Leu Phe
        115                 120                 125

Ala Ser Ala Asp Ala Arg His Arg Arg Ala Arg Pro
    130                 135                 140
```

<210> 197
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(589)
<223> RXA01054

<400> 197

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gacctcctcg ccgacgccgc actttttgca tcggccgacg cccggcaccg acgggctcgg 60

ccttgaacag gcgggcatca aaacaggcac gcgtggggag gtg ctt gtc gac gcc   115
                                            Val Leu Val Asp Ala
                                            1               5

cac ctc cgg acc aac atc gac ggc atc ttc gct gta ggt gat gtc aat   163
His Leu Arg Thr Asn Ile Asp Gly Ile Phe Ala Val Gly Asp Val Asn
                10                  15                  20

ggc ggc ccg cag ttt acc tac gtg tcc tac gat gac cac cgc att gtg   211
Gly Gly Pro Gln Phe Thr Tyr Val Ser Tyr Asp Asp His Arg Ile Val
            25                  30                  35

ctg gat caa cta gcc gga aca ggt aag aaa tcc att gca cac cga ctg   259
Leu Asp Gln Leu Ala Gly Thr Gly Lys Lys Ser Ile Ala His Arg Leu
        40                  45                  50

atc ccc acc acc acg ttc atc gaa ccg ccg tta tcc acc atc ggt gac   307
```

```
Ile Pro Thr Thr Thr Phe Ile Glu Pro Pro Leu Ser Thr Ile Gly Asp
     55                  60                  65

aac act gaa ggg gaa aat gtg gtg gtg aaa aag gcc ttg att gca gat      355
Asn Thr Glu Gly Glu Asn Val Val Val Lys Lys Ala Leu Ile Ala Asp
 70                  75                  80                  85

atg ccg atc gtt ccc cga cca gag att att aac caa cct cac ggt atg      403
Met Pro Ile Val Pro Arg Pro Glu Ile Ile Asn Gln Pro His Gly Met
                 90                  95                 100

gtg aag ttt ttc gtc gac aag caa tct gat gcg ctg ctc ggc gcg acc      451
Val Lys Phe Phe Val Asp Lys Gln Ser Asp Ala Leu Leu Gly Ala Thr
            105                 110                 115

ttg tac tgc gcc gac tcc cag gag ctc atc aac acc gtg gcg ctt gcc      499
Leu Tyr Cys Ala Asp Ser Gln Glu Leu Ile Asn Thr Val Ala Leu Ala
        120                 125                 130

atg cgg cat ggc gtc acc gcc tcc gag ctt ggc gac ggc atc tac acc      547
Met Arg His Gly Val Thr Ala Ser Glu Leu Gly Asp Gly Ile Tyr Thr
    135                 140                 145

cac ccc gcc acc tcg gag atc ttc aac caa tta ttg ggc agt              589
His Pro Ala Thr Ser Glu Ile Phe Asn Gln Leu Leu Gly Ser
150                 155                 160

taacgcagcg gatcgaacgg ctt                                            612


<210> 198
<211> 163
<212> PRT
<213> Corynebacterium glutamicum

<400> 198
Val Leu Val Asp Ala His Leu Arg Thr Asn Ile Asp Gly Ile Phe Ala
  1               5                  10                  15

Val Gly Asp Val Asn Gly Gly Pro Gln Phe Thr Tyr Val Ser Tyr Asp
             20                  25                  30

Asp His Arg Ile Val Leu Asp Gln Leu Ala Gly Thr Gly Lys Lys Ser
         35                  40                  45

Ile Ala His Arg Leu Ile Pro Thr Thr Thr Phe Ile Glu Pro Pro Leu
     50                  55                  60

Ser Thr Ile Gly Asp Asn Thr Glu Gly Glu Asn Val Val Val Lys Lys
 65                  70                  75                  80

Ala Leu Ile Ala Asp Met Pro Ile Val Pro Arg Pro Glu Ile Ile Asn
                 85                  90                  95

Gln Pro His Gly Met Val Lys Phe Phe Val Asp Lys Gln Ser Asp Ala
            100                 105                 110
```

```
Leu Leu Gly Ala Thr Leu Tyr Cys Ala Asp Ser Gln Glu Leu Ile Asn
        115                 120                 125

Thr Val Ala Leu Ala Met Arg His Gly Val Thr Ala Ser Glu Leu Gly
    130                 135                 140

Asp Gly Ile Tyr Thr His Pro Ala Thr Ser Glu Ile Phe Asn Gln Leu
145                 150                 155                 160

Leu Gly Ser



<210> 199
<211> 561
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(538)
<223> RXN03123

<400> 199
agctctacca acgcgcctac accttgacca acgtggatgc cgatgccggt acctttgacc 60

tggcttttgt gctgcacgag ccgctggggc ccgcctcggc gtg ggc gac gcg ctg    115
                                          Val Gly Asp Ala Leu
                                          1               5

cga ggc cgg gga aag cct gaa gtc atg cgc tac cca gga att ccg ttc    163
Arg Gly Arg Gly Lys Pro Glu Val Met Arg Tyr Pro Gly Ile Pro Phe
                10                  15                  20

gcc atc cca gat cca gcg ccg cgt ggc ttc ctt ttc tta ggc gat ctc    211
Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu Phe Leu Gly Asp Leu
            25                  30                  35

acc tct tac cca gcg atc tgc tcg att ctg gag acc ttg gac ggt gaa    259
Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu Thr Leu Asp Gly Glu
        40                  45                  50

atc cct gcg acc gcg tat ctt atc gcc cac gat cca ctt gat tac acc    307
Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp Pro Leu Asp Tyr Thr
    55                  60                  65

ttc gat ttt ccc cag ggc gag cac atc acc gcg cag tgg att tcc aac    355
Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala Gln Trp Ile Ser Asn
70                  75                  80                  85

gaa caa tcc ttc att gat cac atc gct gac acg gat tac acc gat ttt    403
Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr Asp Tyr Thr Asp Phe
                90                  95                  100

tat acc tgg atc ggc gcg gaa tcc tcc gaa acc cgt gcg gcc aag aag    451
Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr Arg Ala Ala Lys Lys
            105                 110                 115
```

```
cat ctg cag acc cac gcc ggc atg ccc aag acg cac atg aac gcg caa    499
His Leu Gln Thr His Ala Gly Met Pro Lys Thr His Met Asn Ala Gln
        120                 125                 130

ggt tat tgg aac aag ggc aga gcc atg ggt aaa agc aat taaaagattt     548
Gly Tyr Trp Asn Lys Gly Arg Ala Met Gly Lys Ser Asn
    135                 140                 145

ttgcttatcg acg                                                     561


&lt;210&gt; 200
&lt;211&gt; 146
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 200
Val Gly Asp Ala Leu Arg Gly Arg Gly Lys Pro Glu Val Met Arg Tyr
  1               5                  10                  15

Pro Gly Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu
             20                  25                  30

Phe Leu Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu
         35                  40                  45

Thr Leu Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp
     50                  55                  60

Pro Leu Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala
 65                  70                  75                  80

Gln Trp Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr
                 85                  90                  95

Asp Tyr Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr
            100                 105                 110

Arg Ala Ala Lys Lys His Leu Gln Thr His Ala Gly Met Pro Lys Thr
        115                 120                 125

His Met Asn Ala Gln Gly Tyr Trp Asn Lys Gly Arg Ala Met Gly Lys
    130                 135                 140

Ser Asn
145


&lt;210&gt; 201
&lt;211&gt; 736
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(736)
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<223> FRXA00993

<400> 201
gctgagctag tgcttttgcg acacacctct tgcgaatgtt gattaggtta ggcaagccat 60

atttacaggg tgttgtgaaa gcataaggga gcaaggaaac atg ggc aag gga ttt 115
Met Gly Lys Gly Phe
1 5

acc ggc gct att ttg acc gtc atg ggc gtg aaa tcg cat atc gcc acc 163
Thr Gly Ala Ile Leu Thr Val Met Gly Val Lys Ser His Ile Ala Thr
10 15 20

acc acg gga aaa acc gtg atc aat gac cgc atg gtg acc att cat ttt 211
Thr Thr Gly Lys Thr Val Ile Asn Asp Arg Met Val Thr Ile His Phe
25 30 35

cat tcc gag acg ctg ctc aac acg gaa ggt gaa gtc ccc ggc gat tgg 259
His Ser Glu Thr Leu Leu Asn Thr Glu Gly Glu Val Pro Gly Asp Trp
40 45 50

ctg cgt ctg tgg ttc ccg cac gag agc cga cct gga aag ctc tac caa 307
Leu Arg Leu Trp Phe Pro His Glu Ser Arg Pro Gly Lys Leu Tyr Gln
55 60 65

cgc gcc tac acc ttg acc aac gtg gat gcc gat gcc ggt acc ttt gac 355
Arg Ala Tyr Thr Leu Thr Asn Val Asp Ala Asp Ala Gly Thr Phe Asp
70 75 80 85

ctg gct ttt gtg ctg cac gag ccg ctg ggg ccc gcc tcg gcg tgg gcg 403
Leu Ala Phe Val Leu His Glu Pro Leu Gly Pro Ala Ser Ala Trp Ala
90 95 100

acg cgc tgc gag gcc ggg gaa agc ctg gaa gtc atg cgc tac cca gga 451
Thr Arg Cys Glu Ala Gly Glu Ser Leu Glu Val Met Arg Tyr Pro Gly
105 110 115

att ccg ttc gcc atc cca gat cca gcg ccg cgt ggc ttc ctt ttc cta 499
Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu Phe Leu
120 125 130

ggc gat ctc acc tct tac cca gcg atc tgc tcg att ctg gag acc ttg 547
Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu Thr Leu
135 140 145

gac ggt gaa atc cct gcg acc gcg tat ctt atc gcc cac gat cca ctt 595
Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp Pro Leu
150 155 160 165

gat tac acc ttc gat ttt ccc cag ggc gag cac atc acc gcg cag tgg 643
Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala Gln Trp
170 175 180

att tcc aac gaa caa tcc ttc att gat cac atc gct gac acg gat tac 691
Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr Asp Tyr
185 190 195

acc gat ttt tat acc tgg atc ggc gcg gaa tcc tcc gaa acc cgt 736
Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr Arg
200 205 210

<210> 202
<211> 212
<212> PRT
<213> Corynebacterium glutamicum

<400> 202
Met Gly Lys Gly Phe Thr Gly Ala Ile Leu Thr Val Met Gly Val Lys
1 5 10 15

Ser His Ile Ala Thr Thr Thr Gly Lys Thr Val Ile Asn Asp Arg Met
20 25 30

Val Thr Ile His Phe His Ser Glu Thr Leu Leu Asn Thr Glu Gly Glu
35 40 45

Val Pro Gly Asp Trp Leu Arg Leu Trp Phe Pro His Glu Ser Arg Pro
50 55 60

Gly Lys Leu Tyr Gln Arg Ala Tyr Thr Leu Thr Asn Val Asp Ala Asp
65 70 75 80

Ala Gly Thr Phe Asp Leu Ala Phe Val Leu His Glu Pro Leu Gly Pro
85 90 95

Ala Ser Ala Trp Ala Thr Arg Cys Glu Ala Gly Glu Ser Leu Glu Val
100 105 110

Met Arg Tyr Pro Gly Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg
115 120 125

Gly Phe Leu Phe Leu Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser
130 135 140

Ile Leu Glu Thr Leu Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile
145 150 155 160

Ala His Asp Pro Leu Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His
165 170 175

Ile Thr Ala Gln Trp Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile
180 185 190

Ala Asp Thr Asp Tyr Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser
195 200 205

Ser Glu Thr Arg
210

<210> 203
<211> 732
<212> DNA

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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXA01051

<400> 203
tgcgacccaa gatactctcg ggcaagctct tcgttgttcg ttaaagattt tgaggaaacc  60

taacagtgaa cacacaggcc atccccctag ggttggccat atg tca acc att cac   115
                                          Met Ser Thr Ile His
                                           1               5

gcc tcc gga atc cag gct cca caa gtg cca cac ggt tcc cac cat gcc   163
Ala Ser Gly Ile Gln Ala Pro Gln Val Pro His Gly Ser His His Ala
                10                  15                  20

ccg cca caa aag gac gaa tca gtg aag aag agc ttc aat gcc tct tct   211
Pro Pro Gln Lys Asp Glu Ser Val Lys Lys Ser Phe Asn Ala Ser Ser
            25                  30                  35

tta ctg ttc gcg ttt tcc ttc ggc gtg tac ctg gtg ctg ctt gtg atg   259
Leu Leu Phe Ala Phe Ser Phe Gly Val Tyr Leu Val Leu Leu Val Met
        40                  45                  50

atg aca ctt ctt aaa agt cgc ctt tct tta ggc gga ctg tgg aac aca   307
Met Thr Leu Leu Lys Ser Arg Leu Ser Leu Gly Gly Leu Trp Asn Thr
    55                  60                  65

gaa gca cac caa tac aga tcc atc gac tta gag ctt ttc aac ggc ttt   355
Glu Ala His Gln Tyr Arg Ser Ile Asp Leu Glu Leu Phe Asn Gly Phe
70                  75                  80                  85

gct gat cca cca att tgg tgg ggg cct tgg acc aac act ttt ggc aac   403
Ala Asp Pro Pro Ile Trp Trp Gly Pro Trp Thr Asn Thr Phe Gly Asn
                90                  95                  100

atc gca ctg ttc atg cca ttt ggg ttt ttc ctg tac aaa atg ctc cgt   451
Ile Ala Leu Phe Met Pro Phe Gly Phe Phe Leu Tyr Lys Met Leu Arg
            105                 110                 115

aga ttc aac cat cga ttc ccc ttc gta gaa acc atc ctg ttt gcc agc   499
Arg Phe Asn His Arg Phe Pro Phe Val Glu Thr Ile Leu Phe Ala Ser
        120                 125                 130

gtc acc agc ctc agt atc gaa gtt ctg caa tgg gtg ttt gct att gga   547
Val Thr Ser Leu Ser Ile Glu Val Leu Gln Trp Val Phe Ala Ile Gly
    135                 140                 145

tat tca gat gtc gat gac ctg ttg ttt aat acg atc ggc gga ctc att   595
Tyr Ser Asp Val Asp Asp Leu Leu Phe Asn Thr Ile Gly Gly Leu Ile
150                 155                 160                 165

gga gca tcc gta gca gcg ctt gtc tcg ctt aaa tcc tcc aag gta gtc   643
Gly Ala Ser Val Ala Ala Leu Val Ser Leu Lys Ser Ser Lys Val Val
                170                 175                 180
```

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agc gga atc atc atg ggc ggt tca cta tct gtg atg gcg atg atg atg    691
Ser Gly Ile Ile Met Gly Gly Ser Leu Ser Val Met Ala Met Met Met
            185                 190                 195

tat tca agt ttt atc gcc tagaaggttt cagcagttcc gct                  732
Tyr Ser Ser Phe Ile Ala
        200


<210> 204
<211> 203
<212> PRT
<213> Corynebacterium glutamicum

<400> 204
Met Ser Thr Ile His Ala Ser Gly Ile Gln Ala Pro Gln Val Pro His
  1               5                  10                  15

Gly Ser His His Ala Pro Pro Gln Lys Asp Glu Ser Val Lys Lys Ser
             20                  25                  30

Phe Asn Ala Ser Ser Leu Leu Phe Ala Phe Ser Phe Gly Val Tyr Leu
         35                  40                  45

Val Leu Leu Val Met Met Thr Leu Leu Lys Ser Arg Leu Ser Leu Gly
     50                  55                  60

Gly Leu Trp Asn Thr Glu Ala His Gln Tyr Arg Ser Ile Asp Leu Glu
 65                  70                  75                  80

Leu Phe Asn Gly Phe Ala Asp Pro Pro Ile Trp Trp Gly Pro Trp Thr
                 85                  90                  95

Asn Thr Phe Gly Asn Ile Ala Leu Phe Met Pro Phe Gly Phe Phe Leu
            100                 105                 110

Tyr Lys Met Leu Arg Arg Phe Asn His Arg Phe Pro Phe Val Glu Thr
        115                 120                 125

Ile Leu Phe Ala Ser Val Thr Ser Leu Ser Ile Glu Val Leu Gln Trp
    130                 135                 140

Val Phe Ala Ile Gly Tyr Ser Asp Val Asp Asp Leu Leu Phe Asn Thr
145                 150                 155                 160

Ile Gly Gly Leu Ile Gly Ala Ser Val Ala Ala Leu Val Ser Leu Lys
                165                 170                 175

Ser Ser Lys Val Val Ser Gly Ile Ile Met Gly Gly Ser Leu Ser Val
            180                 185                 190

Met Ala Met Met Met Tyr Ser Ser Phe Ile Ala
        195                 200


<210> 205
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<211> 1359
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1336)
<223> RXN01873

<400> 205
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ccgtcgttgc ccatggtcac agcctacatg cacaaagtga atcaaaaaca gctatttcta 60

acattttact aatatttgct gttggcgcat gatgaactcc atg agc caa gca ata    115
                                           Met Ser Gln Ala Ile
                                            1               5

gat agc aag gtc gag gca cac gaa ggc cac gaa ggc cac gaa ggc atc    163
Asp Ser Lys Val Glu Ala His Glu Gly His Glu Gly His Glu Gly Ile
                10                  15                  20

gag cga gga aca cgc aat tac aag cgc gct gtg ttt gcg atg ctg gcc    211
Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val Phe Ala Met Leu Ala
            25                  30                  35

gcc ggt ctt gct gct ttc aat ggt ctt tat tgc acg cag gca ttg ctt    259
Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys Thr Gln Ala Leu Leu
        40                  45                  50

ccc acc atg acg gaa gag ttg gga att acg ccc act gag tcc gcg ctg    307
Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro Thr Glu Ser Ala Leu
    55                  60                  65

acg gtg tcg gct acg act gga atg ttg gcg ctg tgt att gtt ccg gcg    355
Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu Cys Ile Val Pro Ala
70                  75                  80                  85

tcg ata ctt tcg gag aaa ttt ggt cgc ggt cgg gtg ctg aca att tca    403
Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg Val Leu Thr Ile Ser
                90                  95                  100

ctc acg ttg gcc atc atc gtg gga tta att ttg ccg ctt gtc ccc aat    451
Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu Pro Leu Val Pro Asn
            105                 110                 115

att act gct ctc atc ctg ctc aga ggt ctc caa ggt gcg ctg ctt gct    499
Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln Gly Ala Leu Leu Ala
        120                 125                 130

ggc act cca gcg gtg gcg atg acc tgg ttg tct gag gaa att cac ccc    547
Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser Glu Glu Ile His Pro
    135                 140                 145

aag gat att ggg cat gcg atg gga att tac atc gcg gga aat act gtc    595
Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile Ala Gly Asn Thr Val
150                 155                 160                 165

ggc ggg ctc act gga cgt atg att ccg gcg gga cta ctt gaa gta act    643
```

```
Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly Leu Leu Glu Val Thr
                170                 175                 180

cat tgg caa aac gca ctg ctg gga agt tct atc gct gcg ctg atc ttc      691
His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile Ala Ala Leu Ile Phe
            185                 190                 195

ggc gta atc atg gtg gtg ttg ctt ccc aag cag cgg aaa ttc cag ccg      739
Gly Val Ile Met Val Val Leu Leu Pro Lys Gln Arg Lys Phe Gln Pro
        200                 205                 210

aag aat atc aat ctg cgc cat gag att tcg gcg atg gct gct cat tgg      787
Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala Met Ala Ala His Trp
    215                 220                 225

cgg aat cct cgt ttg gcg ttg ctt ttt ggt act gcg ttt ttg ggc atg      835
Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr Ala Phe Leu Gly Met
230                 235                 240                 245

ggt act ttt gtg tcg ctg tac aac tat ttg ggt ttc cgc atg att gat      883
Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly Phe Arg Met Ile Asp
                250                 255                 260

cag ttt ggg ctg agt gaa gtg ctg gtt ggt gcg gtg ttc atc atg tat      931
Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala Val Phe Ile Met Tyr
            265                 270                 275

ctg gcc ggg acc tgg agt tcc acc cag gcg ggt gcg ttg agg gag aag      979
Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly Ala Leu Arg Glu Lys
        280                 285                 290

atc ggc aat ggg tca acg gtt att ttc ttg agt ctg acg atg atc gcg     1027
Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser Leu Thr Met Ile Ala
    295                 300                 305

tcg atg gca ctg atg ggg att aat aat ttg tgg gtc acg ttg gtt gcc     1075
Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp Val Thr Leu Val Ala
310                 315                 320                 325

ctg ttt gtg ttt acc gcg gca ttt ttc gca ctg cat tcc agt gct tcg     1123
Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu His Ser Ser Ala Ser
                330                 335                 340

gga tgg atc gga atc atc gca acg aag gat cgc gcg gaa gcc tcc agc     1171
Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg Ala Glu Ala Ser Ser
            345                 350                 355

atg tat ttg ttc tgt tat tac gtg gga tcc tcg gtg att ggt tgg gtt     1219
Met Tyr Leu Phe Cys Tyr Tyr Val Gly Ser Ser Val Ile Gly Trp Val
        360                 365                 370

tct gga ttc gcg ttt acg cat ttg ccg tgg ttg gcg ttc att ggc tgg     1267
Ser Gly Phe Ala Phe Thr His Leu Pro Trp Leu Ala Phe Ile Gly Trp
    375                 380                 385

ttg att ctg ctt ctt tgc gga gtg ctg gcg att tgt gtg acg ctg gca     1315
Leu Ile Leu Leu Leu Cys Gly Val Leu Ala Ile Cys Val Thr Leu Ala
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390 395 400 405

agg ctt gcc cgc aac gcc aat taatacgagt ttgtccgtgt tta 1359
Arg Leu Ala Arg Asn Ala Asn
410

<210> 206
<211> 412
<212> PRT
<213> Corynebacterium glutamicum

<400> 206
Met Ser Gln Ala Ile Asp Ser Lys Val Glu Ala His Glu Gly His Glu
1 5 10 15

Gly His Glu Gly Ile Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val
20 25 30

Phe Ala Met Leu Ala Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys
35 40 45

Thr Gln Ala Leu Leu Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro
50 55 60

Thr Glu Ser Ala Leu Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu
65 70 75 80

Cys Ile Val Pro Ala Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg
85 90 95

Val Leu Thr Ile Ser Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu
100 105 110

Pro Leu Val Pro Asn Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln
115 120 125

Gly Ala Leu Leu Ala Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser
130 135 140

Glu Glu Ile His Pro Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile
145 150 155 160

Ala Gly Asn Thr Val Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly
165 170 175

Leu Leu Glu Val Thr His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile
180 185 190

Ala Ala Leu Ile Phe Gly Val Ile Met Val Val Leu Leu Pro Lys Gln
195 200 205

Arg Lys Phe Gln Pro Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala
210 215 220

Met Ala Ala His Trp Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr
225 230 235 240

```
Ala Phe Leu Gly Met Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly
                245                 250                 255

Phe Arg Met Ile Asp Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala
            260                 265                 270

Val Phe Ile Met Tyr Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly
        275                 280                 285

Ala Leu Arg Glu Lys Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser
    290                 295                 300

Leu Thr Met Ile Ala Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp
305                 310                 315                 320

Val Thr Leu Val Ala Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu
                325                 330                 335

His Ser Ser Ala Ser Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg
            340                 345                 350

Ala Glu Ala Ser Ser Met Tyr Leu Phe Cys Tyr Tyr Val Gly Ser Ser
        355                 360                 365

Val Ile Gly Trp Val Ser Gly Phe Ala Phe Thr His Leu Pro Trp Leu
    370                 375                 380

Ala Phe Ile Gly Trp Leu Ile Leu Leu Leu Cys Gly Val Leu Ala Ile
385                 390                 395                 400

Cys Val Thr Leu Ala Arg Leu Ala Arg Asn Ala Asn
                405                 410


<210> 207
<211> 1215
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1192)
<223> FRXA01873

<400> 207
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acattttact aatatttgct gttggcgcat gatgaactcc atg agc caa gca ata    115
                                           Met Ser Gln Ala Ile
                                           1               5

gat agc aag gtc gag gca cac gaa ggc cac gaa ggc cac gaa ggc atc    163
Asp Ser Lys Val Glu Ala His Glu Gly His Glu Gly His Glu Gly Ile
                10                  15                  20

gag cga gga aca cgc aat tac aag cgc gct gtg ttt gcg atg ctg gcc    211
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Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val Phe Ala Met Leu Ala
            25                  30                  35

gcc ggt ctt gct gct ttc aat ggt ctt tat tgc acg cag gca ttg ctt      259
Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys Thr Gln Ala Leu Leu
        40                  45                  50

ccc acc atg acg gaa gag ttg gga att acg ccc act gag tcc gcg ctg      307
Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro Thr Glu Ser Ala Leu
    55                  60                  65

acg gtg tcg gct acg act gga atg ttg gcg ctg tgt att gtt ccg gcg      355
Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu Cys Ile Val Pro Ala
70                  75                  80                  85

tcg ata ctt tcg gag aaa ttt ggt cgc ggt cgg gtg ctg aca att tca      403
Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg Val Leu Thr Ile Ser
                90                  95                  100

ctc acg ttg gcc atc atc gtg gga tta att ttg ccg ctt gtc ccc aat      451
Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu Pro Leu Val Pro Asn
            105                 110                 115

att act gct ctc atc ctg ctc aga ggt ctc caa ggt gcg ctg ctt gct      499
Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln Gly Ala Leu Leu Ala
        120                 125                 130

ggc act cca gcg gtg gcg atg acc tgg ttg tct gag gaa att cac ccc      547
Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser Glu Glu Ile His Pro
    135                 140                 145

aag gat att ggg cat gcg atg gga att tac atc gcg gga aat act gtc      595
Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile Ala Gly Asn Thr Val
150                 155                 160                 165

ggc ggg ctc act gga cgt atg att ccg gcg gga cta ctt gaa gta act      643
Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly Leu Leu Glu Val Thr
                170                 175                 180

cat tgg caa aac gca ctg ctg gga agt tct atc gct gcg ctg atc ttc      691
His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile Ala Ala Leu Ile Phe
            185                 190                 195

ggc gta atc atg gtg gtg ttg ctt ccc aag cag cgg aaa ttc cag ccg      739
Gly Val Ile Met Val Val Leu Leu Pro Lys Gln Arg Lys Phe Gln Pro
        200                 205                 210

aag aat atc aat ctg cgc cat gag att tcg gcg atg gct gct cat tgg      787
Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala Met Ala Ala His Trp
    215                 220                 225

cgg aat cct cgt ttg gcg ttg ctt ttt ggt act gcg ttt ttg ggc atg      835
Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr Ala Phe Leu Gly Met
230                 235                 240                 245

ggt act ttt gtg tcg ctg tac aac tat ttg ggt ttc cgc atg att gat      883
Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly Phe Arg Met Ile Asp
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            250                 255                 260

cag ttt ggg ctg agt gaa gtg ctg gtt ggt gcg gtg ttc atc atg tat      931
Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala Val Phe Ile Met Tyr
        265                 270                 275

ctg gcc ggg acc tgg agt tcc acc cag gcg ggt gcg ttg agg gag aag      979
Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly Ala Leu Arg Glu Lys
    280                 285                 290

atc ggc aat ggg tca acg gtt att ttc ttg agt ctg acg atg atc gcg      1027
Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser Leu Thr Met Ile Ala
    295                 300                 305

tcg atg gca ctg atg ggg att aat aat ttg tgg gtc acg ttg gtt gcc      1075
Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp Val Thr Leu Val Ala
310                 315                 320                 325

ctg ttt gtg ttt acc gcg gca ttt ttc gca ctg cat tcc agt gct tcg      1123
Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu His Ser Ser Ala Ser
                330                 335                 340

gga tgg atc gga atc atc gca acg aag gat cgc gcg gaa gcc tcc agc      1171
Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg Ala Glu Ala Ser Ser
            345                 350                 355

atg tat ttg ttc tgt gaa tac taggatcctc ggtgattggt tgg                1215
Met Tyr Leu Phe Cys Glu Tyr
        360
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<210> 208
<211> 364
<212> PRT
<213> Corynebacterium glutamicum

<400> 208

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Met Ser Gln Ala Ile Asp Ser Lys Val Glu Ala His Glu Gly His Glu
 1               5                  10                  15

Gly His Glu Gly Ile Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val
            20                  25                  30

Phe Ala Met Leu Ala Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys
        35                  40                  45

Thr Gln Ala Leu Leu Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro
    50                  55                  60

Thr Glu Ser Ala Leu Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu
65                  70                  75                  80

Cys Ile Val Pro Ala Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg
                85                  90                  95

Val Leu Thr Ile Ser Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu
            100                 105                 110
```

```
Pro Leu Val Pro Asn Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln
        115                 120                 125

Gly Ala Leu Leu Ala Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser
    130                 135                 140

Glu Glu Ile His Pro Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile
145                 150                 155                 160

Ala Gly Asn Thr Val Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly
                165                 170                 175

Leu Leu Glu Val Thr His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile
            180                 185                 190

Ala Ala Leu Ile Phe Gly Val Ile Met Val Val Leu Leu Pro Lys Gln
        195                 200                 205

Arg Lys Phe Gln Pro Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala
    210                 215                 220

Met Ala Ala His Trp Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr
225                 230                 235                 240

Ala Phe Leu Gly Met Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly
                245                 250                 255

Phe Arg Met Ile Asp Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala
            260                 265                 270

Val Phe Ile Met Tyr Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly
        275                 280                 285

Ala Leu Arg Glu Lys Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser
    290                 295                 300

Leu Thr Met Ile Ala Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp
305                 310                 315                 320

Val Thr Leu Val Ala Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu
                325                 330                 335

His Ser Ser Ala Ser Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg
            340                 345                 350

Ala Glu Ala Ser Ser Met Tyr Leu Phe Cys Glu Tyr
        355                 360
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<210> 209
<211> 1572
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1549)
<223> RXN00034

<400> 209
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ttttgcaagt ttctatagat tgatagaaaa gggagtttag atg tct tac aca tct 115
Met Ser Tyr Thr Ser
1 5

ttt aaa ggc gat gat aaa gcc ctc atc ggc ata gtt tta tca gtt ctc 163
Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile Val Leu Ser Val Leu
10 15 20

aca ttt tgg ctt ttt gct cag tca acc cta aat atc ggc cca gat atg 211
Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn Ile Gly Pro Asp Met
25 30 35

gca act gat tta ggg atg agc gat ggc acc atg aac ata gct gtc gtg 259
Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met Asn Ile Ala Val Val
40 45 50

gcc gcc gcg tta ttc tgt gga aca ttt atc gtc gca gcc ggc ggc atc 307
Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val Ala Ala Gly Gly Ile
55 60 65

gca gat gtc ttt ggc cga gta cga atc atg atg att ggc aac atc ctt 355
Ala Asp Val Phe Gly Arg Val Arg Ile Met Met Ile Gly Asn Ile Leu
70 75 80 85

aac atc ctg gga tct ctc ctc atc gcc acg gca acg act tct tta gcc 403
Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala Thr Thr Ser Leu Ala
90 95 100

acc caa atg gtg atc acc ggc cga gtt ctc caa gga ctg gca gca gcg 451
Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln Gly Leu Ala Ala Ala
105 110 115

gcc atc atg tct gca tcc cta gca tta gtt aag aca tat tgg tta ggt 499
Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys Thr Tyr Trp Leu Gly
120 125 130

act gac cgc caa cga gca gtc tcc att tgg tcc att ggt tca tgg ggt 547
Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser Ile Gly Ser Trp Gly
135 140 145

ggc acc gga ttc tgc gcg ctt ttc gcg ggt ctt gtt gta gca agc ccc 595
Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu Val Val Ala Ser Pro
150 155 160 165

ttt ggt tgg aga gga atc ttc gcc ctc tgc gcg atc gtc tcc atc gtt 643
Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala Ile Val Ser Ile Val
170 175 180

gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc 691
Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser
185 190 195

```
att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt    739
Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser
        200                 205                 210

gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg    787
Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp
    215                 220                 225

acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt    835
Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu
230                 235                 240                 245

gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac    883
Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp
                250                 255                 260

ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac    931
Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn
            265                 270                 275

ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt    979
Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Val Met Trp Val
        280                 285                 290

cag caa atg gga tgg ggt gtc tcc cca aca atc tcg gga ctc acc agc    1027
Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile Ser Gly Leu Thr Ser
    295                 300                 305

atc ggc ttc gca gcc ttt gtc atc ctt ttc att cga gtt gga gaa aag    1075
Ile Gly Phe Ala Ala Phe Val Ile Leu Phe Ile Arg Val Gly Glu Lys
310                 315                 320                 325

gcc atg cag aaa gtt ggc gcc cga gca gtg atc atc acc gct ggc atc    1123
Ala Met Gln Lys Val Gly Ala Arg Ala Val Ile Ile Thr Ala Gly Ile
                330                 335                 340

ttg gta gcg acc gcg acc gcc ctc cta atg atc acc gcg gtc agc gag    1171
Leu Val Ala Thr Ala Thr Ala Leu Leu Met Ile Thr Ala Val Ser Glu
            345                 350                 355

tca acg tac atc gtc atc tcc ctc gcc ggc ttc tcc ctt tat ggc ctt    1219
Ser Thr Tyr Ile Val Ile Ser Leu Ala Gly Phe Ser Leu Tyr Gly Leu
        360                 365                 370

ggc ctc gga ctc ttc gcc acc cca gtc acc gat act gcg ctt gga aca    1267
Gly Leu Gly Leu Phe Ala Thr Pro Val Thr Asp Thr Ala Leu Gly Thr
    375                 380                 385

ctt ccc aaa gac cgt acc ggc gct ggt gca ggt gta ttc aag atg tcc    1315
Leu Pro Lys Asp Arg Thr Gly Ala Gly Ala Gly Val Phe Lys Met Ser
390                 395                 400                 405

tct tcc ctc ggc gca gca ctc ggc atc gca atc tcc act tca gtg ttc    1363
Ser Ser Leu Gly Ala Ala Leu Gly Ile Ala Ile Ser Thr Ser Val Phe
                410                 415                 420
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ctc gca ctt cgc gac ggc acc tcc atc aac tcc gac gtc gca ctc gcc 1411
Leu Ala Leu Arg Asp Gly Thr Ser Ile Asn Ser Asp Val Ala Leu Ala
425 430 435

gga aca gtt tca ctt ggc atc aac gtt gta ttc gca gca aca gcc acc 1459
Gly Thr Val Ser Leu Gly Ile Asn Val Val Phe Ala Ala Thr Ala Thr
440 445 450

atc acc gca gca gtc ctt att cca aaa gcc gct ggc aaa gtc tca caa 1507
Ile Thr Ala Ala Val Leu Ile Pro Lys Ala Ala Gly Lys Val Ser Gln
455 460 465

acc agc atc acc ctt cct gag cca gct atc gct gta aaa atc 1549
Thr Ser Ile Thr Leu Pro Glu Pro Ala Ile Ala Val Lys Ile
470 475 480

taaaacttca ccaggacaga taa 1572

<210> 210
<211> 483
<212> PRT
<213> Corynebacterium glutamicum

<400> 210
Met Ser Tyr Thr Ser Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile
1 5 10 15

Val Leu Ser Val Leu Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn
20 25 30

Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
35 40 45

Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
50 55 60

Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
65 70 75 80

Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
85 90 95

Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
100 105 110

Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
115 120 125

Thr Tyr Trp Leu Gly Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser
130 135 140

Ile Gly Ser Trp Gly Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu
145 150 155 160

Val Val Ala Ser Pro Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala
165 170 175

```
Ile Val Ser Ile Val Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser
            180                 185                 190

Arg Pro Ala Gln Ser Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile
        195                 200                 205

Val Leu Ala Leu Ser Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly
    210                 215                 220

Glu Ser Leu Gly Trp Thr His Trp Met Thr Trp Thr Leu Leu Ala Val
225                 230                 235                 240

Ser Leu Thr Phe Leu Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser
                245                 250                 255

Trp Pro Val Leu Asp Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly
            260                 265                 270

Ala Thr Ile Thr Asn Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala
        275                 280                 285

Val Val Met Trp Val Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile
    290                 295                 300

Ser Gly Leu Thr Ser Ile Gly Phe Ala Ala Phe Val Ile Leu Phe Ile
305                 310                 315                 320

Arg Val Gly Glu Lys Ala Met Gln Lys Val Gly Ala Arg Ala Val Ile
                325                 330                 335

Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu Leu Met Ile
            340                 345                 350

Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu Ala Gly Phe
        355                 360                 365

Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro Val Thr Asp
    370                 375                 380

Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala Gly Ala Gly
385                 390                 395                 400

Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly Ile Ala Ile
                405                 410                 415

Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser Ile Asn Ser
            420                 425                 430

Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn Val Val Phe
        435                 440                 445

Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro Lys Ala Ala
    450                 455                 460

Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro Ala Ile Ala
465                 470                 475                 480
```

Val Lys Ile

<210> 211
<211> 1045
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1045)
<223> FRXA02273

<400> 211
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taaattttgt ggcactcccc acatttctat caatctatag aaagtatgac ttaaagtcga 60

ttttgcaagt ttctatagat tgatagaaaa gggagtttag atg tct tac aca tct   115
                                            Met Ser Tyr Thr Ser
                                            1               5

ttt aaa ggc gat gat aaa gcc ctc atc ggc ata gtt tta tca gtt ctc   163
Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile Val Leu Ser Val Leu
                10                  15                  20

aca ttt tgg ctt ttt gct cag tca acc cta aat atc ggc cca gat atg   211
Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn Ile Gly Pro Asp Met
            25                  30                  35

gca act gat tta ggg atg agc gat ggc acc atg aac ata gct gtc gtg   259
Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met Asn Ile Ala Val Val
        40                  45                  50

gcc gcc gcg tta ttc tgt gga aca ttt atc gtc gca gcc ggc ggc atc   307
Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val Ala Ala Gly Gly Ile
    55                  60                  65

gca gat gtc ttt ggc cga gta cga atc atg atg att ggc aac atc ctt   355
Ala Asp Val Phe Gly Arg Val Arg Ile Met Met Ile Gly Asn Ile Leu
70                  75                  80                  85

aac atc ctg gga tct ctc ctc atc gcc acg gca acg act tct tta gcc   403
Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala Thr Thr Ser Leu Ala
                90                  95                  100

acc caa atg gtg atc acc ggc cga gtt ctc caa gga ctg gca gca gcg   451
Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln Gly Leu Ala Ala Ala
            105                 110                 115

gcc atc atg tct gca tcc cta gca tta gtt aag aca tat tgg tta ggt   499
Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys Thr Tyr Trp Leu Gly
        120                 125                 130

act gac cgc caa cga gca gtc tcc att tgg tcc att ggt tca tgg ggt   547
Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser Ile Gly Ser Trp Gly
    135                 140                 145
```

ggc acc gga ttc tgc gcg ctt ttc gcg ggt ctt gtt gta gca agc ccc 595
Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu Val Val Ala Ser Pro
150 155 160 165

ttt ggt tgg aga gga atc ttc gcc ctc tgc gcg atc gtc tcc atc gtt 643
Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala Ile Val Ser Ile Val
170 175 180

gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc 691
Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser
185 190 195

att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt 739
Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser
200 205 210

gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg 787
Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp
215 220 225

acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt 835
Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu
230 235 240 245

gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac 883
Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp
250 255 260

ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac 931
Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn
265 270 275

ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt 979
Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Val Met Trp Val
280 285 290

cag caa atg gga tgg ggt gtc tcc cca aca atc tcg gga ctc acc agc 1027
Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile Ser Gly Leu Thr Ser
295 300 305

atc ggc ttc gca gcc ttt 1045
Ile Gly Phe Ala Ala Phe
310 315

<210> 212
<211> 315
<212> PRT
<213> Corynebacterium glutamicum

<400> 212
Met Ser Tyr Thr Ser Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile
1 5 10 15

Val Leu Ser Val Leu Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn
20 25 30

```
Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
        35                  40                  45

Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
    50                  55                  60

Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
65                  70                  75                  80

Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
                85                  90                  95

Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
            100                 105                 110

Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
        115                 120                 125

Thr Tyr Trp Leu Gly Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser
    130                 135                 140

Ile Gly Ser Trp Gly Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu
145                 150                 155                 160

Val Val Ala Ser Pro Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala
                165                 170                 175

Ile Val Ser Ile Val Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser
            180                 185                 190

Arg Pro Ala Gln Ser Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile
        195                 200                 205

Val Leu Ala Leu Ser Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly
    210                 215                 220

Glu Ser Leu Gly Trp Thr His Trp Met Thr Trp Thr Leu Leu Ala Val
225                 230                 235                 240

Ser Leu Thr Phe Leu Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser
                245                 250                 255

Trp Pro Val Leu Asp Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly
            260                 265                 270

Ala Thr Ile Thr Asn Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala
        275                 280                 285

Val Val Met Trp Val Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile
    290                 295                 300

Ser Gly Leu Thr Ser Ile Gly Phe Ala Ala Phe
305                 310                 315
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<210> 213

<211> 826
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(826)
<223> RXN03075

<400> 213
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tgtgcaaaat tgcattcagg ctgaaaaatt cctaaaggga ctccgtccga ataattggaa 60

agcccagaag aacagtcaac tcctagatta aaggataatc gtg gcg aaa ttc ctg   115
                                            Val Ala Lys Phe Leu
                                            1               5

tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg   163
Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala
                10                  15                  20

gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat   211
Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr
            25                  30                  35

gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc   259
Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val
        40                  45                  50

acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca   307
Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala
    55                  60                  65

aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag   355
Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys
70                  75                  80                  85

acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat   403
Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp
                90                  95                  100

gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat   451
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp
            105                 110                 115

cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg   499
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu
        120                 125                 130

gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg   547
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser
    135                 140                 145

att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act   595
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr
150                 155                 160                 165

ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag   643
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Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys
                170                 175                 180

gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc     691
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val
            185                 190                 195

tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc     739
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr
        200                 205                 210

tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc     787
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr
    215                 220                 225

ttc ggt tcg ttc atc gct gcc ggt atg ccg ctg atc tct                 826
Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser
230                 235                 240


<210> 214
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 214
Val Ala Lys Phe Leu Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys
  1               5                  10                  15

Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr
             20                  25                  30

Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
         35                  40                  45

Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
     50                  55                  60

Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65                  70                  75                  80

Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
                 85                  90                  95

Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
            100                 105                 110

Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
        115                 120                 125

Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
    130                 135                 140

Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
145                 150                 155                 160

Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
```

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                165                 170                 175

Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
            180                 185                 190

Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
        195                 200                 205

Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
    210                 215                 220

Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
225                 230                 235                 240

Ile Ser



&lt;210&gt; 215
&lt;211&gt; 826
&lt;212&gt; DNA
&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (101)..(826)
&lt;223&gt; FRXA02907

&lt;400&gt; 215
tgtgcaaaat tgcattcagg ctgaaaaatt cctaaaggga ctccgtccga ataattggaa 60

agcccagaag aacagtcaac tcctagatta aaggataatc gtg gcg aaa ttc ctg    115
                                           Val Ala Lys Phe Leu
                                           1               5

tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg    163
Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala
                10                  15                  20

gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat    211
Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr
            25                  30                  35

gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc    259
Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val
        40                  45                  50

acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca    307
Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala
    55                  60                  65

aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag    355
Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys
70                  75                  80                  85

acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat    403
Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp
```

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                    90                  95                  100

gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat      451
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp
            105                 110                 115

cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg      499
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu
        120                 125                 130

gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg      547
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser
    135                 140                 145

att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act      595
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr
150                 155                 160                 165

ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag      643
Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys
                170                 175                 180

gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc      691
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val
            185                 190                 195

tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc      739
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr
        200                 205                 210

tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc      787
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr
    215                 220                 225

ttc ggt tcg ttc atc gct gcc ggt atg ccg ctg atc tct                  826
Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser
230                 235                 240


&lt;210&gt; 216
&lt;211&gt; 242
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 216
Val Ala Lys Phe Leu Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys
  1               5                  10                  15

Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr
             20                  25                  30

Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
         35                  40                  45

Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
     50                  55                  60
```

```
Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
65                  70                  75                  80

Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
                85                  90                  95

Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
            100                 105                 110

Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
        115                 120                 125

Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
    130                 135                 140

Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
145                 150                 155                 160

Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
                165                 170                 175

Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
            180                 185                 190

Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
        195                 200                 205

Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
    210                 215                 220

Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
225                 230                 235                 240

Ile Ser


<210> 217
<211> 2313
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2290)
<223> RXA00479

<400> 217
tagatcccaa ggctcaaaat ttattactta aacaagttga gcaactagcc agccgcaaat   60

cttagaacta acctttacgc ctttaacgga agtgaatttg atg tct act agc atc    115
                                            Met Ser Thr Ser Ile
                                            1               5

aca aca gag aac aag aag aaa tct ggt cct cct cgc ttg atg aga atc    163
Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro Arg Leu Met Arg Ile
                10                  15                  20
```

```
ttt ctg ccc gcc ttg cta att tta gtt tgg ctt gta gga gct gga gtc     211
Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu Val Gly Ala Gly Val
            25                  30                  35

ggc ggt cct tat ttt ggc aag gtt agt gag gtc tcc tcc aac agc cag     259
Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val Ser Ser Asn Ser Gln
        40                  45                  50

acc aca tat ctg cca gaa tct gcc gat gcc act caa gta cag gaa cag     307
Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr Gln Val Gln Glu Gln
    55                  60                  65

ttg gga gat ttt act gat tct gaa tcc atc cca gcc att gtc gta atg     355
Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro Ala Ile Val Val Met
70                  75                  80                  85

gtc agc gat gaa ccc tta aca cag caa gac atc aca caa ctc aat gaa     403
Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile Thr Gln Leu Asn Glu
                90                  95                  100

gtt gtt gct ggg ctt tca gaa tta gac ata gtt tcc gat gaa gtc tcc     451
Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val Ser Asp Glu Val Ser
            105                 110                 115

cct gct att cca tcc gag gac ggc aga gct gtc caa gtg ttt gtc ccc     499
Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val Gln Val Phe Val Pro
        120                 125                 130

ctc aat cca tca gcg gag ctg acg gaa agc gtc gag aag ctc tct gag     547
Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val Glu Lys Leu Ser Glu
    135                 140                 145

acc ttg acc cag caa acg ccg gac tat gtg agc acc tat gtg acc gga     595
Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser Thr Tyr Val Thr Gly
150                 155                 160                 165

ccg gct ggg ttt acc gct gat ctc agc gca gct ttc gcg ggt att gat     643
Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala Phe Ala Gly Ile Asp
                170                 175                 180

ggg cta ctc cta gca gtc gcc ttg gct gcc gtc ctt gtc att ctt gtc     691
Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val Leu Val Ile Leu Val
            185                 190                 195

atc gtc tat cgc tcc ttc att ctg ccc atc gcc gtg ctt gcc acc agt     739
Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala Val Leu Ala Thr Ser
        200                 205                 210

ttg ttt gcg ctg act gta gct cta ttg gtg gtg tgg tgg cta gct aag     787
Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val Trp Trp Leu Ala Lys
    215                 220                 225

tgg gac atc ctg ctg ctt tcg ggt cag act caa ggc atc ctc ttc att     835
Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln Gly Ile Leu Phe Ile
230                 235                 240                 245
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```
ctg gtc att ggc gcc gcc acc gac tac tca ttg cta tac gtt gct cgt    883
Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu Leu Tyr Val Ala Arg
                250                 255                 260

ttc cgt gaa gag tta cgc gtt caa caa gat aaa ggg ata gcc aca ggg    931
Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys Gly Ile Ala Thr Gly
            265                 270                 275

aaa gcc atc cgg gca tcg gtg gaa ccc att ctt gcc tcg ggc agc act    979
Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu Ala Ser Gly Ser Thr
        280                 285                 290

gtt att gcg ggc ctc ctt tgt ttg cta ttt agt gat ttg aaa tct aac    1027
Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser Asp Leu Lys Ser Asn
    295                 300                 305

tcc acg cta ggt cca gta gct tcg gtg ggc att att ttt gca atg ctt    1075
Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile Ile Phe Ala Met Leu
310                 315                 320                 325

tct gct ctt act ctg cta cca gcc ctg ctg ttt gta ttc ggt cgg gtg    1123
Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe Val Phe Gly Arg Val
                330                 335                 340

gcc ttt tgg ccc aag cga cca aaa tac gaa cct gaa aaa gcc cgt gcg    1171
Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro Glu Lys Ala Arg Ala
            345                 350                 355

aaa aac gac atc ccc gcc agc ggg atc tgg tca aaa gtg gct gat tta    1219
Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser Lys Val Ala Asp Leu
        360                 365                 370

gtg gag cag cat cct cgt gca atc tgg gta tct aca ctt att gtg ctt    1267
Val Glu Gln His Pro Arg Ala Ile Trp Val Ser Thr Leu Ile Val Leu
    375                 380                 385

ctc ttg ggt gcg gct ttc gtt ccc aca cta aaa gcg gac ggt gtg tcc    1315
Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys Ala Asp Gly Val Ser
390                 395                 400                 405

caa tcc gac cta gtt ctg ggt tcc tct gaa gca cgt gat ggc cag cag    1363
Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala Arg Asp Gly Gln Gln
                410                 415                 420

gct tta ggc gaa cac ttc ccc ggt gga tcc ggc agt cct gct tat att    1411
Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly Ser Pro Ala Tyr Ile
            425                 430                 435

atc gtt gat gaa aca cag gca gca cag gct gct gac gta gtc ctt aac    1459
Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala Asp Val Val Leu Asn
        440                 445                 450

aac gac aat ttc gag act gta act gta act agt gct gac tcc ccc tct    1507
Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser Ala Asp Ser Pro Ser
    455                 460                 465

ggc tca gcc cca atc acc gct gac ggt att gtg ccg tta ggt tct ggt    1555
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Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val Pro Leu Gly Ser Gly
470                 475                 480                 485

aca gct cca ggc ccg gta gtt gta gaa ggg caa gtc ctt tta caa gca     1603
Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln Val Leu Leu Gln Ala
                490                 495                 500

aca ctt gtc gaa gca cca gat tcc gaa gaa gct caa aaa gct att cgc     1651
Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala Gln Lys Ala Ile Arg
            505                 510                 515

agt atc cgc caa act ttt gca gat gaa aat ata tca gcg gta gta ggc     1699
Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile Ser Ala Val Val Gly
        520                 525                 530

ggt gtc act gca act tcc gta gac act aac gat gcc tcc atc cat gac     1747
Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp Ala Ser Ile His Asp
    535                 540                 545

cgc aac ctg atc atc cca att gta ttg ctg gtc att ttg gtt att ctc     1795
Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val Ile Leu Val Ile Leu
550                 555                 560                 565

atg ctg ttg ctg cgg tct att gtc gca cca ctc ctg cta gta gtc acc     1843
Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu Leu Leu Val Val Thr
                570                 575                 580

acc gtg gtg tct ttt gct act gct tta ggc gtg gct gct tta ctt ttc     1891
Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val Ala Ala Leu Leu Phe
            585                 590                 595

aat cac gtt ttc agt ttc cca gga gca gac ccc gca gta cct ctc tac     1939
Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro Ala Val Pro Leu Tyr
        600                 605                 610

gga ttt gta ttt tta gta gcc ttg ggc atc gac tac aac att ttc tta     1987
Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp Tyr Asn Ile Phe Leu
    615                 620                 625

gtc acc cga atc cgt gaa gaa acc aaa acc cac ggc aca aga ctt gga     2035
Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His Gly Thr Arg Leu Gly
630                 635                 640                 645

att ctt cga ggc ctg aca gta acc ggc gga gta att acc tca gct gga     2083
Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val Ile Thr Ser Ala Gly
                650                 655                 660

gta gtt ctc gcc gca acg ttc gca gca ctc tat gtc atc cca att cta     2131
Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr Val Ile Pro Ile Leu
            665                 670                 675

ttc ctg gca caa att gcc ttc att gtc gct ttt gga gtt ctt att gat     2179
Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe Gly Val Leu Ile Asp
        680                 685                 690

acc ctg ctc gtt cgc gcc ttc ttg gtg cct gct ttg ttc tac gac atc     2227
Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala Leu Phe Tyr Asp Ile
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695 700 705

gga ccg aaa atc tgg tgg ccg tca aaa ttg tcc aat cag aaa tac cag 2275
Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser Asn Gln Lys Tyr Gln
710 715 720 725

aag cag cct cag cta tgacacacca aaattcgcct ctc 2313
Lys Gln Pro Gln Leu
730

<210> 218
<211> 730
<212> PRT
<213> Corynebacterium glutamicum

<400> 218
Met Ser Thr Ser Ile Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro
1 5 10 15

Arg Leu Met Arg Ile Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu
20 25 30

Val Gly Ala Gly Val Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val
35 40 45

Ser Ser Asn Ser Gln Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr
50 55 60

Gln Val Gln Glu Gln Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro
65 70 75 80

Ala Ile Val Val Met Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile
85 90 95

Thr Gln Leu Asn Glu Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val
100 105 110

Ser Asp Glu Val Ser Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val
115 120 125

Gln Val Phe Val Pro Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val
130 135 140

Glu Lys Leu Ser Glu Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser
145 150 155 160

Thr Tyr Val Thr Gly Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala
165 170 175

Phe Ala Gly Ile Asp Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val
180 185 190

Leu Val Ile Leu Val Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala
195 200 205

Val Leu Ala Thr Ser Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val

210 215 220

Trp Trp Leu Ala Lys Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln
225 230 235 240

Gly Ile Leu Phe Ile Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu
245 250 255

Leu Tyr Val Ala Arg Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys
260 265 270

Gly Ile Ala Thr Gly Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu
275 280 285

Ala Ser Gly Ser Thr Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser
290 295 300

Asp Leu Lys Ser Asn Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile
305 310 315 320

Ile Phe Ala Met Leu Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe
325 330 335

Val Phe Gly Arg Val Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro
340 345 350

Glu Lys Ala Arg Ala Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser
355 360 365

Lys Val Ala Asp Leu Val Glu Gln His Pro Arg Ala Ile Trp Val Ser
370 375 380

Thr Leu Ile Val Leu Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys
385 390 395 400

Ala Asp Gly Val Ser Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala
405 410 415

Arg Asp Gly Gln Gln Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly
420 425 430

Ser Pro Ala Tyr Ile Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala
435 440 445

Asp Val Val Leu Asn Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser
450 455 460

Ala Asp Ser Pro Ser Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val
465 470 475 480

Pro Leu Gly Ser Gly Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln
485 490 495

Val Leu Leu Gln Ala Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala
500 505 510

Gln Lys Ala Ile Arg Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile

515 520 525

Ser Ala Val Val Gly Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp
530 535 540

Ala Ser Ile His Asp Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val
545 550 555 560

Ile Leu Val Ile Leu Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu
565 570 575

Leu Leu Val Val Thr Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val
580 585 590

Ala Ala Leu Leu Phe Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro
595 600 605

Ala Val Pro Leu Tyr Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp
610 615 620

Tyr Asn Ile Phe Leu Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His
625 630 635 640

Gly Thr Arg Leu Gly Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val
645 650 655

Ile Thr Ser Ala Gly Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr
660 665 670

Val Ile Pro Ile Leu Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe
675 680 685

Gly Val Leu Ile Asp Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala
690 695 700

Leu Phe Tyr Asp Ile Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser
705 710 715 720

Asn Gln Lys Tyr Gln Lys Gln Pro Gln Leu
725 730

<210> 219
<211> 983
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(960)
<223> RXN03124

<400> 219
atg act cct acc ctg gcg tcg atg att ggt ctg gct gtc ggt atc gac 48
Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
1 5 10 15

tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag 96
Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
20 25 30

act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc 144
Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
35 40 45

acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc 192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
50 55 60

act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct 240
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
65 70 75 80

ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc 288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
85 90 95

att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc 336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
100 105 110

ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca 384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
115 120 125

cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg 432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
130 135 140

atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac 480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
145 150 155 160

ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc 528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
165 170 175

aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc 576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
180 185 190

gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc 624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
195 200 205

cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag 672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
210 215 220

gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac 720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
225 230 235 240

act gat ggt gtg aag aat gct cag atc act cag acc acg gag aat ttc 768

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Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
                245                 250                 255

gat acc gcg cag atc ctg tta ccc cag aat ttg atg cga tcg atg agc     816
Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
            260                 265                 270

gca cct ctg aga ctc tcg caa ctc ttc gtg cag atg ctg aga cct tcg     864
Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
        275                 280                 285

ctg atg aca ccg gcg cga cgt atg gca tta ctg gcg tca ccc caa ttt     912
Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
    290                 295                 300

acg atg aca tct ctg ctc gcc tcg gcg acg tcc tgg ttc ctt acg ttc     960
Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
305                 310                 315                 320

tgatcgtttt ggttctagcg ttc                                           983


&lt;210&gt; 220
&lt;211&gt; 320
&lt;212&gt; PRT
&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 220
Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
  1               5                  10                  15

Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
             20                  25                  30

Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
         35                  40                  45

Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
     50                  55                  60

Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
 65                  70                  75                  80

Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
                 85                  90                  95

Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
            100                 105                 110

Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
        115                 120                 125

Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
    130                 135                 140

Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
145                 150                 155                 160
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Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
                165                 170                 175

Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
            180                 185                 190

Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
        195                 200                 205

Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
    210                 215                 220

Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
225                 230                 235                 240

Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe
                245                 250                 255

Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser
            260                 265                 270

Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
        275                 280                 285

Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
    290                 295                 300

Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
305                 310                 315                 320
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<210> 221
<211> 762
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(762)
<223> FRXA01180

<400> 221
atg act cct acc ctg gcg tcg atg att ggt ctg gct gtc ggt atc gac      48
Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
  1               5                  10                  15

tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag      96
Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
             20                  25                  30

act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc     144
Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
         35                  40                  45
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acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc     192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
     50                  55                  60

act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct     240
Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
 65                  70                  75                  80

ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc     288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
                 85                  90                  95

att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc     336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
            100                 105                 110

ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca     384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
        115                 120                 125

cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg     432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
    130                 135                 140

atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac     480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
145                 150                 155                 160

ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc     528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
                165                 170                 175

aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc     576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
            180                 185                 190

gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc     624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
        195                 200                 205

cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag     672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
    210                 215                 220

gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac     720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
225                 230                 235                 240

act gat ggt gtg aag aat gct cag atc act cag acc acg gag             762
Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu
                245                 250
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<210> 222
<211> 254
<212> PRT

<213> Corynebacterium glutamicum

<400> 222
Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
1   5   10   15

Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
            20   25   30

Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
        35   40   45

Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
    50   55   60

Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
65   70   75   80

Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
                85   90   95

Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
            100   105   110

Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
        115   120   125

Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
    130   135   140

Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
145   150   155   160

Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
                165   170   175

Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
            180   185   190

Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
        195   200   205

Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu
    210   215   220

Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn
225   230   235   240

Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu
                245   250

<210> 223
<211> 393
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(370)
<223> RXA02586

<400> 223
ttctctgaga tcgtcatgat gaagtacatc gcgttcggca tgatcgcagc gctgattctg 60

gatgccacca tcatccgcat gctgcttgtc ccccgccgtg atg cac ctg ctt cgc    115
                                          Met His Leu Leu Arg
                                           1               5

gac gac aac tgg tgg gca ccc ggc ttc gtt aaa aag gcc tac acc gtc    163
Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys Lys Ala Tyr Thr Val
                10                  15                  20

atg ggt cac ggc tct gag gtg gag gaa gca cct cgc cca acc acc cgt    211
Met Gly His Gly Ser Glu Val Glu Glu Ala Pro Arg Pro Thr Thr Arg
            25                  30                  35

cgc ctc aac gac gat gag gaa gtc acc gtg cat gaa gca gtt gtc gct    259
Arg Leu Asn Asp Asp Glu Glu Val Thr Val His Glu Ala Val Val Ala
        40                  45                  50

ggc gat acc gtg gca tct cgc ggt ggt ttg agc acg cag gaa aac cgt    307
Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser Thr Gln Glu Asn Arg
    55                  60                  65

gat ctg gtg tcc ttc gtg gaa ctt aag gct cgt ttg gaa aag cgc agg    355
Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg Leu Glu Lys Arg Arg
70                  75                  80                  85

ctt gag gat cta gat taaatctatg cgaggatttt tca                      393
Leu Glu Asp Leu Asp
                90


<210> 224
<211> 90
<212> PRT
<213> Corynebacterium glutamicum

<400> 224
Met His Leu Leu Arg Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys
1               5                   10                  15

Lys Ala Tyr Thr Val Met Gly His Gly Ser Glu Val Glu Glu Ala Pro
            20                  25                  30

Arg Pro Thr Thr Arg Arg Leu Asn Asp Asp Glu Glu Val Thr Val His
        35                  40                  45

Glu Ala Val Val Ala Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser
    50                  55                  60

Thr Gln Glu Asn Arg Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg
65                  70                  75                  80
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Leu Glu Lys Arg Arg Leu Glu Asp Leu Asp
                85                  90


<210> 225
<211> 2214
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2191)
<223> RXA02587

<400> 225
agcctggata acctgccaga cggtggcgca tggctgcagc cgttccgccc tctgactgcc 60

ttgttatcca accgccacaa ttcccaggag taatccaccc gtg ttt tct aaa tgg   115
                                           Val Phe Ser Lys Trp
                                           1               5

ggc cac ttt gct tac aga ttt agg cgc att gtt ccg tta gtc gtc atc   163
Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val Pro Leu Val Val Ile
                10                  15                  20

gcc gcg att ttg gct ttg ttt gtc att ttc ggc acc aag ctg ggc gac   211
Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly Thr Lys Leu Gly Asp
            25                  30                  35

cgc atg agc cag gaa gga tgg gat gat cct ggt tct tcc tcg acc gct   259
Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly Ser Ser Ser Thr Ala
        40                  45                  50

gcg gcg cgc atc gag ttg gag acc ttt ggg cgt gac aat gac ggc gat   307
Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg Asp Asn Asp Gly Asp
    55                  60                  65

gtc gtg ttg ctg ttt act gcg cct gaa ggc act tct ttc gat gat gca   355
Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr Ser Phe Asp Asp Ala
70                  75                  80                  85

gag gtg ttc tcc agc atc tct ggc tac tta gat ggg cta atc gag aac   403
Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp Gly Leu Ile Glu Asn
                90                  95                  100

aac cct gat gaa gtc agc cac atc aac agc tac ttt gac act cgt aat   451
Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr Phe Asp Thr Arg Asn
            105                 110                 115

caa aat ctc ctc agc aaa gac ggc acc caa acc ttt gca gct ctc ggg   499
Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr Phe Ala Ala Leu Gly
        120                 125                 130

ctc aaa ggt gac ggc gag caa acg ctg aag gac ttc cgg gag att gaa   547
Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp Phe Arg Glu Ile Glu
    135                 140                 145
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gat cag ctc cat ccg gac aac ctt gcc ggt ggc gtc acc act gag gtc    595
Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly Val Thr Thr Glu Val
150                 155                 160                 165

gcg ggt gcc acc gct gta gcc gac gca ctc gat gag ggc atg gct ggc    643
Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp Glu Gly Met Ala Gly
                170                 175                 180

gat att tca cgc gcc gaa gtt ttt gcg ctg cct ttc gtg gct atc ttg    691
Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro Phe Val Ala Ile Leu
            185                 190                 195

ctg ctc atc gtg ttt ggc tca gtt gtt gcc gcg gcg atg cca ttg atc    739
Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala Ala Met Pro Leu Ile
        200                 205                 210

gtg ggc att ttg tcc atc ttg ggt tcg ctg ggc atc ttg gca att ttg    787
Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly Ile Leu Ala Ile Leu
    215                 220                 225

gct gga ttc ttc cag gtc aac gta ttt gca caa tct gtt gtg acc ctt    835
Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln Ser Val Val Thr Leu
230                 235                 240                 245

ctg ggc ttg ggt ctt gcc att gac tat ggc tta ttc atg gtc tct cgt    883
Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu Phe Met Val Ser Arg
                250                 255                 260

ttc cgt gag gaa atg gat aag ggc acc ccg gtt gaa cag gct gtt gcc    931
Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val Glu Gln Ala Val Ala
            265                 270                 275

acc act acg gcg acc gcg ggt aag act gtg gtg ttc tct gca gcg atg    979
Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val Phe Ser Ala Ala Met
        280                 285                 290

gtg gct gtg gcg ctg tcc ggg ttg ttt gtt ttc cca cag gct ttc ttg    1027
Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe Pro Gln Ala Phe Leu
    295                 300                 305

aag tcg gtg gca ttc ggt gcg att tcc gcg gtt ggc ctt gct gct ttg    1075
Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val Gly Leu Ala Ala Leu
310                 315                 320                 325

atg tcg gtg acg gtg ttg ccg tcg ctg ttc agc atg ttg ggt aag aat    1123
Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser Met Leu Gly Lys Asn
                330                 335                 340

atc gat aag tgg agt ttg cgt cgc act gct cga aca gcg cgc cgt ttg    1171
Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg Thr Ala Arg Arg Leu
            345                 350                 355

gaa gac acc att tgg tac cgc gtg ccg gca tgg gca atg cgc cat gcc    1219
Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp Ala Met Arg His Ala
        360                 365                 370
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aag gca gtg acc gtg ggc gtc gta ttg ctc ttg ctt gct ctt aca gtg 1267
Lys Ala Val Thr Val Gly Val Val Leu Leu Leu Leu Ala Leu Thr Val
375 380 385

ccg ttg acg ggc gtg aaa ttc ggc ggc atc aat gaa acg tat ctg cca 1315
Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn Glu Thr Tyr Leu Pro
390 395 400 405

cca gct aac gac acc cgc gtc gcc caa gag cgt ttc gac gag gcg ttt 1363
Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg Phe Asp Glu Ala Phe
410 415 420

ccc gcc ttc cgc acc gag ccg gtc aag ctt gtg gtc acc ggg gcg gac 1411
Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val Val Thr Gly Ala Asp
425 430 435

aac aac cag ctg atc gat atc tat gtt cag gcc aac gaa gtt gag gga 1459
Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala Asn Glu Val Glu Gly
440 445 450

ctg aca gat cgt ttc acc gca ggt gcg act acc gat gat ggc acc acg 1507
Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr Asp Asp Gly Thr Thr
455 460 465

gtg ttg tct act ggt att cag gat cgt tcc ctc aat gag cag gta gtg 1555
Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu Asn Glu Gln Val Val
470 475 480 485

gag cag ctt cgc gct att tcc gtc cct gag ggc gtt gag gtg cag atc 1603
Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly Val Glu Val Gln Ile
490 495 500

ggt ggc act cca gcc atg gag atc gaa tcc att gag gcg ctc ttt gaa 1651
Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile Glu Ala Leu Phe Glu
505 510 515

aag ctc ctc tgg atg gct ctc tac att gtg ctg gcc act ttc atc ctc 1699
Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu Ala Thr Phe Ile Leu
520 525 530

atg gca ttg gta ttt ggt tcg gtg att ttg ccg gcg aag gcc atc atc 1747
Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro Ala Lys Ala Ile Ile
535 540 545

atg acc att ctg ggt atg ggt gcc acc ttg ggt att ctc acc ttg atg 1795
Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly Ile Leu Thr Leu Met
550 555 560 565

ttc gtc gat ggc gtg ggt gcc agc gca ttg aac ttc tcc cct ggc cca 1843
Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn Phe Ser Pro Gly Pro
570 575 580

ctg atg agt cca gtg ctg gtg ctg atc atg gct att att tac gga ctt 1891
Leu Met Ser Pro Val Leu Val Leu Ile Met Ala Ile Ile Tyr Gly Leu
585 590 595

tcc acc gac tat gag gtg ttc ctg gta tct cgc atg gtg gag gcc cgc 1939

Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg Met Val Glu Ala Arg
600 605 610

gat aaa ggc gaa tcc acc gac gac gcc atc aga tac ggc act gca cac 1987
Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg Tyr Gly Thr Ala His
615 620 625

acc gga tct atc atc acc gcg gcc gca ctg atc atg att gtg gtc tgt 2035
Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile Met Ile Val Val Cys
630 635 640 645

gga gcg ttt ggt ttc tct gag atc gtc atg atg aag tac atc gcg ttc 2083
Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met Lys Tyr Ile Ala Phe
650 655 660

ggc atg atc gca gcg ctg att ctg gat gcc acc atc atc cgc atg ctg 2131
Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr Ile Ile Arg Met Leu
665 670 675

ctt gtc ccc cgc cgt gat gca cct gct tcg cga cga caa ctg gtg ggc 2179
Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg Arg Gln Leu Val Gly
680 685 690

acc cgg ctt cgt taaaaaggcc tacaccgtca tgg 2214
Thr Arg Leu Arg
695

<210> 226
<211> 697
<212> PRT
<213> Corynebacterium glutamicum

<400> 226
Val Phe Ser Lys Trp Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val
1 5 10 15

Pro Leu Val Val Ile Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly
20 25 30

Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly
35 40 45

Ser Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg
50 55 60

Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr
65 70 75 80

Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp
85 90 95

Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr
100 105 110

Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr
115 120 125

Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp
130 135 140

Phe Arg Glu Ile Glu Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly
145 150 155 160

Val Thr Thr Glu Val Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp
165 170 175

Glu Gly Met Ala Gly Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro
180 185 190

Phe Val Ala Ile Leu Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala
195 200 205

Ala Met Pro Leu Ile Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly
210 215 220

Ile Leu Ala Ile Leu Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln
225 230 235 240

Ser Val Val Thr Leu Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu
245 250 255

Phe Met Val Ser Arg Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val
260 265 270

Glu Gln Ala Val Ala Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val
275 280 285

Phe Ser Ala Ala Met Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe
290 295 300

Pro Gln Ala Phe Leu Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val
305 310 315 320

Gly Leu Ala Ala Leu Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser
325 330 335

Met Leu Gly Lys Asn Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg
340 345 350

Thr Ala Arg Arg Leu Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp
355 360 365

Ala Met Arg His Ala Lys Ala Val Thr Val Gly Val Val Leu Leu Leu
370 375 380

Leu Ala Leu Thr Val Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn
385 390 395 400

Glu Thr Tyr Leu Pro Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg
405 410 415

Phe Asp Glu Ala Phe Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val
420 425 430

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Val Thr Gly Ala Asp Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala
        435                 440                 445

Asn Glu Val Glu Gly Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr
    450                 455                 460

Asp Asp Gly Thr Thr Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu
465                 470                 475                 480

Asn Glu Gln Val Val Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly
                485                 490                 495

Val Glu Val Gln Ile Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile
            500                 505                 510

Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu
        515                 520                 525

Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro
    530                 535                 540

Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly
545                 550                 555                 560

Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn
                565                 570                 575

Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala
            580                 585                 590

Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg
        595                 600                 605

Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg
    610                 615                 620

Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile
625                 630                 635                 640

Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met
                645                 650                 655

Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr
            660                 665                 670

Ile Ile Arg Met Leu Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg
        675                 680                 685

Arg Gln Leu Val Gly Thr Arg Leu Arg
    690                 695
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<210> 227
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(706)
<223> RXN03042

<400> 227
atgacaccgg cgcgacgtat ggcattactg gcgtacccca atttacgatg acatctctgc 60

tcgcctcggc gacgtcctgg ttccttacgt tctgatcgtt ttg gtt cta gcg ttc   115
                                           Leu Val Leu Ala Phe
                                            1               5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg   163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
                10                  15                  20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg   211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
            25                  30                  35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca   259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
        40                  45                  50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg   307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu
    55                  60                  65

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc   355
Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe
70                  75                  80                  85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac   403
Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His
                90                  95                  100

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc   451
Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe
            105                 110                 115

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt   499
Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe
        120                 125                 130

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg   547
Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met
    135                 140                 145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta   595
Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu
150                 155                 160                 165

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag   643
Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu
                170                 175                 180
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```
ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat    691
Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn
            185                 190                 195

gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta                      729
Val Gly Val Gly Ala
        200


<210> 228
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 228
Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp
 1               5                  10                  15

Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
            20                  25                  30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
        35                  40                  45

Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
    50                  55                  60

Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
65                  70                  75                  80

Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
                85                  90                  95

Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
            100                 105                 110

Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
        115                 120                 125

Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
    130                 135                 140

Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
145                 150                 155                 160

Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
                165                 170                 175

Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
            180                 185                 190

Glu Leu Lys Glu Asn Val Gly Val Gly Ala
        195                 200


<210> 229
<211> 729
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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> FRXA02893

<400> 229
atgacaccgg cgcgacgtat ggcattactg gcgtacccca atttacgatg acatctctgc 60

tcgcctcggc gacgtcctgg ttccttacgt tctgatcgtt ttg gtt cta gcg ttc 115
Leu Val Leu Ala Phe
1 5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
10 15 20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
25 30 35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
40 45 50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg 307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu
55 60 65

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc 355
Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe
70 75 80 85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac 403
Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His
90 95 100

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc 451
Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe
105 110 115

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt 499
Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe
120 125 130

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg 547
Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met
135 140 145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta 595
Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu
150 155 160 165

cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag 643
Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu

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                170                 175                 180

ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat      691
Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn
            185                 190                 195

gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta                         729
Val Gly Val Gly Ala
        200


<210> 230
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

<400> 230
Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp
  1               5                  10                  15

Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
            20                  25                  30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
        35                  40                  45

Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
    50                  55                  60

Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
65                  70                  75                  80

Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
                85                  90                  95

Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
            100                 105                 110

Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
        115                 120                 125

Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
    130                 135                 140

Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
145                 150                 155                 160

Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
                165                 170                 175

Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
            180                 185                 190

Glu Leu Lys Glu Asn Val Gly Val Gly Ala
        195                 200
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<210> 231
<211> 1605
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1582)
<223> RXA01616

<400> 231
cctacgattt ccgacgtctt aaatcgccac acagcgccgt ggtctaaaac accaacaaaa 60

gagttgtaac tgtaccgacc attcgttaca gttacgatcc atg act tca gaa acc 115
Met Thr Ser Glu Thr
1 5

tta cag gcg caa gcg cct acg aaa acc caa cgt tgg gct ttc ctc gcc 163
Leu Gln Ala Gln Ala Pro Thr Lys Thr Gln Arg Trp Ala Phe Leu Ala
10 15 20

gtt atc agc ggt ggt ctc ttt ctg atc ggt gta gac aac tcg att ctc 211
Val Ile Ser Gly Gly Leu Phe Leu Ile Gly Val Asp Asn Ser Ile Leu
25 30 35

tac acc gca ctc cct ctg ctg cgt gaa cag ctc gca gcc tcc gaa acc 259
Tyr Thr Ala Leu Pro Leu Leu Arg Glu Gln Leu Ala Ala Ser Glu Thr
40 45 50

caa gcg ttg tgg atc atc aac gca tat ccc ctg ctc atg gcg ggc ctt 307
Gln Ala Leu Trp Ile Ile Asn Ala Tyr Pro Leu Leu Met Ala Gly Leu
55 60 65

cgt ttg ggt gcc ggc act ttg ggt gac aaa aac ggc cac cgc cgg atg 355
Arg Leu Gly Ala Gly Thr Leu Gly Asp Lys Asn Gly His Arg Arg Met
70 75 80 85

ttc ctc atg ggc ttg agc att ttc gga atc gct tca ctt ggt gct gcg 403
Phe Leu Met Gly Leu Ser Ile Phe Gly Ile Ala Ser Leu Gly Ala Ala
90 95 100

ttt gct cca act gcg tgg gct ctt gtt gct gcg aga gct ttc ctt ggc 451
Phe Ala Pro Thr Ala Trp Ala Leu Val Ala Ala Arg Ala Phe Leu Gly
105 110 115

atc ggt gcg gca acg atg atg cct gca acc ttg gct ctg atc cgc att 499
Ile Gly Ala Ala Thr Met Met Pro Ala Thr Leu Ala Leu Ile Arg Ile
120 125 130

acg ttt gag gat gag cgt gag cgc aac act gca att ggt att tgg ggt 547
Thr Phe Glu Asp Glu Arg Glu Arg Asn Thr Ala Ile Gly Ile Trp Gly
135 140 145

tcc gtg gca att ctt ggc gct gcg gca ggc ccg atc att ggt ggt gcg 595
Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro Ile Ile Gly Gly Ala
150 155 160 165

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ctg ttg gaa ttc ttc tgg tgg ggt tcg gtt ttc ctc att aac gtt ccg     643
Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe Leu Ile Asn Val Pro
                170                 175                 180

gtg gct gtt atc gcg ttg atc gct acg ctt ttt gtg gcg ccg gcc aat     691
Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe Val Ala Pro Ala Asn
            185                 190                 195

atc gcg aat ccg tct aag cat tgg gat ttc ttg tcg tcg ttc tat gcg     739
Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu Ser Ser Phe Tyr Ala
        200                 205                 210

ctg ctc aca ctt gct ggg ttg atc atc acg atc aag gaa tct gtg aat     787
Leu Leu Thr Leu Ala Gly Leu Ile Ile Thr Ile Lys Glu Ser Val Asn
    215                 220                 225

act gca cgc cat atg cct ctt ctt ttg ggt gca gtc atc atg ttg atc     835
Thr Ala Arg His Met Pro Leu Leu Leu Gly Ala Val Ile Met Leu Ile
230                 235                 240                 245

att ggt gcg gtg ttg ttt agc agt cgt cag aag aag atc gag gag cca     883
Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys Lys Ile Glu Glu Pro
                250                 255                 260

ctt cta gat ctg tcg ttg ttc cgt aat cgc ctt ttc tta ggc ggt gtg     931
Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu Phe Leu Gly Gly Val
            265                 270                 275

gtt gct gcg ggc atg gcg atg ttt act gtg tcc ggt ttg gaa atg act     979
Val Ala Ala Gly Met Ala Met Phe Thr Val Ser Gly Leu Glu Met Thr
        280                 285                 290

acc tcg cag cgt ttc cag ttg tct gtg ggt ttc act cca ctt gag gct     1027
Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe Thr Pro Leu Glu Ala
    295                 300                 305

ggt ttg ctc atg atc cca gct gca ttg ggt agc ttc ccg atg tct att     1075
Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser Phe Pro Met Ser Ile
310                 315                 320                 325

atc ggt ggt gca aac ctg cat cgt tgg ggc ttc aaa ccg ctg atc agt     1123
Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe Lys Pro Leu Ile Ser
                330                 335                 340

ggt ggt ttt gct gcc act gcc gtt ggc atc gcc ctg tgt att tgg ggc     1171
Gly Gly Phe Ala Ala Thr Ala Val Gly Ile Ala Leu Cys Ile Trp Gly
            345                 350                 355

gcg act cat act gat ggt ttg ccg ttt ttc atc gcg ggt cta ttc ttc     1219
Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile Ala Gly Leu Phe Phe
        360                 365                 370

atg ggc gcg ggt gct ggt tcg gta atg tct gtg tct tcc act gcg att     1267
Met Gly Ala Gly Ala Gly Ser Val Met Ser Val Ser Ser Thr Ala Ile
    375                 380                 385

atc ggt tcc gcg ccg gtg cgt aag gct ggc atg gcg tcg tcg atc gaa     1315
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```
Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met Ala Ser Ser Ile Glu
390                 395                 400                 405

gag gtc tct tat gag ttc ggc acg ctg ttg tct gtc gcg att ttg ggt      1363
Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser Val Ala Ile Leu Gly
                410                 415                 420

agc ttg ttc cca ttc ttc tac tcg ctg cat gcc ccg gca gag gtt gcg      1411
Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala Pro Ala Glu Val Ala
            425                 430                 435

gat aac ttc tcg gcg ggt gtt cac cac gcg att gat ggc gat gcg gcg      1459
Asp Asn Phe Ser Ala Gly Val His His Ala Ile Asp Gly Asp Ala Ala
        440                 445                 450

cgt gca tct ttg gac acc gca tac att aac gtg ttg atc att gcc cta      1507
Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val Leu Ile Ile Ala Leu
    455                 460                 465

gta tgc gca gta gcg gct gct ctg atc agc agt tac ctt ttc cgc gga      1555
Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser Tyr Leu Phe Arg Gly
470                 475                 480                 485

aat ccg aag gga gcc aat aat gcg cac tagtaaaaaa gagatgattc            1602
Asn Pro Lys Gly Ala Asn Asn Ala His
                490

tgc                                                                  1605


<210> 232
<211> 494
<212> PRT
<213> Corynebacterium glutamicum

<400> 232
Met Thr Ser Glu Thr Leu Gln Ala Gln Ala Pro Thr Lys Thr Gln Arg
 1               5                  10                  15

Trp Ala Phe Leu Ala Val Ile Ser Gly Gly Leu Phe Leu Ile Gly Val
            20                  25                  30

Asp Asn Ser Ile Leu Tyr Thr Ala Leu Pro Leu Leu Arg Glu Gln Leu
        35                  40                  45

Ala Ala Ser Glu Thr Gln Ala Leu Trp Ile Ile Asn Ala Tyr Pro Leu
    50                  55                  60

Leu Met Ala Gly Leu Arg Leu Gly Ala Gly Thr Leu Gly Asp Lys Asn
65                  70                  75                  80

Gly His Arg Arg Met Phe Leu Met Gly Leu Ser Ile Phe Gly Ile Ala
                85                  90                  95

Ser Leu Gly Ala Ala Phe Ala Pro Thr Ala Trp Ala Leu Val Ala Ala
            100                 105                 110
```

Arg Ala Phe Leu Gly Ile Gly Ala Ala Thr Met Met Pro Ala Thr Leu
115 120 125

Ala Leu Ile Arg Ile Thr Phe Glu Asp Glu Arg Glu Arg Asn Thr Ala
130 135 140

Ile Gly Ile Trp Gly Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro
145 150 155 160

Ile Ile Gly Gly Ala Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe
165 170 175

Leu Ile Asn Val Pro Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe
180 185 190

Val Ala Pro Ala Asn Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu
195 200 205

Ser Ser Phe Tyr Ala Leu Leu Thr Leu Ala Gly Leu Ile Ile Thr Ile
210 215 220

Lys Glu Ser Val Asn Thr Ala Arg His Met Pro Leu Leu Leu Gly Ala
225 230 235 240

Val Ile Met Leu Ile Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys
245 250 255

Lys Ile Glu Glu Pro Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu
260 265 270

Phe Leu Gly Gly Val Val Ala Ala Gly Met Ala Met Phe Thr Val Ser
275 280 285

Gly Leu Glu Met Thr Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe
290 295 300

Thr Pro Leu Glu Ala Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser
305 310 315 320

Phe Pro Met Ser Ile Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe
325 330 335

Lys Pro Leu Ile Ser Gly Gly Phe Ala Ala Thr Ala Val Gly Ile Ala
340 345 350

Leu Cys Ile Trp Gly Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile
355 360 365

Ala Gly Leu Phe Phe Met Gly Ala Gly Ala Gly Ser Val Met Ser Val
370 375 380

Ser Ser Thr Ala Ile Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met
385 390 395 400

Ala Ser Ser Ile Glu Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser
405 410 415

```
Val Ala Ile Leu Gly Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala
            420                 425                 430

Pro Ala Glu Val Ala Asp Asn Phe Ser Ala Gly Val His His Ala Ile
        435                 440                 445

Asp Gly Asp Ala Ala Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val
    450                 455                 460

Leu Ile Ile Ala Leu Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser
465                 470                 475                 480

Tyr Leu Phe Arg Gly Asn Pro Lys Gly Ala Asn Asn Ala His
                485                 490


<210> 233
<211> 1500
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1477)
<223> RXA01666

<400> 233
cgacgcgccc ctccaccttt tcagtagcgt cacgggcgcc aatcctgtat ttttagcagc 60

agtttgaggg tttttgctcc ccatctttag gagacacccc gtg tcc acg ttt cat    115
                                            Val Ser Thr Phe His
                                            1               5

aaa gtt ttg atc aac acc atg atc tcc aac gtc acc act gga ttt ctg    163
Lys Val Leu Ile Asn Thr Met Ile Ser Asn Val Thr Thr Gly Phe Leu
                10                  15                  20

ttc ttt gcc gtg gtg ttt tgg atg tat ctt tcc act ggc aac gtc gca    211
Phe Phe Ala Val Val Phe Trp Met Tyr Leu Ser Thr Gly Asn Val Ala
            25                  30                  35

ctg acc ggc atc gtc agt gga att tac atg ggt ttg atc gcc gtt tgt    259
Leu Thr Gly Ile Val Ser Gly Ile Tyr Met Gly Leu Ile Ala Val Cys
        40                  45                  50

tcc atc ttt ttc gga acc gtt gtt gat cac aat cgc aag aag tcc gtc    307
Ser Ile Phe Phe Gly Thr Val Val Asp His Asn Arg Lys Lys Ser Val
    55                  60                  65

atg ctg ttt tcc agc gtc acc aca ctc gtg ttt tat tgt ctc agt gcc    355
Met Leu Phe Ser Ser Val Thr Thr Leu Val Phe Tyr Cys Leu Ser Ala
70                  75                  80                  85

ctg gtg tgg gtg ttt tgg ctg gag gaa gac ggc ctg agc atc gga aat    403
Leu Val Trp Val Phe Trp Leu Glu Glu Asp Gly Leu Ser Ile Gly Asn
                90                  95                  100
```

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acc gcc ctg tgg gtg ttc gtt tct ttc atc ctc atc gga tca atc gtg      451
Thr Ala Leu Trp Val Phe Val Ser Phe Ile Leu Ile Gly Ser Ile Val
            105                 110                 115

gaa cac atg cgc aac atc gca ctg tcc acc gtg gtc acg ctg ttg gtt      499
Glu His Met Arg Asn Ile Ala Leu Ser Thr Val Val Thr Leu Leu Val
        120                 125                 130

cct gaa gct gaa cgc gac aaa gca aac ggc ctg gta gga gcc gtg caa      547
Pro Glu Ala Glu Arg Asp Lys Ala Asn Gly Leu Val Gly Ala Val Gln
    135                 140                 145

ggt gtt gga ttt tta gtc acc agc gtc att gct ggt tcc gcc atc ggg      595
Gly Val Gly Phe Leu Val Thr Ser Val Ile Ala Gly Ser Ala Ile Gly
150                 155                 160                 165

ttc ttg ggc atg gaa atc acc ctg tgg atc tgc ctt ggg ctc tca ctt      643
Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys Leu Gly Leu Ser Leu
                170                 175                 180

gtc gcg ctg ctg cac ctg ctg ccg att cgc gtc gac gaa ccg gaa atc      691
Val Ala Leu Leu His Leu Leu Pro Ile Arg Val Asp Glu Pro Glu Ile
            185                 190                 195

atc acc caa gaa gac gca cag cct act gtt tct gac gat tca gtt ccc      739
Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser Asp Asp Ser Val Pro
        200                 205                 210

aca cct acc tcc gat ttg gcg atc gtg tcc aaa ggc atc gac cta aaa      787
Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys Gly Ile Asp Leu Lys
    215                 220                 225

gga tca atg aaa atc atc ctg agt gtt ccg gga ctg ctc gcg ctt gtg      835
Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly Leu Leu Ala Leu Val
230                 235                 240                 245

ttg ttt gcg tcc ttc aac aac ctc atc ggc ggc gtg tac tcc gca ctc      883
Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly Val Tyr Ser Ala Leu
                250                 255                 260

atg gac cct tac ggc ctg gaa ctt ttc agc cca cag ctg tgg ggg cta      931
Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro Gln Leu Trp Gly Leu
            265                 270                 275

ctg ctt gga ctc acc agc ctc ggc ttc atc gtt ggt ggt gct gtg atc      979
Leu Leu Gly Leu Thr Ser Leu Gly Phe Ile Val Gly Gly Ala Val Ile
        280                 285                 290

tcc aaa act ggc ttg ggc aaa aac cct gtg cgc acc ttg ctg ctg gtt     1027
Ser Lys Thr Gly Leu Gly Lys Asn Pro Val Arg Thr Leu Leu Leu Val
    295                 300                 305

aat gtt ggt gtg gct ttt gtt ggc atg tta ttt gcc att cgc gaa tgg     1075
Asn Val Gly Val Ala Phe Val Gly Met Leu Phe Ala Ile Arg Glu Trp
310                 315                 320                 325

tgg tgg ctc tac atc ctg ggc att ttc atc ttc atg gct atc acc cca     1123
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Trp Trp Leu Tyr Ile Leu Gly Ile Phe Ile Phe Met Ala Ile Thr Pro
                330                 335                 340

gct gcc gaa gcc gca gaa caa acc atc ctt caa cga gtc gtc cca ttc    1171
Ala Ala Glu Ala Ala Glu Gln Thr Ile Leu Gln Arg Val Val Pro Phe
            345                 350                 355

cgc caa caa ggc cgc gta ttt gga cta gcc atg gca gtg gaa atg gca    1219
Arg Gln Gln Gly Arg Val Phe Gly Leu Ala Met Ala Val Glu Met Ala
        360                 365                 370

gcc aac ccg ctc tcc aca gtg atc gtg gcg att ttg gcc gaa gcc tac    1267
Ala Asn Pro Leu Ser Thr Val Ile Val Ala Ile Leu Ala Glu Ala Tyr
    375                 380                 385

ctc att cca tgg atg gct ggc ccc ggc gcg gac acc atc tgg ggc gtg    1315
Leu Ile Pro Trp Met Ala Gly Pro Gly Ala Asp Thr Ile Trp Gly Val
390                 395                 400                 405

atc ctc ggc gag ggt aaa gct cgc ggc atg gca ctg atg ttc ctc gca    1363
Ile Leu Gly Glu Gly Lys Ala Arg Gly Met Ala Leu Met Phe Leu Ala
                410                 415                 420

tca ggt gcc atc atg ttg gtt gtc gtg ctg ttg gca ttc atg tcg agg    1411
Ser Gly Ala Ile Met Leu Val Val Val Leu Leu Ala Phe Met Ser Arg
            425                 430                 435

tcc tac cgg aaa ctc agc cag tac tac gcc acc acc agc caa gac att    1459
Ser Tyr Arg Lys Leu Ser Gln Tyr Tyr Ala Thr Thr Ser Gln Asp Ile
        440                 445                 450

gcg gga gct gct gag aag taagtgctct agaccgttgt ttg                  1500
Ala Gly Ala Ala Glu Lys
    455


<210> 234
<211> 459
<212> PRT
<213> Corynebacterium glutamicum

<400> 234
Val Ser Thr Phe His Lys Val Leu Ile Asn Thr Met Ile Ser Asn Val
  1               5                  10                  15

Thr Thr Gly Phe Leu Phe Phe Ala Val Val Phe Trp Met Tyr Leu Ser
             20                  25                  30

Thr Gly Asn Val Ala Leu Thr Gly Ile Val Ser Gly Ile Tyr Met Gly
         35                  40                  45

Leu Ile Ala Val Cys Ser Ile Phe Phe Gly Thr Val Val Asp His Asn
     50                  55                  60

Arg Lys Lys Ser Val Met Leu Phe Ser Ser Val Thr Thr Leu Val Phe
 65                  70                  75                  80
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Tyr Cys Leu Ser Ala Leu Val Trp Val Phe Trp Leu Glu Glu Asp Gly
                85                  90                  95

Leu Ser Ile Gly Asn Thr Ala Leu Trp Val Phe Val Ser Phe Ile Leu
            100                 105                 110

Ile Gly Ser Ile Val Glu His Met Arg Asn Ile Ala Leu Ser Thr Val
        115                 120                 125

Val Thr Leu Leu Val Pro Glu Ala Glu Arg Asp Lys Ala Asn Gly Leu
    130                 135                 140

Val Gly Ala Val Gln Gly Val Gly Phe Leu Val Thr Ser Val Ile Ala
145                 150                 155                 160

Gly Ser Ala Ile Gly Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys
                165                 170                 175

Leu Gly Leu Ser Leu Val Ala Leu Leu His Leu Leu Pro Ile Arg Val
            180                 185                 190

Asp Glu Pro Glu Ile Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser
        195                 200                 205

Asp Asp Ser Val Pro Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys
    210                 215                 220

Gly Ile Asp Leu Lys Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly
225                 230                 235                 240

Leu Leu Ala Leu Val Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly
                245                 250                 255

Val Tyr Ser Ala Leu Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro
            260                 265                 270

Gln Leu Trp Gly Leu Leu Leu Gly Leu Thr Ser Leu Gly Phe Ile Val
        275                 280                 285

Gly Gly Ala Val Ile Ser Lys Thr Gly Leu Gly Lys Asn Pro Val Arg
    290                 295                 300

Thr Leu Leu Leu Val Asn Val Gly Val Ala Phe Val Gly Met Leu Phe
305                 310                 315                 320

Ala Ile Arg Glu Trp Trp Trp Leu Tyr Ile Leu Gly Ile Phe Ile Phe
                325                 330                 335

Met Ala Ile Thr Pro Ala Ala Glu Ala Ala Glu Gln Thr Ile Leu Gln
            340                 345                 350

Arg Val Val Pro Phe Arg Gln Gln Gly Arg Val Phe Gly Leu Ala Met
        355                 360                 365

Ala Val Glu Met Ala Ala Asn Pro Leu Ser Thr Val Ile Val Ala Ile
    370                 375                 380
```

Leu Ala Glu Ala Tyr Leu Ile Pro Trp Met Ala Gly Pro Gly Ala Asp
385 390 395 400

Thr Ile Trp Gly Val Ile Leu Gly Glu Gly Lys Ala Arg Gly Met Ala
405 410 415

Leu Met Phe Leu Ala Ser Gly Ala Ile Met Leu Val Val Val Leu Leu
420 425 430

Ala Phe Met Ser Arg Ser Tyr Arg Lys Leu Ser Gln Tyr Tyr Ala Thr
435 440 445

Thr Ser Gln Asp Ile Ala Gly Ala Ala Glu Lys
450 455

<210> 235
<211> 1521
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1498)
<223> RXA00062

<400> 235
cttcaacata ggcgttgggg ctgactttta aacaggtacc agtagtaccg gcataagcga 60

tcactgttgc gttttcttgc tgccatcaaa aattagtcac atg att tta agc atc 115
Met Ile Leu Ser Ile
1 5

gtc ctt ttg ggc tac ttc atg att ctg ctt gac acc tcc atc gtc att 163
Val Leu Leu Gly Tyr Phe Met Ile Leu Leu Asp Thr Ser Ile Val Ile
10 15 20

acg ggt cta cct gcc atc ggc agt gaa ctt ggc atc gat ccc gtg cac 211
Thr Gly Leu Pro Ala Ile Gly Ser Glu Leu Gly Ile Asp Pro Val His
25 30 35

ctg tca tgg gtg cag agt tcc tac aca tta gtc ttc ggc gca ctt ctt 259
Leu Ser Trp Val Gln Ser Ser Tyr Thr Leu Val Phe Gly Ala Leu Leu
40 45 50

ctg ctg gga gct cgt gcc ggt gat atc ttc ggc cga aag aaa gtg ctc 307
Leu Leu Gly Ala Arg Ala Gly Asp Ile Phe Gly Arg Lys Lys Val Leu
55 60 65

tac att ggt ctc gcg ttg ttt gcg gct tca tcg ttg gca att gcg ctt 355
Tyr Ile Gly Leu Ala Leu Phe Ala Ala Ser Ser Leu Ala Ile Ala Leu
70 75 80 85

tct cca aat gct gcg gtc ctc att gga gca cgc gta gtt caa ggc gcg 403
Ser Pro Asn Ala Ala Val Leu Ile Gly Ala Arg Val Val Gln Gly Ala
90 95 100

gga gct gcg att atc gct cca gcg aca ctt gcg ttg att act gag ttc 451
Gly Ala Ala Ile Ile Ala Pro Ala Thr Leu Ala Leu Ile Thr Glu Phe
105 110 115

ttc ccc gaa ggc cca gct cgc ctt cgt gct acc tct gct tat ggt gct 499
Phe Pro Glu Gly Pro Ala Arg Leu Arg Ala Thr Ser Ala Tyr Gly Ala
120 125 130

gtt gcc ggc atc ggt gtg gca gca ggc cta gtg atc ggc ggc gta ttt 547
Val Ala Gly Ile Gly Val Ala Ala Gly Leu Val Ile Gly Gly Val Phe
135 140 145

gct gat ctt ttg tcg tgg cgc atc ggc ttc ttt atc aac gtc ccc atc 595
Ala Asp Leu Leu Ser Trp Arg Ile Gly Phe Phe Ile Asn Val Pro Ile
150 155 160 165

gcc gca gtg ttg gcc tac ata gtg cac aaa gcc att ccc gca acc ttc 643
Ala Ala Val Leu Ala Tyr Ile Val His Lys Ala Ile Pro Ala Thr Phe
170 175 180

agc agg cct gga tca ctc gac atc ttc gga gca att acc tcc acg gca 691
Ser Arg Pro Gly Ser Leu Asp Ile Phe Gly Ala Ile Thr Ser Thr Ala
185 190 195

ggt atc gcc gcg gtg ctc tac gca att gtc cgc agc gcc gat tac agc 739
Gly Ile Ala Ala Val Leu Tyr Ala Ile Val Arg Ser Ala Asp Tyr Ser
200 205 210

tgg aca gat ccg ttt gtg ttg att tcc ctc gtg ctg ggc atc gca gtg 787
Trp Thr Asp Pro Phe Val Leu Ile Ser Leu Val Leu Gly Ile Ala Val
215 220 225

ttc atc tgg ttc ctg cgc cat gaa tcc tca gcc aaa gaa cca ctt ctg 835
Phe Ile Trp Phe Leu Arg His Glu Ser Ser Ala Lys Glu Pro Leu Leu
230 235 240 245

ccc ctg ggg ctc ttt aaa aac cgc agg cga aac acc atc ttg gcc agc 883
Pro Leu Gly Leu Phe Lys Asn Arg Arg Arg Asn Thr Ile Leu Ala Ser
250 255 260

cgc ttt ctt ctg gtt ggc tcc gtg atg tca ttc ttc ttc ttt gcc acc 931
Arg Phe Leu Leu Val Gly Ser Val Met Ser Phe Phe Phe Phe Ala Thr
265 270 275

cag ctg ttc cag gac acc atg gga atg aat gct ctc cag gca ggc ctt 979
Gln Leu Phe Gln Asp Thr Met Gly Met Asn Ala Leu Gln Ala Gly Leu
280 285 290

gcg ttc atg ccg cta tct ctg ctg cag ttt gcc agc gcc gcg atg gtg 1027
Ala Phe Met Pro Leu Ser Leu Leu Gln Phe Ala Ser Ala Ala Met Val
295 300 305

cca cgg ctt tcc cga gca ggc gta tct gat tcc atg ctc acc gtc atc 1075
Pro Arg Leu Ser Arg Ala Gly Val Ser Asp Ser Met Leu Thr Val Ile
310 315 320 325

ggt ttc gcc atc atg gtc atc ggc atg gca ggc ctc gca ttt gta cca 1123

Gly Phe Ala Ile Met Val Ile Gly Met Ala Gly Leu Ala Phe Val Pro
330 335 340

aac acg atg atc gcg ctg atc cta cca ata gtt ttg gtg gga ttt ggc 1171
Asn Thr Met Ile Ala Leu Ile Leu Pro Ile Val Leu Val Gly Phe Gly
345 350 355

caa ggc ttc gct ttc gga cca atg aca gct ctg gca gtt caa ggt gca 1219
Gln Gly Phe Ala Phe Gly Pro Met Thr Ala Leu Ala Val Gln Gly Ala
360 365 370

ccg aag gac caa tcc ggc gcc gtt tct ggc ctg gtg aat tcc ctt cac 1267
Pro Lys Asp Gln Ser Gly Ala Val Ser Gly Leu Val Asn Ser Leu His
375 380 385

caa atc ggc ggc acc ttc ggt ttg ggt gtg ttc tcc tcc ttg gct gtc 1315
Gln Ile Gly Gly Thr Phe Gly Leu Gly Val Phe Ser Ser Leu Ala Val
390 395 400 405

gct gtc atc gga cat gat gca aca tca gag atg atc agc gac cgc gca 1363
Ala Val Ile Gly His Asp Ala Thr Ser Glu Met Ile Ser Asp Arg Ala
410 415 420

cac ttc gga ttc ttg ctc tcc acc gtg acg ctg acg ctg gcc acc atc 1411
His Phe Gly Phe Leu Leu Ser Thr Val Thr Leu Thr Leu Ala Thr Ile
425 430 435

ttt gcg gtc aca ctg ctg aag cgc cac gaa acc cga aag agt agc gag 1459
Phe Ala Val Thr Leu Leu Lys Arg His Glu Thr Arg Lys Ser Ser Glu
440 445 450

cgc cca acc cag ctc gtc gac gaa aag gca gtt acc tct tagtgcgctg 1508
Arg Pro Thr Gln Leu Val Asp Glu Lys Ala Val Thr Ser
455 460 465

cagcatccca gtt 1521

<210> 236
<211> 466
<212> PRT
<213> Corynebacterium glutamicum

<400> 236
Met Ile Leu Ser Ile Val Leu Leu Gly Tyr Phe Met Ile Leu Leu Asp
1 5 10 15

Thr Ser Ile Val Ile Thr Gly Leu Pro Ala Ile Gly Ser Glu Leu Gly
20 25 30

Ile Asp Pro Val His Leu Ser Trp Val Gln Ser Ser Tyr Thr Leu Val
35 40 45

Phe Gly Ala Leu Leu Leu Leu Gly Ala Arg Ala Gly Asp Ile Phe Gly
50 55 60

Arg Lys Lys Val Leu Tyr Ile Gly Leu Ala Leu Phe Ala Ala Ser Ser

65 70 75 80

Leu Ala Ile Ala Leu Ser Pro Asn Ala Ala Val Leu Ile Gly Ala Arg
85 90 95

Val Val Gln Gly Ala Gly Ala Ala Ile Ile Ala Pro Ala Thr Leu Ala
100 105 110

Leu Ile Thr Glu Phe Phe Pro Glu Gly Pro Ala Arg Leu Arg Ala Thr
115 120 125

Ser Ala Tyr Gly Ala Val Ala Gly Ile Gly Val Ala Ala Gly Leu Val
130 135 140

Ile Gly Gly Val Phe Ala Asp Leu Leu Ser Trp Arg Ile Gly Phe Phe
145 150 155 160

Ile Asn Val Pro Ile Ala Ala Val Leu Ala Tyr Ile Val His Lys Ala
165 170 175

Ile Pro Ala Thr Phe Ser Arg Pro Gly Ser Leu Asp Ile Phe Gly Ala
180 185 190

Ile Thr Ser Thr Ala Gly Ile Ala Ala Val Leu Tyr Ala Ile Val Arg
195 200 205

Ser Ala Asp Tyr Ser Trp Thr Asp Pro Phe Val Leu Ile Ser Leu Val
210 215 220

Leu Gly Ile Ala Val Phe Ile Trp Phe Leu Arg His Glu Ser Ser Ala
225 230 235 240

Lys Glu Pro Leu Leu Pro Leu Gly Leu Phe Lys Asn Arg Arg Arg Asn
245 250 255

Thr Ile Leu Ala Ser Arg Phe Leu Leu Val Gly Ser Val Met Ser Phe
260 265 270

Phe Phe Phe Ala Thr Gln Leu Phe Gln Asp Thr Met Gly Met Asn Ala
275 280 285

Leu Gln Ala Gly Leu Ala Phe Met Pro Leu Ser Leu Leu Gln Phe Ala
290 295 300

Ser Ala Ala Met Val Pro Arg Leu Ser Arg Ala Gly Val Ser Asp Ser
305 310 315 320

Met Leu Thr Val Ile Gly Phe Ala Ile Met Val Ile Gly Met Ala Gly
325 330 335

Leu Ala Phe Val Pro Asn Thr Met Ile Ala Leu Ile Leu Pro Ile Val
340 345 350

Leu Val Gly Phe Gly Gln Gly Phe Ala Phe Gly Pro Met Thr Ala Leu
355 360 365

Ala Val Gln Gly Ala Pro Lys Asp Gln Ser Gly Ala Val Ser Gly Leu

370 375 380

Val Asn Ser Leu His Gln Ile Gly Gly Thr Phe Gly Leu Gly Val Phe
385 390 395 400

Ser Ser Leu Ala Val Ala Val Ile Gly His Asp Ala Thr Ser Glu Met
405 410 415

Ile Ser Asp Arg Ala His Phe Gly Phe Leu Leu Ser Thr Val Thr Leu
420 425 430

Thr Leu Ala Thr Ile Phe Ala Val Thr Leu Leu Lys Arg His Glu Thr
435 440 445

Arg Lys Ser Ser Glu Arg Pro Thr Gln Leu Val Asp Glu Lys Ala Val
450 455 460

Thr Ser
465

<210> 237
<211> 1584
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1561)
<223> RXA00215

<400> 237
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ccttttccag gcgccctcgt gcgtgaaaga ataactcaac gtg tct gac aaa aag 115
Val Ser Asp Lys Lys
1 5

cag gat cta aca tcc tcc gca gca ggt agt gct gca ccc caa acc aag 163
Gln Asp Leu Thr Ser Ser Ala Ala Gly Ser Ala Ala Pro Gln Thr Lys
10 15 20

gcc tac ccc gcc atg ccc ttg cct gaa aag caa gct tgg cca gct cta 211
Ala Tyr Pro Ala Met Pro Leu Pro Glu Lys Gln Ala Trp Pro Ala Leu
25 30 35

att gcc ttg tgc att ggg ttt ttc atg atc ctg ttg gat caa acc atc 259
Ile Ala Leu Cys Ile Gly Phe Phe Met Ile Leu Leu Asp Gln Thr Ile
40 45 50

gtg gcc gtc tct acc cca gcg tta cag gca gac atg ggc gcg tcc tac 307
Val Ala Val Ser Thr Pro Ala Leu Gln Ala Asp Met Gly Ala Ser Tyr
55 60 65

aac gag gtc atc tgg gta acc tcg gtg tat ctc ctc act ttc gcg gtg 355
Asn Glu Val Ile Trp Val Thr Ser Val Tyr Leu Leu Thr Phe Ala Val
70 75 80 85

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cca ctg ctt gtt act ggc cgt ttg ggc gac aag tac ggt ccg aaa aat     403
Pro Leu Leu Val Thr Gly Arg Leu Gly Asp Lys Tyr Gly Pro Lys Asn
                 90                  95                  100

gtc tat gtc gca ggc atg gtt atc ttc aca gtg agc tct ttg gcc tgt     451
Val Tyr Val Ala Gly Met Val Ile Phe Thr Val Ser Ser Leu Ala Cys
            105                 110                 115

ggt ttg gcc cca gac atg ttc acg ttg att atc gct cgt ggc gtt caa     499
Gly Leu Ala Pro Asp Met Phe Thr Leu Ile Ile Ala Arg Gly Val Gln
        120                 125                 130

ggt ttg ggc gca gcc ctt ttg act cca caa acc atg gca aca atc aac     547
Gly Leu Gly Ala Ala Leu Leu Thr Pro Gln Thr Met Ala Thr Ile Asn
    135                 140                 145

cgc atc ttt gct ttt gag cgc cgc ggt gca gct ctt gga gtg tgg ggt     595
Arg Ile Phe Ala Phe Glu Arg Arg Gly Ala Ala Leu Gly Val Trp Gly
150                 155                 160                 165

tct aca gct ggc ctt gca tcc cta gca gga ccg atc ctg ggt ggt gtc     643
Ser Thr Ala Gly Leu Ala Ser Leu Ala Gly Pro Ile Leu Gly Gly Val
                170                 175                 180

atc acc gaa aac tgg ggt tgg caa tgg gtc ttc tac atc aac gtg ccc     691
Ile Thr Glu Asn Trp Gly Trp Gln Trp Val Phe Tyr Ile Asn Val Pro
            185                 190                 195

atc ggc gtg atc tcg gtg atc gca gta atg aag tac gtt cct gaa ttc     739
Ile Gly Val Ile Ser Val Ile Ala Val Met Lys Tyr Val Pro Glu Phe
        200                 205                 210

cca ccg ctg acc cga ccg ctt gat ccg ctt tct atc gtg ttg tcc atc     787
Pro Pro Leu Thr Arg Pro Leu Asp Pro Leu Ser Ile Val Leu Ser Ile
    215                 220                 225

gtg gcc gtg ttc ttc ctg gtg ttt gct ttc cag gaa ggc gaa ggc gct     835
Val Ala Val Phe Phe Leu Val Phe Ala Phe Gln Glu Gly Glu Gly Ala
230                 235                 240                 245

ggc tgg gcg gca tgg gtg tgg atc atg atc gta gcc gcc ttt gcg ctc     883
Gly Trp Ala Ala Trp Val Trp Ile Met Ile Val Ala Ala Phe Ala Leu
                250                 255                 260

ttt gcg tgg ttt atc tac caa caa agc agg gcc gag aaa tcc gga aac     931
Phe Ala Trp Phe Ile Tyr Gln Gln Ser Arg Ala Glu Lys Ser Gly Asn
            265                 270                 275

gat cct ctc gtc cca ctg gag att ttc aag ttt aga aac ttc agc ctc     979
Asp Pro Leu Val Pro Leu Glu Ile Phe Lys Phe Arg Asn Phe Ser Leu
        280                 285                 290

ggc aat atc tgc atc atg gcc atg gga ttc acc gtg gct ggt act cct    1027
Gly Asn Ile Cys Ile Met Ala Met Gly Phe Thr Val Ala Gly Thr Pro
    295                 300                 305
```

```
ctg ccc atc atg ttg tac ttc cag caa gca cac gga atg aac gcc atg    1075
Leu Pro Ile Met Leu Tyr Phe Gln Gln Ala His Gly Met Asn Ala Met
310                 315                 320                 325

gaa gcg ggt ttc atg atg gtg cct caa gct ctc atg gca gca gta ctg    1123
Glu Ala Gly Phe Met Met Val Pro Gln Ala Leu Met Ala Ala Val Leu
                330                 335                 340

tca cca ttt gtt gga aag ctg gtt gat cga tcc aac cct gga ctc atg    1171
Ser Pro Phe Val Gly Lys Leu Val Asp Arg Ser Asn Pro Gly Leu Met
            345                 350                 355

gca gcc ctc ggt ttt agc aca gtg gct gtg tcc att gta ctg ctg tca    1219
Ala Ala Leu Gly Phe Ser Thr Val Ala Val Ser Ile Val Leu Leu Ser
        360                 365                 370

atg gta atg att ttc gat acg ggt cta gtc tgg gca ctt gtt tcg atg    1267
Met Val Met Ile Phe Asp Thr Gly Leu Val Trp Ala Leu Val Ser Met
    375                 380                 385

act ttg ctc ggc atc gga aac gcc ttt gtg tgg gca ccg aac tcg acc    1315
Thr Leu Leu Gly Ile Gly Asn Ala Phe Val Trp Ala Pro Asn Ser Thr
390                 395                 400                 405

tcc act atg cgc gac ctg cca cac aag ttc atg gga gcg ggc tct ggc    1363
Ser Thr Met Arg Asp Leu Pro His Lys Phe Met Gly Ala Gly Ser Gly
                410                 415                 420

gtg ttc aat aca acc cgc caa tta ggt tca gtc atc ggc gcc gct gcc    1411
Val Phe Asn Thr Thr Arg Gln Leu Gly Ser Val Ile Gly Ala Ala Ala
            425                 430                 435

atc ggc gcg gta atg cag att cga ctg gca gca ggc gat gag ggc gca    1459
Ile Gly Ala Val Met Gln Ile Arg Leu Ala Ala Gly Asp Glu Gly Ala
        440                 445                 450

gct ttt ggt caa gca ctt cta ctt gcc gct gcg gtg ctg gtt atc ggc    1507
Ala Phe Gly Gln Ala Leu Leu Leu Ala Ala Ala Val Leu Val Ile Gly
    455                 460                 465

att gtg gca tca acg atg gca gga aaa aat gca cac cca gcg ccg gta    1555
Ile Val Ala Ser Thr Met Ala Gly Lys Asn Ala His Pro Ala Pro Val
470                 475                 480                 485

aag cct taaaggtcgc atgaatcctt cga                                  1584
Lys Pro
```

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<210> 238
<211> 487
<212> PRT
<213> Corynebacterium glutamicum

<400> 238
Val Ser Asp Lys Lys Gln Asp Leu Thr Ser Ser Ala Ala Gly Ser Ala
  1               5                  10                  15
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Ala Pro Gln Thr Lys Ala Tyr Pro Ala Met Pro Leu Pro Glu Lys Gln
20 25 30

Ala Trp Pro Ala Leu Ile Ala Leu Cys Ile Gly Phe Phe Met Ile Leu
35 40 45

Leu Asp Gln Thr Ile Val Ala Val Ser Thr Pro Ala Leu Gln Ala Asp
50 55 60

Met Gly Ala Ser Tyr Asn Glu Val Ile Trp Val Thr Ser Val Tyr Leu
65 70 75 80

Leu Thr Phe Ala Val Pro Leu Leu Val Thr Gly Arg Leu Gly Asp Lys
85 90 95

Tyr Gly Pro Lys Asn Val Tyr Val Ala Gly Met Val Ile Phe Thr Val
100 105 110

Ser Ser Leu Ala Cys Gly Leu Ala Pro Asp Met Phe Thr Leu Ile Ile
115 120 125

Ala Arg Gly Val Gln Gly Leu Gly Ala Ala Leu Leu Thr Pro Gln Thr
130 135 140

Met Ala Thr Ile Asn Arg Ile Phe Ala Phe Glu Arg Arg Gly Ala Ala
145 150 155 160

Leu Gly Val Trp Gly Ser Thr Ala Gly Leu Ala Ser Leu Ala Gly Pro
165 170 175

Ile Leu Gly Gly Val Ile Thr Glu Asn Trp Gly Trp Gln Trp Val Phe
180 185 190

Tyr Ile Asn Val Pro Ile Gly Val Ile Ser Val Ile Ala Val Met Lys
195 200 205

Tyr Val Pro Glu Phe Pro Pro Leu Thr Arg Pro Leu Asp Pro Leu Ser
210 215 220

Ile Val Leu Ser Ile Val Ala Val Phe Phe Leu Val Phe Ala Phe Gln
225 230 235 240

Glu Gly Glu Gly Ala Gly Trp Ala Ala Trp Val Trp Ile Met Ile Val
245 250 255

Ala Ala Phe Ala Leu Phe Ala Trp Phe Ile Tyr Gln Gln Ser Arg Ala
260 265 270

Glu Lys Ser Gly Asn Asp Pro Leu Val Pro Leu Glu Ile Phe Lys Phe
275 280 285

Arg Asn Phe Ser Leu Gly Asn Ile Cys Ile Met Ala Met Gly Phe Thr
290 295 300

Val Ala Gly Thr Pro Leu Pro Ile Met Leu Tyr Phe Gln Gln Ala His
305 310 315 320

```
Gly Met Asn Ala Met Glu Ala Gly Phe Met Met Val Pro Gln Ala Leu
                325                 330                 335

Met Ala Ala Val Leu Ser Pro Phe Val Gly Lys Leu Val Asp Arg Ser
            340                 345                 350

Asn Pro Gly Leu Met Ala Ala Leu Gly Phe Ser Thr Val Ala Val Ser
        355                 360                 365

Ile Val Leu Leu Ser Met Val Met Ile Phe Asp Thr Gly Leu Val Trp
    370                 375                 380

Ala Leu Val Ser Met Thr Leu Leu Gly Ile Gly Asn Ala Phe Val Trp
385                 390                 395                 400

Ala Pro Asn Ser Thr Ser Thr Met Arg Asp Leu Pro His Lys Phe Met
                405                 410                 415

Gly Ala Gly Ser Gly Val Phe Asn Thr Thr Arg Gln Leu Gly Ser Val
            420                 425                 430

Ile Gly Ala Ala Ala Ile Gly Ala Val Met Gln Ile Arg Leu Ala Ala
        435                 440                 445

Gly Asp Glu Gly Ala Ala Phe Gly Gln Ala Leu Leu Leu Ala Ala Ala
    450                 455                 460

Val Leu Val Ile Gly Ile Val Ala Ser Thr Met Ala Gly Lys Asn Ala
465                 470                 475                 480

His Pro Ala Pro Val Lys Pro
                485


<210> 239
<211> 1455
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1432)
<223> RXN03064

<400> 239
tggagccttg tcttcctcca gcaatcccac aacggagcag gttgggatcc cgagaaatgt 60

tgtcatcatc ttggctgtat tagtttttac agcctttgtc atg atg ttg aat gag   115
                                            Met Met Leu Asn Glu
                                            1               5

act act ctg gca gtc gcg ttg ccg tcg atc atg gcg gac ttt gac att   163
Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
                10                  15                  20

gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg   211
```

Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly Phe Met Leu Thr Met
25 30 35

gct gtg gtt ctt cca gct act ggt tgg atg ttg gaa cgt ttt acc act 259
Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu Glu Arg Phe Thr Thr
40 45 50

cgt agt gtg ttt att ttc gcc acg gtg gtc ttc ctg atc ggt act gtg 307
Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe Leu Ile Gly Thr Val
55 60 65

acg gct gcg ttg tct cct act ttt gcg att atg ctt gca gcc cgc gtc 355
Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met Leu Ala Ala Arg Val
70 75 80 85

gct cag gcg att ggt acc gct gtg atc atg ccg ctg ctg atg act gtc 403
Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro Leu Leu Met Thr Val
90 95 100

gcg atg acc gtt gtt cct cca gag cgc cgt ggc gcc gtc atg ggt ttg 451
Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly Ala Val Met Gly Leu
105 110 115

att gcg gtc gtg atg gcc gtt ggt cct gct ctt gga cct agt gtg gct 499
Ile Ala Val Val Met Ala Val Gly Pro Ala Leu Gly Pro Ser Val Ala
120 125 130

ggt ttc gta ctc agc ttg tct tcg tgg cac gcg att ttc tgg gtc atg 547
Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala Ile Phe Trp Val Met
135 140 145

gtt ccg ttg gtg ttt gtg gca agc ctg atc ggt acc ctg cgt ctg acc 595
Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly Thr Leu Arg Leu Thr
150 155 160 165

aac gtc agt gag cct aaa aag act cct ttg gat gtt att tcc ttc ctg 643
Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp Val Ile Ser Phe Leu
170 175 180

att tcc gca gtg gct ttc ggt ggc ctt gtg tac gcc ttg agc tcg att 691
Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr Ala Leu Ser Ser Ile
185 190 195

ggc atc att ttg gaa ggt gac aga agc gct ttg gtc gtg ttg gct gtc 739
Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu Val Val Leu Ala Val
200 205 210

ggc atc att gcg ttg gtg gtg ttt gtg tgg cgc cag att gcc atg ggt 787
Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg Gln Ile Ala Met Gly
215 220 225

aag cag gat aag gcg ctg ttg gat ctg cgt ccg ttg gcg att cgt gag 835
Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro Leu Ala Ile Arg Glu
230 235 240 245

tac acc att ccg ctg gtt gtg ctt ttg acg ctg ttc ggt gcg ctg ctc 883
Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu Phe Gly Ala Leu Leu

```
            250                 255                 260

ggt gtc atg aat aca ctg ccg ctc tac ctg cag gga tcc ttg atg gtc     931
Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln Gly Ser Leu Met Val
            265                 270                 275

acc gcc ttg gtc gcg ggt cta gtg ctg ttg cca ggt ggt ctt ttg gaa     979
Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro Gly Gly Leu Leu Glu
        280                 285                 290

ggt gtg ctg tcg cca ttt gtg ggt cga att tat gat cgt cat ggt cca     1027
Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr Asp Arg His Gly Pro
    295                 300                 305

cgc gga ctc gtg atc ggc ggt atg tca ctc gtt gtg atc tcc ctg ttt     1075
Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val Val Ile Ser Leu Phe
310                 315                 320                 325

gca ctg tcc acc gtc gat gag ttc gcc aac gtg tgg ttc atc atc ggc     1123
Ala Leu Ser Thr Val Asp Glu Phe Ala Asn Val Trp Phe Ile Ile Gly
                330                 335                 340

gta cac atc gtg ttc tcc atc ggc ctt gcg ctg ctg ttc acc cca ctg     1171
Val His Ile Val Phe Ser Ile Gly Leu Ala Leu Leu Phe Thr Pro Leu
            345                 350                 355

atg aca gtc gcg ctc gca tcc gtc ccc gac aac atg tac ggc cac ggc     1219
Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly
        360                 365                 370

tcc gcg atc ctc aac acc ctc caa cag ctc gcc ggc gcc gca ggc acc     1267
Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
    375                 380                 385

gcg gtc atg att gcg gtt tat tcc acc gtc agc aac aac gcg ctt atc     1315
Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile
390                 395                 400                 405

gac ggc gca acc caa caa acc gcc ctc gcc gac ggc gcc aac tct gca     1363
Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala
                410                 415                 420

ttc ttc gcc tca gcg tgc gtg gca gtg ttt gca ctg atc gtg ggc ttc     1411
Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe
            425                 430                 435

ttt gta aag agg cca gcc cgc taagctaggt cgcatgatca gca               1455
Phe Val Lys Arg Pro Ala Arg
        440
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<210> 240
<211> 444
<212> PRT
<213> Corynebacterium glutamicum

<400> 240

Met Met Leu Asn Glu Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met
1 5 10 15

Ala Asp Phe Asp Ile Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly
20 25 30

Phe Met Leu Thr Met Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu
35 40 45

Glu Arg Phe Thr Thr Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe
50 55 60

Leu Ile Gly Thr Val Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met
65 70 75 80

Leu Ala Ala Arg Val Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro
85 90 95

Leu Leu Met Thr Val Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly
100 105 110

Ala Val Met Gly Leu Ile Ala Val Val Met Ala Val Gly Pro Ala Leu
115 120 125

Gly Pro Ser Val Ala Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala
130 135 140

Ile Phe Trp Val Met Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly
145 150 155 160

Thr Leu Arg Leu Thr Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp
165 170 175

Val Ile Ser Phe Leu Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr
180 185 190

Ala Leu Ser Ser Ile Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu
195 200 205

Val Val Leu Ala Val Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg
210 215 220

Gln Ile Ala Met Gly Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro
225 230 235 240

Leu Ala Ile Arg Glu Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu
245 250 255

Phe Gly Ala Leu Leu Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln
260 265 270

Gly Ser Leu Met Val Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro
275 280 285

Gly Gly Leu Leu Glu Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr
290 295 300

Asp Arg His Gly Pro Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val
305 310 315 320

Val Ile Ser Leu Phe Ala Leu Ser Thr Val Asp Glu Phe Ala Asn Val
325 330 335

Trp Phe Ile Ile Gly Val His Ile Val Phe Ser Ile Gly Leu Ala Leu
340 345 350

Leu Phe Thr Pro Leu Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn
355 360 365

Met Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala
370 375 380

Gly Ala Ala Gly Thr Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser
385 390 395 400

Asn Asn Ala Leu Ile Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp
405 410 415

Gly Ala Asn Ser Ala Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala
420 425 430

Leu Ile Val Gly Phe Phe Val Lys Arg Pro Ala Arg
435 440

<210> 241
<211> 1093
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1093)
<223> FRXA00565

<400> 241
tggagccttg tcttcctcca gcaatcccac aacggagcag gttgggatcc cgagaaatgt 60

tgtcatcatc ttggctgtat tagtttttac agcctttgtc atg atg ttg aat gag 115
Met Met Leu Asn Glu
1 5

act act ctg gca gtc gcg ttg ccg tcg atc atg gcg gac ttt gac att 163
Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
10 15 20

gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg 211
Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly Phe Met Leu Thr Met
25 30 35

gct gtg gtt ctt cca gct act ggt tgg atg ttg gaa cgt ttt acc act 259
Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu Glu Arg Phe Thr Thr
40 45 50

cgt agt gtg ttt att ttc gcc acg gtg gtc ttc ctg atc ggt act gtg 307
Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe Leu Ile Gly Thr Val
55 60 65

acg gct gcg ttg tct cct act ttt gcg att atg ctt gca gcc cgc gtc 355
Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met Leu Ala Ala Arg Val
70 75 80 85

gct cag gcg att ggt acc gct gtg atc atg ccg ctg ctg atg act gtc 403
Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro Leu Leu Met Thr Val
90 95 100

gcg atg acc gtt gtt cct cca gag cgc cgt ggc gcc gtc atg ggt ttg 451
Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly Ala Val Met Gly Leu
105 110 115

att gcg gtc gtg atg gcc gtt ggt cct gct ctt gga cct agt gtg gct 499
Ile Ala Val Val Met Ala Val Gly Pro Ala Leu Gly Pro Ser Val Ala
120 125 130

ggt ttc gta ctc agc ttg tct tcg tgg cac gcg att ttc tgg gtc atg 547
Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala Ile Phe Trp Val Met
135 140 145

gtt ccg ttg gtg ttt gtg gca agc ctg atc ggt acc ctg cgt ctg acc 595
Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly Thr Leu Arg Leu Thr
150 155 160 165

aac gtc agt gag cct aaa aag act cct ttg gat gtt att tcc ttc ctg 643
Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp Val Ile Ser Phe Leu
170 175 180

att tcc gca gtg gct ttc ggt ggc ctt gtg tac gcc ttg agc tcg att 691
Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr Ala Leu Ser Ser Ile
185 190 195

ggc atc att ttg gaa ggt gac aga agc gct ttg gtc gtg ttg gct gtc 739
Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu Val Val Leu Ala Val
200 205 210

ggc atc att gcg ttg gtg gtg ttt gtg tgg cgc cag att gcc atg ggt 787
Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg Gln Ile Ala Met Gly
215 220 225

aag cag gat aag gcg ctg ttg gat ctg cgt ccg ttg gcg att cgt gag 835
Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro Leu Ala Ile Arg Glu
230 235 240 245

tac acc att ccg ctg gtt gtg ctt ttg acg ctg ttc ggt gcg ctg ctc 883
Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu Phe Gly Ala Leu Leu
250 255 260

ggt gtc atg aat aca ctg ccg ctc tac ctg cag gga tcc ttg atg gtc 931
Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln Gly Ser Leu Met Val
265 270 275

acc gcc ttg gtc gcg ggt cta gtg ctg ttg cca ggt ggt ctt ttg gaa 979

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Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro Gly Gly Leu Leu Glu
        280                 285                 290

ggt gtg ctg tcg cca ttt gtg ggt cga att tat gat cgt cat ggt cca      1027
Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr Asp Arg His Gly Pro
    295                 300                 305

cgc gga ctc gtg atc ggc ggt atg tca ctc gtt gtg atc tcc ctg ttt      1075
Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val Val Ile Ser Leu Phe
310                 315                 320                 325

gca ctg tcc acc gtc gat                                              1093
Ala Leu Ser Thr Val Asp
                330


<210> 242
<211> 331
<212> PRT
<213> Corynebacterium glutamicum

<400> 242
Met Met Leu Asn Glu Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met
  1               5                  10                  15

Ala Asp Phe Asp Ile Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly
             20                  25                  30

Phe Met Leu Thr Met Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu
         35                  40                  45

Glu Arg Phe Thr Thr Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe
     50                  55                  60

Leu Ile Gly Thr Val Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met
 65                  70                  75                  80

Leu Ala Ala Arg Val Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro
                 85                  90                  95

Leu Leu Met Thr Val Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly
            100                 105                 110

Ala Val Met Gly Leu Ile Ala Val Val Met Ala Val Gly Pro Ala Leu
        115                 120                 125

Gly Pro Ser Val Ala Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala
    130                 135                 140

Ile Phe Trp Val Met Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly
145                 150                 155                 160

Thr Leu Arg Leu Thr Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp
                165                 170                 175

Val Ile Ser Phe Leu Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr
            180                 185                 190
```

```
Ala Leu Ser Ser Ile Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu
        195                 200                 205

Val Val Leu Ala Val Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg
    210                 215                 220

Gln Ile Ala Met Gly Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro
225                 230                 235                 240

Leu Ala Ile Arg Glu Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu
                245                 250                 255

Phe Gly Ala Leu Leu Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln
            260                 265                 270

Gly Ser Leu Met Val Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro
        275                 280                 285

Gly Gly Leu Leu Glu Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr
    290                 295                 300

Asp Arg His Gly Pro Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val
305                 310                 315                 320

Val Ile Ser Leu Phe Ala Leu Ser Thr Val Asp
                325                 330


<210> 243
<211> 380
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(357)
<223> FRXA02878

<400> 243
tgc ctg tcc acc gtc gat gag ttc gcc acg tgt tgg tca tca ttc gcg      48
Cys Leu Ser Thr Val Asp Glu Phe Ala Thr Cys Trp Ser Ser Phe Ala
  1               5                  10                  15

gac aca tcg tgg ttc tca tcg gcc ctt gcg ctg ctg ttc acc cca ctg      96
Asp Thr Ser Trp Phe Ser Ser Ala Leu Ala Leu Leu Phe Thr Pro Leu
             20                  25                  30

atg aca gtc gcg ctc gca tcc gtc ccc gac aac atg tac ggc cac ggc     144
Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly
         35                  40                  45

tcc gcg atc ctc aac acc ctc caa cag ctc gcc ggc gcc gca ggc acc     192
Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
     50                  55                  60

gcg gtc atg att gcg gtt tat tcc acc gtc agc aac aac gcg ctt atc     240
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```
Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile
65                  70                  75                  80

gac ggc gca acc caa caa acc gcc ctc gcc gac ggc gcc aac tct gca    288
Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala
                85                  90                  95

ttc ttc gcc tca gcg tgc gtg gca gtg ttt gca ctg atc gtg ggc ttc    336
Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe
            100                 105                 110

ttt gta aag agg cca gcc cgc taagctaggt cgcatgatca gca             380
Phe Val Lys Arg Pro Ala Arg
        115


<210> 244
<211> 119
<212> PRT
<213> Corynebacterium glutamicum

<400> 244
Cys Leu Ser Thr Val Asp Glu Phe Ala Thr Cys Trp Ser Ser Phe Ala
1               5                   10                  15

Asp Thr Ser Trp Phe Ser Ser Ala Leu Ala Leu Leu Phe Thr Pro Leu
            20                  25                  30

Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly
        35                  40                  45

Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
    50                  55                  60

Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile
65                  70                  75                  80

Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala
                85                  90                  95

Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe
            100                 105                 110

Phe Val Lys Arg Pro Ala Arg
        115


<210> 245
<211> 1533
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1510)
<223> RXA00648
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<400> 245
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gtttgccagc tattgcatct tgcacaaaat gtgtaccata cacataatgt catcgagtcc 60

tcccgaatca gccacaccac agatcaaata cggcctgctg gtg gtc act ctc gcc   115
                                           Val Val Thr Leu Ala
                                           1               5

tca gct ggt atc act gtt tcc cta gcg cag acc ctg gtt att ccg atc   163
Ser Ala Gly Ile Thr Val Ser Leu Ala Gln Thr Leu Val Ile Pro Ile
                10                  15                  20

att ggt cgg ttg ccc gag atc ttc aac acc acg gct gct aat gcc tct   211
Ile Gly Arg Leu Pro Glu Ile Phe Asn Thr Thr Ala Ala Asn Ala Ser
            25                  30                  35

tgg atc att act gtg acg ctg ttg gtg ggc gca gtg gcg act cct gtg   259
Trp Ile Ile Thr Val Thr Leu Leu Val Gly Ala Val Ala Thr Pro Val
        40                  45                  50

atg ggc agg ctt gca gat atg tac ggc aag aaa aag atg atg ctc atc   307
Met Gly Arg Leu Ala Asp Met Tyr Gly Lys Lys Lys Met Met Leu Ile
    55                  60                  65

tca ctt gtc ccg ttc att ctt gga tca gtg atc tgc gct gtg tcg gtg   355
Ser Leu Val Pro Phe Ile Leu Gly Ser Val Ile Cys Ala Val Ser Val
70                  75                  80                  85

gat ttg att ccg atg atc atc ggc cgt ggt ttt cag ggg ctt ggc tct   403
Asp Leu Ile Pro Met Ile Ile Gly Arg Gly Phe Gln Gly Leu Gly Ser
                90                  95                  100

ggc ctg att cct ctt ggc att tct ctc atg cat gat ttg ttg ccc cgg   451
Gly Leu Ile Pro Leu Gly Ile Ser Leu Met His Asp Leu Leu Pro Arg
            105                 110                 115

gag aaa gca ggg tct gcc att gct ttg atg agt tct tcc atg ggc att   499
Glu Lys Ala Gly Ser Ala Ile Ala Leu Met Ser Ser Ser Met Gly Ile
        120                 125                 130

ggc ggt gca ctc ggt cta ccg ctg gct gct gct att gcc cag ttt gcg   547
Gly Gly Ala Leu Gly Leu Pro Leu Ala Ala Ala Ile Ala Gln Phe Ala
    135                 140                 145

tcc tgg cgg gtg ctg ttc tgg ttc acc gct ctg gta gcg ctt aca gtt   595
Ser Trp Arg Val Leu Phe Trp Phe Thr Ala Leu Val Ala Leu Thr Val
150                 155                 160                 165

ggc gcg gtc att tgg aag gcg att cct gct aga ccc agg atc gtg agg   643
Gly Ala Val Ile Trp Lys Ala Ile Pro Ala Arg Pro Arg Ile Val Arg
                170                 175                 180

agt ggc ggc ttt gat tat ttc ggt gct ctc ggc ctt gca atg gga ctt   691
Ser Gly Gly Phe Asp Tyr Phe Gly Ala Leu Gly Leu Ala Met Gly Leu
            185                 190                 195

atc gca ttg ttg ctc gcg gtg tcc aag gga tca gaa tgg ggc tgg aga   739
Ile Ala Leu Leu Leu Ala Val Ser Lys Gly Ser Glu Trp Gly Trp Arg
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200 205 210

agt gcc ctg acc att ggg tta ttc gtg gca gcg ctg gtg att ttg gtg 787
Ser Ala Leu Thr Ile Gly Leu Phe Val Ala Ala Leu Val Ile Leu Val
215 220 225

ggt tgg ggc tgg ttc gaa acc cgc cag aaa tcc cct ttg att gat ctg 835
Gly Trp Gly Trp Phe Glu Thr Arg Gln Lys Ser Pro Leu Ile Asp Leu
230 235 240 245

cgc acc act att cgg gcg acc gtg ttg atg aca aat att gcg tcc atc 883
Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr Asn Ile Ala Ser Ile
250 255 260

ctc atc ggt ttc acc atg tat gga atg aat ctg atc ctg cct cag gtc 931
Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu Ile Leu Pro Gln Val
265 270 275

atg cag ctg cct gta att ctg ggc tac ggt cta ggc cag agc atg ctt 979
Met Gln Leu Pro Val Ile Leu Gly Tyr Gly Leu Gly Gln Ser Met Leu
280 285 290

cag atg ggc atc tgg ctg atc ccg atg ggt cta ggc atg atg ttg att 1027
Gln Met Gly Ile Trp Leu Ile Pro Met Gly Leu Gly Met Met Leu Ile
295 300 305

tcg aat gca ggt gca gcc att agc gct gct cat ggt cct cgt gtg acg 1075
Ser Asn Ala Gly Ala Ala Ile Ser Ala Ala His Gly Pro Arg Val Thr
310 315 320 325

ctg aca att gcg ggt gtt gtg atc gca gtc ggt tat gca ctt act gcc 1123
Leu Thr Ile Ala Gly Val Val Ile Ala Val Gly Tyr Ala Leu Thr Ala
330 335 340

aca gtg ttg ttc act atc ggc aac cgc aca ccg gga gga gat gca gac 1171
Thr Val Leu Phe Thr Ile Gly Asn Arg Thr Pro Gly Gly Asp Ala Asp
345 350 355

aac gca ctt att ttg acc acc ctg gtg ctg ttc tca gtg tgt agt ctc 1219
Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe Ser Val Cys Ser Leu
360 365 370

gtg gtc ggt atc ggc att ggc ctg gca ttt ggt tcc atg cct gcc ttg 1267
Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly Ser Met Pro Ala Leu
375 380 385

atc atg ggt gcc gta cca gcc acg gag aaa gcc gca gcg aat ggt ttc 1315
Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala Ala Ala Asn Gly Phe
390 395 400 405

aac tct ctt atg cgt tca ctg ggc acc acc ggc tca tca gct gtc atc 1363
Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly Ser Ser Ala Val Ile
410 415 420

ggt gca gtg ttg gcc gga atg atg agt ggc gga gta ccc acc tta ggg 1411
Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly Val Pro Thr Leu Gly
425 430 435

gga ttc atg acc act ctg atc atc gga tgc tgc gcc gcg ctt gtg gct 1459
Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys Ala Ala Leu Val Ala
440 445 450

gcg gtc atc tcc tat ttc atc ccc acc aca acc act gtg gtg gaa gca 1507
Ala Val Ile Ser Tyr Phe Ile Pro Thr Thr Thr Thr Val Val Glu Ala
455 460 465

aaa taatcccggc agcgactcga cca 1533
Lys
470

<210> 246
<211> 470
<212> PRT
<213> Corynebacterium glutamicum

<400> 246
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1 5 10 15

Leu Val Ile Pro Ile Ile Gly Arg Leu Pro Glu Ile Phe Asn Thr Thr
20 25 30

Ala Ala Asn Ala Ser Trp Ile Ile Thr Val Thr Leu Leu Val Gly Ala
35 40 45

Val Ala Thr Pro Val Met Gly Arg Leu Ala Asp Met Tyr Gly Lys Lys
50 55 60

Lys Met Met Leu Ile Ser Leu Val Pro Phe Ile Leu Gly Ser Val Ile
65 70 75 80

Cys Ala Val Ser Val Asp Leu Ile Pro Met Ile Ile Gly Arg Gly Phe
85 90 95

Gln Gly Leu Gly Ser Gly Leu Ile Pro Leu Gly Ile Ser Leu Met His
100 105 110

Asp Leu Leu Pro Arg Glu Lys Ala Gly Ser Ala Ile Ala Leu Met Ser
115 120 125

Ser Ser Met Gly Ile Gly Gly Ala Leu Gly Leu Pro Leu Ala Ala Ala
130 135 140

Ile Ala Gln Phe Ala Ser Trp Arg Val Leu Phe Trp Phe Thr Ala Leu
145 150 155 160

Val Ala Leu Thr Val Gly Ala Val Ile Trp Lys Ala Ile Pro Ala Arg
165 170 175

Pro Arg Ile Val Arg Ser Gly Gly Phe Asp Tyr Phe Gly Ala Leu Gly
180 185 190

Leu Ala Met Gly Leu Ile Ala Leu Leu Leu Ala Val Ser Lys Gly Ser

195 200 205

Glu Trp Gly Trp Arg Ser Ala Leu Thr Ile Gly Leu Phe Val Ala Ala
210 215 220

Leu Val Ile Leu Val Gly Trp Gly Trp Phe Glu Thr Arg Gln Lys Ser
225 230 235 240

Pro Leu Ile Asp Leu Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr
245 250 255

Asn Ile Ala Ser Ile Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu
260 265 270

Ile Leu Pro Gln Val Met Gln Leu Pro Val Ile Leu Gly Tyr Gly Leu
275 280 285

Gly Gln Ser Met Leu Gln Met Gly Ile Trp Leu Ile Pro Met Gly Leu
290 295 300

Gly Met Met Leu Ile Ser Asn Ala Gly Ala Ala Ile Ser Ala Ala His
305 310 315 320

Gly Pro Arg Val Thr Leu Thr Ile Ala Gly Val Val Ile Ala Val Gly
325 330 335

Tyr Ala Leu Thr Ala Thr Val Leu Phe Thr Ile Gly Asn Arg Thr Pro
340 345 350

Gly Gly Asp Ala Asp Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe
355 360 365

Ser Val Cys Ser Leu Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly
370 375 380

Ser Met Pro Ala Leu Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala
385 390 395 400

Ala Ala Asn Gly Phe Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly
405 410 415

Ser Ser Ala Val Ile Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly
420 425 430

Val Pro Thr Leu Gly Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys
435 440 445

Ala Ala Leu Val Ala Ala Val Ile Ser Tyr Phe Ile Pro Thr Thr Thr
450 455 460

Thr Val Val Glu Ala Lys
465 470

<210> 247
<211> 1770
<212> DNA

<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1747)
<223> RXN01320

<400> 247
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caattaaaaa tacttttctt cttagaggtg gattttcaga atg aca tca cag gtc 115
Met Thr Ser Gln Val
1 5

aag ccg gac gac gaa cgt ccg gta aca aca att tca aaa agt ggt gca 163
Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile Ser Lys Ser Gly Ala
10 15 20

cct tcg gcc cac acc tca gca cca tat ggt gca gca gca act gaa gaa 211
Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala Ala Ala Thr Glu Glu
25 30 35

gct gtc gag gaa aaa acc aaa ggt cgc gtt gga ttt atc atc gca gcc 259
Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly Phe Ile Ile Ala Ala
40 45 50

ctc atg ttg gcg atg ctt ctt agc tcc ttg ggt cag acc att ttc ggt 307
Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly Gln Thr Ile Phe Gly
55 60 65

tct gcc ctg cca acg att gtt ggt gag ctt ggc ggc gtt aac cac atg 355
Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asn His Met
70 75 80 85

acc tgg gtg att acc gcc ttc ctc ttg ggc cag acc att tca ttg cct 403
Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln Thr Ile Ser Leu Pro
90 95 100

att ttc ggc aag ttg ggt gac cag ttt ggt cgc aaa tac ctc ttc atg 451
Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg Lys Tyr Leu Phe Met
105 110 115

ttt gcc atc gca ctg ttc gtg gtg ggt tcc atc atc ggt gct ttg gct 499
Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile Ile Gly Ala Leu Ala
120 125 130

cag aac atg acc acc ttg att gtg gct cgt gca ctg cag ggt atc gcc 547
Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala Leu Gln Gly Ile Ala
135 140 145

ggt ggt ggc ttg atg att ctt tct cag gca att acc gct gat gtc acc 595
Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Thr Ala Asp Val Thr
150 155 160 165

acc gcc cgt gag cgt gca aag tac atg ggc atc atg ggt tcc gtt ttc 643
Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile Met Gly Ser Val Phe
170 175 180

gga ctg tcc tcc atc ctt ggc cca ttg ctt ggt ggc tgg ttc act gac 691
Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp
185 190 195

ggt cca ggc tgg cgt tgg ggt ctg tgg ttg aac gtt cca atc ggc atc 739
Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn Val Pro Ile Gly Ile
200 205 210

atc gca ctg gtt gct atc gct gtg ctg ctg aaa ctt cca gct cgt gaa 787
Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys Leu Pro Ala Arg Glu
215 220 225

cgt ggc aag gtc tcc gtt gac tgg ttg gga agc atc ttc atg gct atc 835
Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser Ile Phe Met Ala Ile
230 235 240 245

gcc acc acc gca ttt gtc ctc gca gtg acc tgg ggt ggc aat gaa tat 883
Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp Gly Gly Asn Glu Tyr
250 255 260

gag tgg gca tca cca atg atc atc ggt ttg ttc atc acg aca ttg gtc 931
Glu Trp Ala Ser Pro Met Ile Ile Gly Leu Phe Ile Thr Thr Leu Val
265 270 275

gct gcg ata gtg ttc gtt ttc gtc gaa aag cgt gct gtt gac cca ctg 979
Ala Ala Ile Val Phe Val Phe Val Glu Lys Arg Ala Val Asp Pro Leu
280 285 290

gtc ccc atg ggc ctt ttc tcg aac cgc aac ttc gtg ctc acc gcc gtc 1027
Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val Leu Thr Ala Val
295 300 305

gcc ggt atc ggc gta ggc ctg ttt atg atg ggc acc atc gcg tac atg 1075
Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr Ile Ala Tyr Met
310 315 320 325

cct acc tac ctg cag atg gtt cat ggt ctg aac cca acg caa gct ggt 1123
Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro Thr Gln Ala Gly
330 335 340

ctg atg ctg atc cca atg atg atc ggc ctg att ggt aca tcc act gtg 1171
Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly Thr Ser Thr Val
345 350 355

gtg ggc aac atc gtg tcc aag act ggc aag tac aag tgg tac cca ttc 1219
Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys Trp Tyr Pro Phe
360 365 370

atc ggc atg ctc atc atg gtc ctt gcc cta gta ctg cta tcg acg ctg 1267
Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu Leu Ser Thr Leu
375 380 385

aca cct tcg gca agc ttg gct ctc att gga ctg tac ttc ttc gtc ttc 1315
Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr Phe Phe Val Phe
390 395 400 405

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gga ttc ggc ctg ggc tgt gca atg cag att ttg gtt ctc atc gtg cag      1363
Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val Leu Ile Val Gln
                410                 415                 420

aac tcc ttc cca atc acc atg gtt ggc acc gcg acc ggt tcc aac aac      1411
Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr Gly Ser Asn Asn
            425                 430                 435

ttc ttc cgc caa atc ggt gga gca gta ggt tcc gca ctg atc ggt ggc      1459
Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala Leu Ile Gly Gly
        440                 445                 450

ctg ttt atc tcc aac ctg tcc gac cga ttc acc gaa aac gtc ccc gca      1507
Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu Asn Val Pro Ala
    455                 460                 465

gca gtg gct tcc atg ggt gaa gaa ggc gca caa tac gcc tca gca atg      1555
Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr Ala Ser Ala Met
470                 475                 480                 485

tcc gat ttc tcc ggt gca tcc aac ctc act cca cac ctt gtt gaa tca      1603
Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His Leu Val Glu Ser
                490                 495                 500

ctt cca caa gca ctc cgt gaa gca att caa ctt tct tac aac gac gcc      1651
Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser Tyr Asn Asp Ala
            505                 510                 515

ctg aca cca atc ttc ttg gcg ctc acc ccg atc gca gta gtc gcc gcg      1699
Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala Val Val Ala Ala
        520                 525                 530

atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag gaa acg cac gaa      1747
Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys Glu Thr His Glu
    535                 540                 545

taatgacaca cgaaacttcc gtc                                            1770


<210> 248
<211> 549
<212> PRT
<213> Corynebacterium glutamicum

<400> 248
Met Thr Ser Gln Val Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile
  1               5                  10                  15

Ser Lys Ser Gly Ala Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala
            20                  25                  30

Ala Ala Thr Glu Glu Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly
        35                  40                  45

Phe Ile Ile Ala Ala Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly
    50                  55                  60
```

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Gln Thr Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
 65                 70                  75                  80

Gly Val Asn His Met Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln
                85                  90                  95

Thr Ile Ser Leu Pro Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg
            100                 105                 110

Lys Tyr Leu Phe Met Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile
        115                 120                 125

Ile Gly Ala Leu Ala Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala
    130                 135                 140

Leu Gln Gly Ile Ala Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile
145                 150                 155                 160

Thr Ala Asp Val Thr Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile
                165                 170                 175

Met Gly Ser Val Phe Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly
            180                 185                 190

Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn
        195                 200                 205

Val Pro Ile Gly Ile Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys
    210                 215                 220

Leu Pro Ala Arg Glu Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser
225                 230                 235                 240

Ile Phe Met Ala Ile Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp
                245                 250                 255

Gly Gly Asn Glu Tyr Glu Trp Ala Ser Pro Met Ile Ile Gly Leu Phe
            260                 265                 270

Ile Thr Thr Leu Val Ala Ala Ile Val Phe Val Phe Val Glu Lys Arg
        275                 280                 285

Ala Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe
    290                 295                 300

Val Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly
305                 310                 315                 320

Thr Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn
                325                 330                 335

Pro Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile
            340                 345                 350

Gly Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr
        355                 360                 365
```

```
Lys Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val
    370                 375                 380

Leu Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu
385                 390                 395                 400

Tyr Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu
                405                 410                 415

Val Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala
            420                 425                 430

Thr Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser
        435                 440                 445

Ala Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr
    450                 455                 460

Glu Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln
465                 470                 475                 480

Tyr Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro
                485                 490                 495

His Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu
            500                 505                 510

Ser Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile
        515                 520                 525

Ala Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu
    530                 535                 540

Lys Glu Thr His Glu
545


<210> 249
<211> 841
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> FRXA01314

<400> 249
gtgaatggca cgacatgcca caaggcacgc aagctgattt ccaagcctgc tgtcgcaaag 60

caattaaaaa tacttttctt cttagaggtg gattttcaga atg aca tca cag gtc   115
                                           Met Thr Ser Gln Val
                                           1               5

aag ccg gac gac gaa cgt ccg gta aca aca att tca aaa agt ggt gca   163
Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile Ser Lys Ser Gly Ala
                10                  15                  20
```

```
cct tcg gcc cac acc tca gca cca tat ggt gca gca gca act gaa gaa     211
Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala Ala Ala Thr Glu Glu
            25                  30                  35

gct gtc gag gaa aaa acc aaa ggt cgc gtt gga ttt atc atc gca gcc     259
Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly Phe Ile Ile Ala Ala
        40                  45                  50

ctc atg ttg gcg atg ctt ctt agc tcc ttg ggt cag acc att ttc ggt     307
Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly Gln Thr Ile Phe Gly
    55                  60                  65

tct gcc ctg cca acg att gtt ggt gag ctt ggc ggc gtt aac cac atg     355
Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asn His Met
70                  75                  80                  85

acc tgg gtg att acc gcc ttc ctc ttg ggc cag acc att tca ttg cct     403
Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln Thr Ile Ser Leu Pro
                90                  95                  100

att ttc ggc aag ttg ggt gac cag ttt ggt cgc aaa tac ctc ttc atg     451
Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg Lys Tyr Leu Phe Met
            105                 110                 115

ttt gcc atc gca ctg ttc gtg gtg ggt tcc atc atc ggt gct ttg gct     499
Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile Ile Gly Ala Leu Ala
        120                 125                 130

cag aac atg acc acc ttg att gtg gct cgt gca ctg cag ggt atc gcc     547
Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala Leu Gln Gly Ile Ala
    135                 140                 145

ggt ggt ggc ttg atg att ctt tct cag gca att acc gct gat gtc acc     595
Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Thr Ala Asp Val Thr
150                 155                 160                 165

acc gcc cgt gag cgt gca aag tac atg ggc atc atg ggt tcc gtt ttc     643
Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile Met Gly Ser Val Phe
                170                 175                 180

gga ctg tcc tcc atc ctt ggc cca ttg ctt ggt ggc tgg ttc act gac     691
Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp
            185                 190                 195

ggt cca ggc tgg cgt tgg ggt ctg tgg ttg aac gtt cca atc ggc atc     739
Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn Val Pro Ile Gly Ile
        200                 205                 210

atc gca ctg gtt gct atc gct gtg ctg ctg aaa ctt cca gct cgt gaa     787
Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys Leu Pro Ala Arg Glu
    215                 220                 225

cgt ggc aag gtc tcc gtt gac tgg ttg gga agc atc ttc atg gct atc     835
Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser Ile Phe Met Ala Ile
230                 235                 240                 245
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gcc acc 841
Ala Thr

<210> 250
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 250
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  1               5                  10                  15

Ser Lys Ser Gly Ala Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala
             20                  25                  30

Ala Ala Thr Glu Glu Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly
         35                  40                  45

Phe Ile Ile Ala Ala Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly
     50                  55                  60

Gln Thr Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
 65                  70                  75                  80

Gly Val Asn His Met Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln
                 85                  90                  95

Thr Ile Ser Leu Pro Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg
            100                 105                 110

Lys Tyr Leu Phe Met Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile
        115                 120                 125

Ile Gly Ala Leu Ala Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala
    130                 135                 140

Leu Gln Gly Ile Ala Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile
145                 150                 155                 160

Thr Ala Asp Val Thr Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile
                165                 170                 175

Met Gly Ser Val Phe Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly
            180                 185                 190

Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn
        195                 200                 205

Val Pro Ile Gly Ile Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys
    210                 215                 220

Leu Pro Ala Arg Glu Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser
225                 230                 235                 240

Ile Phe Met Ala Ile Ala Thr
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245

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<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(780)
<223> FRXA01320

<400> 251
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Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val
1 5 10 15

ctc acc gcc gtc gcc ggt atc ggc gta ggc ctg ttt atg atg ggc acc 96
Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr
20 25 30

atc gcg tac atg cct acc tac ctg cag atg gtt cat ggt ctg aac cca 144
Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro
35 40 45

acg caa gct ggt ctg atg ctg atc cca atg atg atc ggc ctg att ggt 192
Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly
50 55 60

aca tcc act gtg gtg ggc aac atc gtg tcc aag act ggc aag tac aag 240
Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys
65 70 75 80

tgg tac cca ttc atc ggc atg ctc atc atg gtc ctt gcc cta gta ctg 288
Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu
85 90 95

cta tcg acg ctg aca cct tcg gca agc ttg gct ctc att gga ctg tac 336
Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr
100 105 110

ttc ttc gtc ttc gga ttc ggc ctg ggc tgt gca atg cag att ttg gtt 384
Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val
115 120 125

ctc atc gtg cag aac tcc ttc cca atc acc atg gtt ggc acc gcg acc 432
Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr
130 135 140

ggt tcc aac aac ttc ttc cgc caa atc ggt gga gca gta ggt tcc gca 480
Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala
145 150 155 160

ctg atc ggt ggc ctg ttt atc tcc aac ctg tcc gac cga ttc acc gaa 528
Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu
165 170 175

aac gtc ccc gca gca gtg gct tcc atg ggt gaa gaa ggc gca caa tac 576
Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr
180 185 190

gcc tca gca atg tcc gat ttc tcc ggt gca tcc aac ctc act cca cac 624
Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His
195 200 205

ctt gtt gaa tca ctt cca caa gca ctc cgt gaa gca att caa ctt tct 672
Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser
210 215 220

tac aac gac gcc ctg aca cca atc ttc ttg gcg ctc acc ccg atc gca 720
Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala
225 230 235 240

gta gtc gcc gcg atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag 768
Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys
245 250 255

gaa acg cac gaa taatgacaca cgaaacttcc gtc 803
Glu Thr His Glu
260

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<212> PRT
<213> Corynebacterium glutamicum

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Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val
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Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr
20 25 30

Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro
35 40 45

Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly
50 55 60

Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys
65 70 75 80

Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu
85 90 95

Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr
100 105 110

Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val
115 120 125

Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr

130 135 140

Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala
145 150 155 160

Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu
165 170 175

Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr
180 185 190

Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His
195 200 205

Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser
210 215 220

Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala
225 230 235 240

Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys
245 250 255

Glu Thr His Glu
260

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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1732)
<223> RXN02926

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ttttcatccg tgaagatcac ctcaaggaaa cgcacgaata atg aca cac gaa act 115
Met Thr His Glu Thr
1 5

tcc gtc ccc gga cct gcc gac gcg cag gtc gca gga gat acg aag ctg 163
Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala Gly Asp Thr Lys Leu
10 15 20

cgc aaa ggc cgc gcg aag aag gaa aaa act cct tca tca atg acg cct 211
Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro Ser Ser Met Thr Pro
25 30 35

gaa caa caa aag aaa gtc tgg tgg gtc ctc agc gcg ctg atg gtc gcc 259
Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser Ala Leu Met Val Ala
40 45 50

atg atg atg gcc tcc ctt gac cag atg att ttc ggc aca gcc ctg cca 307

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Met Met Met Ala Ser Leu Asp Gln Met Ile Phe Gly Thr Ala Leu Pro
     55                  60                  65

aca atc gtc ggt gaa ctc ggc ggc gtt gac cac atg atg tgg gtc atc     355
Thr Ile Val Gly Glu Leu Gly Gly Val Asp His Met Met Trp Val Ile
 70                  75                  80                  85

acc gca tac cta ctt gcc gaa acc atc atg ctg ccg atc tac gga aag     403
Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu Pro Ile Tyr Gly Lys
                 90                  95                 100

ctc ggc gac ctg gtt gga cgt aaa ggt ctc ttc atc gga gcc ctc ggc     451
Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe Ile Gly Ala Leu Gly
            105                 110                 115

atc ttc ctg atc ggc tcc gtc atc ggc ggg ctt gca gga aat atg acc     499
Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu Ala Gly Asn Met Thr
        120                 125                 130

tgg ttg atc gtc ggc cgt gcc gta cag ggc atc ggt ggc ggt gga ctg     547
Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile Gly Gly Gly Gly Leu
    135                 140                 145

atg atc ctc tcg cag gca atc atc gcg gac gtt gtt cca gca cgt gaa     595
Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val Val Pro Ala Arg Glu
150                 155                 160                 165

cgt ggc cgc tac atg ggt gtc atg ggt gga gtc ttc gga ctc tct gca     643
Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val Phe Gly Leu Ser Ala
                170                 175                 180

gtt ctt ggc cca cta ctc ggt ggc tgg ttc acc gaa gga cca ggc tgg     691
Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Glu Gly Pro Gly Trp
            185                 190                 195

cgc tgg gca ttc tgg atg aac atc cca ctg gga atc atc gcc atc ggt     739
Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly Ile Ile Ala Ile Gly
        200                 205                 210

gtc gcc att tac ttc ctg gac att cca aag aag agc gtc aag ttc cgc     787
Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys Ser Val Lys Phe Arg
    215                 220                 225

tgg gat tac ctg ggc act ttc ttc atg atc gtt gcc gca acc agc ctg     835
Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val Ala Ala Thr Ser Leu
230                 235                 240                 245

atc ctg ttc acc acc tgg ggt gga tcc cag tac gag tgg tct gat cca     883
Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr Glu Trp Ser Asp Pro
                250                 255                 260

atc atc att gga ctg atc atc acc acc atc gtt gcc gct gca ctg ctg     931
Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val Ala Ala Ala Leu Leu
            265                 270                 275

gtt gtt gtg gaa ctg cgc gca aaa gat cca ttg gtt cca atg tcc ttc     979
Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu Val Pro Met Ser Phe
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        280                 285                 290

ttc caa aac cgc aac ttc acg ctc acc acc att gca ggc ctg atc ctg    1027
Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile Ala Gly Leu Ile Leu
    295                 300                 305

ggt atc gca atg ttc ggc atc atc ggc tac ctt ccg acc tac ctc cag    1075
Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu Pro Thr Tyr Leu Gln
310                 315                 320                 325

atg gtc cac gga atc aac gcc acc gaa gcc ggc tac atg ctg atc cca    1123
Met Val His Gly Ile Asn Ala Thr Glu Ala Gly Tyr Met Leu Ile Pro
                330                 335                 340

atg atg gtc ggc atg atg ggt acc tcc atc tgg act ggt atc cgc atc    1171
Met Met Val Gly Met Met Gly Thr Ser Ile Trp Thr Gly Ile Arg Ile
            345                 350                 355

tcc aac aca gga aag tac aaa ctc ttc cca cca atc ggc atg gtg gtt    1219
Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro Ile Gly Met Val Val
        360                 365                 370

acc ttc gtg gca ctg atc ttc ttt gcc cga atg gaa gtg tcc acc acc    1267
Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met Glu Val Ser Thr Thr
    375                 380                 385

ctg tgg cag atc gga atc tac ctc ttc gtc ctc ggc gtc ggc ctg ggt    1315
Leu Trp Gln Ile Gly Ile Tyr Leu Phe Val Leu Gly Val Gly Leu Gly
390                 395                 400                 405

cta gcc atg cag gtt ctg gtc ctg atc gtt cag aac acc ctg cca acc    1363
Leu Ala Met Gln Val Leu Val Leu Ile Val Gln Asn Thr Leu Pro Thr
                410                 415                 420

gcg gtg gtc gga tcc gca acc gct gtg aac aac ttc ttc cgt caa atc    1411
Ala Val Val Gly Ser Ala Thr Ala Val Asn Asn Phe Phe Arg Gln Ile
            425                 430                 435

ggt tcc tca ctc gga tcc gcg ctg gtc ggt ggc atg ttc gtt ggc aac    1459
Gly Ser Ser Leu Gly Ser Ala Leu Val Gly Gly Met Phe Val Gly Asn
        440                 445                 450

ttg gga acc ctc atg gaa gaa aga atg cca gca gcc atg gca caa ctt    1507
Leu Gly Thr Leu Met Glu Glu Arg Met Pro Ala Ala Met Ala Gln Leu
    455                 460                 465

tca cca gaa gaa caa gcc gcc atg gca gcc caa ggc gga ctg gac tcc    1555
Ser Pro Glu Glu Gln Ala Ala Met Ala Ala Gln Gly Gly Leu Asp Ser
470                 475                 480                 485

aac gaa ttg acg ccg gca atc gtc aat caa ttg cca acc gcg ctc cac    1603
Asn Glu Leu Thr Pro Ala Ile Val Asn Gln Leu Pro Thr Ala Leu His
                490                 495                 500

gat gcg ttc gcc ggt tcc tac aac gac gca ctc atc cca gtg ttc tac    1651
Asp Ala Phe Ala Gly Ser Tyr Asn Asp Ala Leu Ile Pro Val Phe Tyr
            505                 510                 515
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gtg atg atg cca ctg atc ggc atc gcg ctg ctt ctc ttg ctg ttt att   1699
Val Met Met Pro Leu Ile Gly Ile Ala Leu Leu Leu Leu Leu Phe Ile
        520                 525                 530

aag caa gaa aaa cta cgc gaa acc acc aca gac taaacacaaa acaaatgaga 1752
Lys Gln Glu Lys Leu Arg Glu Thr Thr Thr Asp
    535                 540

cct                                                                1755


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<212> PRT
<213> Corynebacterium glutamicum

<400> 254
Met Thr His Glu Thr Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala
  1               5                  10                  15

Gly Asp Thr Lys Leu Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro
             20                  25                  30

Ser Ser Met Thr Pro Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser
        35                  40                  45

Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe
    50                  55                  60

Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His
 65                  70                  75                  80

Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu
                 85                  90                  95

Pro Ile Tyr Gly Lys Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe
            100                 105                 110

Ile Gly Ala Leu Gly Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu
        115                 120                 125

Ala Gly Asn Met Thr Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile
    130                 135                 140

Gly Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val
145                 150                 155                 160

Val Pro Ala Arg Glu Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val
                165                 170                 175

Phe Gly Leu Ser Ala Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr
            180                 185                 190

Glu Gly Pro Gly Trp Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly
        195                 200                 205
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Ile Ile Ala Ile Gly Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys
210 215 220

Ser Val Lys Phe Arg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val
225 230 235 240

Ala Ala Thr Ser Leu Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr
245 250 255

Glu Trp Ser Asp Pro Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val
260 265 270

Ala Ala Ala Leu Leu Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu
275 280 285

Val Pro Met Ser Phe Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile
290 295 300

Ala Gly Leu Ile Leu Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu
305 310 315 320

Pro Thr Tyr Leu Gln Met Val His Gly Ile Asn Ala Thr Glu Ala Gly
325 330 335

Tyr Met Leu Ile Pro Met Met Val Gly Met Met Gly Thr Ser Ile Trp
340 345 350

Thr Gly Ile Arg Ile Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro
355 360 365

Ile Gly Met Val Val Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met
370 375 380

Glu Val Ser Thr Thr Leu Trp Gln Ile Gly Ile Tyr Leu Phe Val Leu
385 390 395 400

Gly Val Gly Leu Gly Leu Ala Met Gln Val Leu Val Leu Ile Val Gln
405 410 415

Asn Thr Leu Pro Thr Ala Val Val Gly Ser Ala Thr Ala Val Asn Asn
420 425 430

Phe Phe Arg Gln Ile Gly Ser Ser Leu Gly Ser Ala Leu Val Gly Gly
435 440 445

Met Phe Val Gly Asn Leu Gly Thr Leu Met Glu Glu Arg Met Pro Ala
450 455 460

Ala Met Ala Gln Leu Ser Pro Glu Glu Gln Ala Ala Met Ala Ala Gln
465 470 475 480

Gly Gly Leu Asp Ser Asn Glu Leu Thr Pro Ala Ile Val Asn Gln Leu
485 490 495

Pro Thr Ala Leu His Asp Ala Phe Ala Gly Ser Tyr Asn Asp Ala Leu
500 505 510

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Ile Pro Val Phe Tyr Val Met Met Pro Leu Ile Gly Ile Ala Leu Leu
        515                 520                 525

Leu Leu Leu Phe Ile Lys Gln Glu Lys Leu Arg Glu Thr Thr Thr Asp
    530                 535                 540
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<211> 1294
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1294)
<223> FRXA01319

<400> 255

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ttttcatccg tgaagatcac ctcaaggaaa cgcacgaata atg aca cac gaa act    115
                                          Met Thr His Glu Thr
                                            1               5

tcc gtc ccc gga cct gcc gac gcg cag gtc gca gga gat acg aag ctg    163
Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala Gly Asp Thr Lys Leu
                 10                  15                  20

cgc aaa ggc cgc gcg aag aag gaa aaa act cct tca tca atg acg cct    211
Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro Ser Ser Met Thr Pro
             25                  30                  35

gaa caa caa aag aaa gtc tgg tgg gtc ctc agc gcg ctg atg gtc gcc    259
Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser Ala Leu Met Val Ala
         40                  45                  50

atg atg atg gcc tcc ctt gac cag atg att ttc ggc aca gcc ctg cca    307
Met Met Met Ala Ser Leu Asp Gln Met Ile Phe Gly Thr Ala Leu Pro
     55                  60                  65

aca atc gtc ggt gaa ctc ggc ggc gtt gac cac atg atg tgg gtc atc    355
Thr Ile Val Gly Glu Leu Gly Gly Val Asp His Met Met Trp Val Ile
 70                  75                  80                  85

acc gca tac cta ctt gcc gaa acc atc atg ctg ccg atc tac gga aag    403
Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu Pro Ile Tyr Gly Lys
                 90                  95                 100

ctc ggc gac ctg gtt gga cgt aaa ggt ctc ttc atc gga gcc ctc ggc    451
Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe Ile Gly Ala Leu Gly
            105                 110                 115

atc ttc ctg atc ggc tcc gtc atc ggc ggg ctt gca gga aat atg acc    499
Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu Ala Gly Asn Met Thr
```

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        120                 125                 130

tgg ttg atc gtc ggc cgt gcc gta cag ggc atc ggt ggc ggt gga ctg      547
Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile Gly Gly Gly Gly Leu
    135                 140                 145

atg atc ctc tcg cag gca atc atc gcg gac gtt gtt cca gca cgt gaa      595
Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val Val Pro Ala Arg Glu
150                 155                 160                 165

cgt ggc cgc tac atg ggt gtc atg ggt gga gtc ttc gga ctc tct gca      643
Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val Phe Gly Leu Ser Ala
                170                 175                 180

gtt ctt ggc cca cta ctc ggt ggc tgg ttc acc gaa gga cca ggc tgg      691
Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Glu Gly Pro Gly Trp
            185                 190                 195

cgc tgg gca ttc tgg atg aac atc cca ctg gga atc atc gcc atc ggt      739
Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly Ile Ile Ala Ile Gly
        200                 205                 210

gtc gcc att tac ttc ctg gac att cca aag aag agc gtc aag ttc cgc      787
Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys Ser Val Lys Phe Arg
    215                 220                 225

tgg gat tac ctg ggc act ttc ttc atg atc gtt gcc gca acc agc ctg      835
Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val Ala Ala Thr Ser Leu
230                 235                 240                 245

atc ctg ttc acc acc tgg ggt gga tcc cag tac gag tgg tct gat cca      883
Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr Glu Trp Ser Asp Pro
                250                 255                 260

atc atc att gga ctg atc atc acc acc atc gtt gcc gct gca ctg ctg      931
Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val Ala Ala Ala Leu Leu
            265                 270                 275

gtt gtt gtg gaa ctg cgc gca aaa gat cca ttg gtt cca atg tcc ttc      979
Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu Val Pro Met Ser Phe
        280                 285                 290

ttc caa aac cgc aac ttc acg ctc acc acc att gca ggc ctg atc ctg     1027
Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile Ala Gly Leu Ile Leu
    295                 300                 305

ggt atc gca atg ttc ggc atc atc ggc tac ctt ccg acc tac ctc cag     1075
Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu Pro Thr Tyr Leu Gln
310                 315                 320                 325

atg gtc cac gga atc aac gcc acc gaa gcc ggc tac atg ctg atc cca     1123
Met Val His Gly Ile Asn Ala Thr Glu Ala Gly Tyr Met Leu Ile Pro
                330                 335                 340

atg atg gtc ggc atg atg ggt acc tcc atc tgg act ggt atc cgc atc     1171
Met Met Val Gly Met Met Gly Thr Ser Ile Trp Thr Gly Ile Arg Ile
            345                 350                 355
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tcc aac aca gga aag tac aaa ctc ttc cca cca atc ggc atg gtg gtt      1219
Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro Ile Gly Met Val Val
        360                 365                 370

acc ttc gtg gca ctg atc ttc ttt gcc cga atg gaa gtg tcc acc acc      1267
Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met Glu Val Ser Thr Thr
    375                 380                 385

ctg tgg cag atc gga atc tac ctc ttc                                  1294
Leu Trp Gln Ile Gly Ile Tyr Leu Phe
390                 395


<210> 256
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<212> PRT
<213> Corynebacterium glutamicum

<400> 256
Met Thr His Glu Thr Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala
  1               5                  10                  15

Gly Asp Thr Lys Leu Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro
             20                  25                  30

Ser Ser Met Thr Pro Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser
         35                  40                  45

Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe
     50                  55                  60

Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His
 65                  70                  75                  80

Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu
                 85                  90                  95

Pro Ile Tyr Gly Lys Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe
            100                 105                 110

Ile Gly Ala Leu Gly Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu
        115                 120                 125

Ala Gly Asn Met Thr Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile
    130                 135                 140

Gly Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val
145                 150                 155                 160

Val Pro Ala Arg Glu Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val
                165                 170                 175

Phe Gly Leu Ser Ala Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr
            180                 185                 190

Glu Gly Pro Gly Trp Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly
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        195                 200                 205

Ile Ile Ala Ile Gly Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys
    210                 215                 220

Ser Val Lys Phe Arg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val
225                 230                 235                 240

Ala Ala Thr Ser Leu Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr
                245                 250                 255

Glu Trp Ser Asp Pro Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val
            260                 265                 270

Ala Ala Ala Leu Leu Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu
        275                 280                 285

Val Pro Met Ser Phe Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile
    290                 295                 300

Ala Gly Leu Ile Leu Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu
305                 310                 315                 320

Pro Thr Tyr Leu Gln Met Val His Gly Ile Asn Ala Thr Glu Ala Gly
                325                 330                 335

Tyr Met Leu Ile Pro Met Met Val Gly Met Met Gly Thr Ser Ile Trp
            340                 345                 350

Thr Gly Ile Arg Ile Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro
        355                 360                 365

Ile Gly Met Val Val Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met
    370                 375                 380

Glu Val Ser Thr Thr Leu Trp Gln Ile Gly Ile Tyr Leu Phe
385                 390                 395


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<213> Corynebacterium glutamicum

<220>
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<222> (93)..(1487)
<223> RXA01578

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gtaaaacctc ggccgccaca gtcataccat tgatg atc gcc ctg ctg gtc gcg    113
                                     Met Ile Ala Leu Leu Val Ala
                                     1               5

gta ttc gcc ttc cag ctc aac gcc tcc atg ctg gcg ccg gca ctg gcc   161
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Val Phe Ala Phe Gln Leu Asn Ala Ser Met Leu Ala Pro Ala Leu Ala
        10                  15                  20

acc atg gaa act gaa ctt aat gca aca gct gcc caa atc ggc atg acg      209
Thr Met Glu Thr Glu Leu Asn Ala Thr Ala Ala Gln Ile Gly Met Thr
    25                  30                  35

cag act gct ttc ttc acc gcg gcg gcg ctg ttt tcc ctg ttc ctg cca      257
Gln Thr Ala Phe Phe Thr Ala Ala Ala Leu Phe Ser Leu Phe Leu Pro
40                  45                  50                  55

cgt tgg ggc gat ctg att ggt cgc cgc aaa gtg ctg gtc ggc atg atg      305
Arg Trp Gly Asp Leu Ile Gly Arg Arg Lys Val Leu Val Gly Met Met
                60                  65                  70

att gtc acc ggt att gga tgt gtt gtc gct gcc ttt gct ccg aat gtg      353
Ile Val Thr Gly Ile Gly Cys Val Val Ala Ala Phe Ala Pro Asn Val
            75                  80                  85

acc atc ctc ttc ctg ggc cgc ctg att caa ggt gtt gct ggc cca acc      401
Thr Ile Leu Phe Leu Gly Arg Leu Ile Gln Gly Val Ala Gly Pro Thr
        90                  95                  100

gtg cca ctg tgt ctg atc att ctg cgc cag cag gta acc aat gaa aag      449
Val Pro Leu Cys Leu Ile Ile Leu Arg Gln Gln Val Thr Asn Glu Lys
    105                 110                 115

caa tat gcg cta ctt ctc gga att gtt acc tct gtc aac ggt ggt atc      497
Gln Tyr Ala Leu Leu Leu Gly Ile Val Thr Ser Val Asn Gly Gly Ile
120                 125                 130                 135

ggc ggc gtg gac gcg ctt gct ggt ggc tgg ttg gct gaa aca ctt ggt      545
Gly Gly Val Asp Ala Leu Ala Gly Gly Trp Leu Ala Glu Thr Leu Gly
                140                 145                 150

ttc cgt tcc atc ttc tgg gtc atg gct gct ttc tgc gct gtc gct gcc      593
Phe Arg Ser Ile Phe Trp Val Met Ala Ala Phe Cys Ala Val Ala Ala
            155                 160                 165

ctc gca ctg cct ttc agc gtg aag gaa tcc acc gct gaa gaa acc ccg      641
Leu Ala Leu Pro Phe Ser Val Lys Glu Ser Thr Ala Glu Glu Thr Pro
        170                 175                 180

aag atg gac tgg ctt ggt gtg ctg cca ctg gcg gtg tcc att gga tct      689
Lys Met Asp Trp Leu Gly Val Leu Pro Leu Ala Val Ser Ile Gly Ser
    185                 190                 195

ttg ctc atg gct ttc aac gag gcc ggc aaa ctc ggt gcc gcg aac tgg      737
Leu Leu Met Ala Phe Asn Glu Ala Gly Lys Leu Gly Ala Ala Asn Trp
200                 205                 210                 215

att ctg gtg gtt gtg ctg ttc atc atc ggt atc gcc gga gtc atc ttc      785
Ile Leu Val Val Val Leu Phe Ile Ile Gly Ile Ala Gly Val Ile Phe
                220                 225                 230

ttc tac aac att gaa aag cgc gtt aag cac ccg ctg gtc agt gtt gaa      833
Phe Tyr Asn Ile Glu Lys Arg Val Lys His Pro Leu Val Ser Val Glu
```

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            235                    240                    245

tac ctc ggt caa cga cgc acc tgg gca ttg ctg ctg agc acc ctt ctc     881
Tyr Leu Gly Gln Arg Arg Thr Trp Ala Leu Leu Leu Ser Thr Leu Leu
        250                 255                 260

aca atg acc ggt gta ttc gcc gta atg aat ggt ctg ctg ccc aac ctt     929
Thr Met Thr Gly Val Phe Ala Val Met Asn Gly Leu Leu Pro Asn Leu
    265                 270                 275

gcg cag gat gct gcc aac ggt gcc ggc atg tca gcg agc gtg gtg tcc     977
Ala Gln Asp Ala Ala Asn Gly Ala Gly Met Ser Ala Ser Val Val Ser
280                 285                 290                 295

tgg tgg aca ctt acc cca tat gcg ctg gct ggc ttg gta ttc ggt cca     1025
Trp Trp Thr Leu Thr Pro Tyr Ala Leu Ala Gly Leu Val Phe Gly Pro
                300                 305                 310

atc gcc gga att ctc gcc gga aaa ttt gga tac aag atc gtc ctg caa     1073
Ile Ala Gly Ile Leu Ala Gly Lys Phe Gly Tyr Lys Ile Val Leu Gln
            315                 320                 325

att ggt atc gct gcc acc atc atc ggc gtt gcc gga gcc acc ttc tta     1121
Ile Gly Ile Ala Ala Thr Ile Ile Gly Val Ala Gly Ala Thr Phe Leu
        330                 335                 340

gtc gga agc acc tcg cat ctc gcg tac ctc ggc atc tcc atc ttc gtg     1169
Val Gly Ser Thr Ser His Leu Ala Tyr Leu Gly Ile Ser Ile Phe Val
    345                 350                 355

ggt att acc tat gca ggt att gcc aac atc atg ctc aac ggc ctg ggc     1217
Gly Ile Thr Tyr Ala Gly Ile Ala Asn Ile Met Leu Asn Gly Leu Gly
360                 365                 370                 375

atc gtg ctc tcc cct gct aac aac caa ggc tat ctg cct ggc atg aac     1265
Ile Val Leu Ser Pro Ala Asn Asn Gln Gly Tyr Leu Pro Gly Met Asn
                380                 385                 390

gca ggt gcc ttc aac cta ggt gca ggt att tcc ttc gcc atc ctc ttc     1313
Ala Gly Ala Phe Asn Leu Gly Ala Gly Ile Ser Phe Ala Ile Leu Phe
            395                 400                 405

gca gtt tcc acg gca ttc agt gac aac ggc gga gga tac gcc gca ggc     1361
Ala Val Ser Thr Ala Phe Ser Asp Asn Gly Gly Gly Tyr Ala Ala Gly
        410                 415                 420

atg tgg gct ggc gtg atc atc ttg gtc cta gcc ttc ctc tgc tcc ctg     1409
Met Trp Ala Gly Val Ile Ile Leu Val Leu Ala Phe Leu Cys Ser Leu
    425                 430                 435

ctg atc cca cgc cca gaa tca atc acc gat aca gtg gca gcc aaa gtc     1457
Leu Ile Pro Arg Pro Glu Ser Ile Thr Asp Thr Val Ala Ala Lys Val
440                 445                 450                 455

cag gct gaa gaa gcc gct caa gcc gcc agc taaatccaca aactgaacta       1507
Gln Ala Glu Glu Ala Ala Gln Ala Ala Ser
                460                 465
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agg 1510

<210> 258
<211> 465
<212> PRT
<213> Corynebacterium glutamicum

<400> 258
Met Ile Ala Leu Leu Val Ala Val Phe Ala Phe Gln Leu Asn Ala Ser
1   5   10   15

Met Leu Ala Pro Ala Leu Ala Thr Met Glu Thr Glu Leu Asn Ala Thr
            20   25   30

Ala Ala Gln Ile Gly Met Thr Gln Thr Ala Phe Phe Thr Ala Ala Ala
        35   40   45

Leu Phe Ser Leu Phe Leu Pro Arg Trp Gly Asp Leu Ile Gly Arg Arg
    50   55   60

Lys Val Leu Val Gly Met Met Ile Val Thr Gly Ile Gly Cys Val Val
65   70   75   80

Ala Ala Phe Ala Pro Asn Val Thr Ile Leu Phe Leu Gly Arg Leu Ile
                85   90   95

Gln Gly Val Ala Gly Pro Thr Val Pro Leu Cys Leu Ile Ile Leu Arg
            100   105   110

Gln Gln Val Thr Asn Glu Lys Gln Tyr Ala Leu Leu Leu Gly Ile Val
        115   120   125

Thr Ser Val Asn Gly Gly Ile Gly Gly Val Asp Ala Leu Ala Gly Gly
    130   135   140

Trp Leu Ala Glu Thr Leu Gly Phe Arg Ser Ile Phe Trp Val Met Ala
145   150   155   160

Ala Phe Cys Ala Val Ala Ala Leu Ala Leu Pro Phe Ser Val Lys Glu
                165   170   175

Ser Thr Ala Glu Glu Thr Pro Lys Met Asp Trp Leu Gly Val Leu Pro
            180   185   190

Leu Ala Val Ser Ile Gly Ser Leu Leu Met Ala Phe Asn Glu Ala Gly
        195   200   205

Lys Leu Gly Ala Ala Asn Trp Ile Leu Val Val Val Leu Phe Ile Ile
    210   215   220

Gly Ile Ala Gly Val Ile Phe Phe Tyr Asn Ile Glu Lys Arg Val Lys
225   230   235   240

His Pro Leu Val Ser Val Glu Tyr Leu Gly Gln Arg Arg Thr Trp Ala
                245   250   255

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Leu Leu Leu Ser Thr Leu Leu Thr Met Thr Gly Val Phe Ala Val Met
            260                 265                 270

Asn Gly Leu Leu Pro Asn Leu Ala Gln Asp Ala Ala Asn Gly Ala Gly
        275                 280                 285

Met Ser Ala Ser Val Val Ser Trp Trp Thr Leu Thr Pro Tyr Ala Leu
    290                 295                 300

Ala Gly Leu Val Phe Gly Pro Ile Ala Gly Ile Leu Ala Gly Lys Phe
305                 310                 315                 320

Gly Tyr Lys Ile Val Leu Gln Ile Gly Ile Ala Ala Thr Ile Ile Gly
                325                 330                 335

Val Ala Gly Ala Thr Phe Leu Val Gly Ser Thr Ser His Leu Ala Tyr
            340                 345                 350

Leu Gly Ile Ser Ile Phe Val Gly Ile Thr Tyr Ala Gly Ile Ala Asn
        355                 360                 365

Ile Met Leu Asn Gly Leu Gly Ile Val Leu Ser Pro Ala Asn Asn Gln
    370                 375                 380

Gly Tyr Leu Pro Gly Met Asn Ala Gly Ala Phe Asn Leu Gly Ala Gly
385                 390                 395                 400

Ile Ser Phe Ala Ile Leu Phe Ala Val Ser Thr Ala Phe Ser Asp Asn
                405                 410                 415

Gly Gly Gly Tyr Ala Ala Gly Met Trp Ala Gly Val Ile Ile Leu Val
            420                 425                 430

Leu Ala Phe Leu Cys Ser Leu Leu Ile Pro Arg Pro Glu Ser Ile Thr
        435                 440                 445

Asp Thr Val Ala Ala Lys Val Gln Ala Glu Glu Ala Ala Gln Ala Ala
    450                 455                 460

Ser
465


<210> 259
<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1447)
<223> RXA02087

<400> 259
aatcggattc atgctgtgtg gtgtgatcag tttgctggct gcggtcgcat ggatcttcgg 60
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ccgggagacg ctgccaacgg cgaaagtcga gcaggtataa atg acg cca att gtg   115
                                            Met Thr Pro Ile Val
                                             1               5

gag tcc agg gcg tgg aaa gct ctg ggc gct tta agt gtt ggg ctg ttt   163
Glu Ser Arg Ala Trp Lys Ala Leu Gly Ala Leu Ser Val Gly Leu Phe
                10                  15                  20

ctc aca ctg ctt gac caa tcg ttg gtg gct gtc gcg ctg cca aag att   211
Leu Thr Leu Leu Asp Gln Ser Leu Val Ala Val Ala Leu Pro Lys Ile
            25                  30                  35

caa gag gat ttg ggt gcg agc ctg aac caa gcg gtg tgg gtg tca gcg   259
Gln Glu Asp Leu Gly Ala Ser Leu Asn Gln Ala Val Trp Val Ser Ala
        40                  45                  50

gtt tat ttg ctc act ttt gcg gtg cca ctg ttg att act ggg cgc ttg   307
Val Tyr Leu Leu Thr Phe Ala Val Pro Leu Leu Ile Thr Gly Arg Leu
    55                  60                  65

ggt gat cgt tat gga cag cga aat att tat ctt gcc ggc atg gct gtg   355
Gly Asp Arg Tyr Gly Gln Arg Asn Ile Tyr Leu Ala Gly Met Ala Val
70                  75                  80                  85

ttt acc ctc gcg gcg ttg gcc tgt gta ttt gca cca agc atc gaa tgg   403
Phe Thr Leu Ala Ala Leu Ala Cys Val Phe Ala Pro Ser Ile Glu Trp
                90                  95                  100

ttg att gct gct cgc gcg gtg cag ggc ctg ggc gga tct ctt ctt aat   451
Leu Ile Ala Ala Arg Ala Val Gln Gly Leu Gly Gly Ser Leu Leu Asn
            105                 110                 115

ccg cag ccc ctg agc atc att cac aag att ttc gcg cat gat cgt agg   499
Pro Gln Pro Leu Ser Ile Ile His Lys Ile Phe Ala His Asp Arg Arg
        120                 125                 130

gga gcc gcc acc ggg gtg tgg agt gct gtt gcc tca tca gct gga ctt   547
Gly Ala Ala Thr Gly Val Trp Ser Ala Val Ala Ser Ser Ala Gly Leu
    135                 140                 145

ttc ggg cca gtt atc ggt ggt gtt ctg gtg ggg tgg atc agc tgg cgt   595
Phe Gly Pro Val Ile Gly Gly Val Leu Val Gly Trp Ile Ser Trp Arg
150                 155                 160                 165

gct gtg ttc ttg gtt tat gtg ccg ctc gga ttg atc tcc cta ttt atg   643
Ala Val Phe Leu Val Tyr Val Pro Leu Gly Leu Ile Ser Leu Phe Met
                170                 175                 180

gtg gcg cgt tat gtg cct aaa ctt ccc acg gga acc tcg aag atc gat   691
Val Ala Arg Tyr Val Pro Lys Leu Pro Thr Gly Thr Ser Lys Ile Asp
            185                 190                 195

tgg ctc tcg ggt gcg gtc tca ctt gtt gct gta ctt ggt gtg gtt ctt   739
Trp Leu Ser Gly Ala Val Ser Leu Val Ala Val Leu Gly Val Val Leu
        200                 205                 210

gcc ttg cag cag ggg cca gaa ctt ggg tgg gga aca ctg att tgg gtg   787
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Ala Leu Gln Gln Gly Pro Glu Leu Gly Trp Gly Thr Leu Ile Trp Val
    215                 220                 225

tcc ctt gcc gtt ggt att gct gca gct gtg ctc ttt ata tgg atg caa     835
Ser Leu Ala Val Gly Ile Ala Ala Ala Val Leu Phe Ile Trp Met Gln
230                 235                 240                 245

aca aga tcc aag gcg cca ctg atg ccg ttg agg att ttc aag acg cgc     883
Thr Arg Ser Lys Ala Pro Leu Met Pro Leu Arg Ile Phe Lys Thr Arg
                250                 255                 260

aac ttc gcg atc ggt gca ttt tcg atc ttc agc ctg ggc ttt acg gtg     931
Asn Phe Ala Ile Gly Ala Phe Ser Ile Phe Ser Leu Gly Phe Thr Val
            265                 270                 275

tat tcc gtt aat ttg ccc atc atg ttg tat ctg caa acg gct cag gga     979
Tyr Ser Val Asn Leu Pro Ile Met Leu Tyr Leu Gln Thr Ala Gln Gly
        280                 285                 290

atg tcg tcg cag ttg gcc ggt ttg atg ttg gtt ccg atg ggc atc atc     1027
Met Ser Ser Gln Leu Ala Gly Leu Met Leu Val Pro Met Gly Ile Ile
    295                 300                 305

tct gtg gtg atg tca cca gta att gga cga ttg gtg gat cgc ctg gca     1075
Ser Val Val Met Ser Pro Val Ile Gly Arg Leu Val Asp Arg Leu Ala
310                 315                 320                 325

cca gga atg atc tcc aag atc gga ttc ggc gcg ctg att ttc tcg atg     1123
Pro Gly Met Ile Ser Lys Ile Gly Phe Gly Ala Leu Ile Phe Ser Met
                330                 335                 340

gcg ttg atg gct gtc ttt atg atc gcc aac cta tcg ccg tgg tgg cta     1171
Ala Leu Met Ala Val Phe Met Ile Ala Asn Leu Ser Pro Trp Trp Leu
            345                 350                 355

ctc atc ccg att att ttg ttc ggt agc tcc aac gcg atg agt ttt gca     1219
Leu Ile Pro Ile Ile Leu Phe Gly Ser Ser Asn Ala Met Ser Phe Ala
        360                 365                 370

ccg aac tct gtg att gct ctg cgt gat gtt ccg cag gat tta gtg ggc     1267
Pro Asn Ser Val Ile Ala Leu Arg Asp Val Pro Gln Asp Leu Val Gly
    375                 380                 385

tct gct tct ggt ttt tac aac acc tca cgc cag gtg ggc gct gtt ttg     1315
Ser Ala Ser Gly Phe Tyr Asn Thr Ser Arg Gln Val Gly Ala Val Leu
390                 395                 400                 405

ggc gcc gct acc ttg ggc gct gtg atg caa ata gga gtg ggc acg gtg     1363
Gly Ala Ala Thr Leu Gly Ala Val Met Gln Ile Gly Val Gly Thr Val
                410                 415                 420

tcc ttc ggt gtt gcc atg ggt gcg gca atc ctg gtg aca ctc gtg ccc     1411
Ser Phe Gly Val Ala Met Gly Ala Ala Ile Leu Val Thr Leu Val Pro
            425                 430                 435

tta atc ttt ggg ttc cta gcg gta acc caa ttt aga tagttgctcc          1457
Leu Ile Phe Gly Phe Leu Ala Val Thr Gln Phe Arg
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440 445

gattttctca cga 1470

<210> 260
<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 260
Met Thr Pro Ile Val Glu Ser Arg Ala Trp Lys Ala Leu Gly Ala Leu
1 5 10 15

Ser Val Gly Leu Phe Leu Thr Leu Leu Asp Gln Ser Leu Val Ala Val
20 25 30

Ala Leu Pro Lys Ile Gln Glu Asp Leu Gly Ala Ser Leu Asn Gln Ala
35 40 45

Val Trp Val Ser Ala Val Tyr Leu Leu Thr Phe Ala Val Pro Leu Leu
50 55 60

Ile Thr Gly Arg Leu Gly Asp Arg Tyr Gly Gln Arg Asn Ile Tyr Leu
65 70 75 80

Ala Gly Met Ala Val Phe Thr Leu Ala Ala Leu Ala Cys Val Phe Ala
85 90 95

Pro Ser Ile Glu Trp Leu Ile Ala Ala Arg Ala Val Gln Gly Leu Gly
100 105 110

Gly Ser Leu Leu Asn Pro Gln Pro Leu Ser Ile Ile His Lys Ile Phe
115 120 125

Ala His Asp Arg Arg Gly Ala Ala Thr Gly Val Trp Ser Ala Val Ala
130 135 140

Ser Ser Ala Gly Leu Phe Gly Pro Val Ile Gly Gly Val Leu Val Gly
145 150 155 160

Trp Ile Ser Trp Arg Ala Val Phe Leu Val Tyr Val Pro Leu Gly Leu
165 170 175

Ile Ser Leu Phe Met Val Ala Arg Tyr Val Pro Lys Leu Pro Thr Gly
180 185 190

Thr Ser Lys Ile Asp Trp Leu Ser Gly Ala Val Ser Leu Val Ala Val
195 200 205

Leu Gly Val Val Leu Ala Leu Gln Gln Gly Pro Glu Leu Gly Trp Gly
210 215 220

Thr Leu Ile Trp Val Ser Leu Ala Val Gly Ile Ala Ala Ala Val Leu
225 230 235 240

Phe Ile Trp Met Gln Thr Arg Ser Lys Ala Pro Leu Met Pro Leu Arg

245 250 255

Ile Phe Lys Thr Arg Asn Phe Ala Ile Gly Ala Phe Ser Ile Phe Ser
260 265 270

Leu Gly Phe Thr Val Tyr Ser Val Asn Leu Pro Ile Met Leu Tyr Leu
275 280 285

Gln Thr Ala Gln Gly Met Ser Ser Gln Leu Ala Gly Leu Met Leu Val
290 295 300

Pro Met Gly Ile Ile Ser Val Val Met Ser Pro Val Ile Gly Arg Leu
305 310 315 320

Val Asp Arg Leu Ala Pro Gly Met Ile Ser Lys Ile Gly Phe Gly Ala
325 330 335

Leu Ile Phe Ser Met Ala Leu Met Ala Val Phe Met Ile Ala Asn Leu
340 345 350

Ser Pro Trp Trp Leu Leu Ile Pro Ile Ile Leu Phe Gly Ser Ser Asn
355 360 365

Ala Met Ser Phe Ala Pro Asn Ser Val Ile Ala Leu Arg Asp Val Pro
370 375 380

Gln Asp Leu Val Gly Ser Ala Ser Gly Phe Tyr Asn Thr Ser Arg Gln
385 390 395 400

Val Gly Ala Val Leu Gly Ala Ala Thr Leu Gly Ala Val Met Gln Ile
405 410 415

Gly Val Gly Thr Val Ser Phe Gly Val Ala Met Gly Ala Ala Ile Leu
420 425 430

Val Thr Leu Val Pro Leu Ile Phe Gly Phe Leu Ala Val Thr Gln Phe
435 440 445

Arg

<210> 261
<211> 1338
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1315)
<223> RXA02088

<400> 261
agagcaccca agcgacattg ttcgataata tgttctatta ttggtattaa tactggtcag 60

ctagatataa aaggggcgca gggctagcct tgggtgtgaa atg tta act caa aaa 115
Met Leu Thr Gln Lys

```
                                                  1               5

ata gaa tta gag gct aaa cca aaa atc cca gag gag atc tgg gtg ctg      163
Ile Glu Leu Glu Ala Lys Pro Lys Ile Pro Glu Glu Ile Trp Val Leu
                10                  15                  20

gtt gtg gct gcg ttt att att gcg ctg ggc tat ggc ctg att gcg ccg      211
Val Val Ala Ala Phe Ile Ile Ala Leu Gly Tyr Gly Leu Ile Ala Pro
            25                  30                  35

att ttg cca cag ttt gtg gtc ggt ttt gat gta agt ttt gca gct gcc      259
Ile Leu Pro Gln Phe Val Val Gly Phe Asp Val Ser Phe Ala Ala Ala
        40                  45                  50

agt gcg gtg gtg tcc atc ttt gcg ggc gcc cgg ttg ttg ttt gcg ccg      307
Ser Ala Val Val Ser Ile Phe Ala Gly Ala Arg Leu Leu Phe Ala Pro
    55                  60                  65

atg tcg ggg agt ttg atc gat aag atc ggt tcc cgt cgt gtg tat ctc      355
Met Ser Gly Ser Leu Ile Asp Lys Ile Gly Ser Arg Arg Val Tyr Leu
70                  75                  80                  85

act ggt tta ctc acc gtg gct atc acc acg ggg ctt gtt gcg ttg gcg      403
Thr Gly Leu Leu Thr Val Ala Ile Thr Thr Gly Leu Val Ala Leu Ala
                90                  95                  100

cag gaa tac tgg cag att ctg ctg ctt cgt ggc atc gca ggt att ggt      451
Gln Glu Tyr Trp Gln Ile Leu Leu Leu Arg Gly Ile Ala Gly Ile Gly
            105                 110                 115

tcc acc atg ttt acg gtc tct gcc atg ggc ctg atc gtg aag atg gcg      499
Ser Thr Met Phe Thr Val Ser Ala Met Gly Leu Ile Val Lys Met Ala
        120                 125                 130

ccg gtg gag atc cgc ggg cgg tgt tcg tcg gta tat gcc agt tcg ttc      547
Pro Val Glu Ile Arg Gly Arg Cys Ser Ser Val Tyr Ala Ser Ser Phe
    135                 140                 145

ctg ttt ggc aat att att ggc ccg gtt gtg ggt gct gcg atg tcc ggt      595
Leu Phe Gly Asn Ile Ile Gly Pro Val Val Gly Ala Ala Met Ser Gly
150                 155                 160                 165

ttg ggc atg cgg tgg ccg ttc gcg att tat ggt gct tcc gtt ggc tta      643
Leu Gly Met Arg Trp Pro Phe Ala Ile Tyr Gly Ala Ser Val Gly Leu
                170                 175                 180

gct gca ctt gtt gtg tgg tgg cgg atg ccg aaa acc aac gat tca ctt      691
Ala Ala Leu Val Val Trp Trp Arg Met Pro Lys Thr Asn Asp Ser Leu
            185                 190                 195

cgg aag gct gat agc aat agt gtg ccg gcg ttg cgc ttt gct gag gca      739
Arg Lys Ala Asp Ser Asn Ser Val Pro Ala Leu Arg Phe Ala Glu Ala
        200                 205                 210

att aag gat tct gcc tac cgc tcg gcg ttg ttt agt gct ttt gcc aat      787
Ile Lys Asp Ser Ala Tyr Arg Ser Ala Leu Phe Ser Ala Phe Ala Asn
    215                 220                 225
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ggt tgg tcg aac ttt ggt gtg cgt gtg gcg gtt ctt cca ctg ttt gcc 835
Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val Leu Pro Leu Phe Ala
230 235 240 245

gca gct gca ttt agc aat ggc gga gct att gcg ggt ttt gcc atg gct 883
Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala Gly Phe Ala Met Ala
250 255 260

gcg ttc gcc gct gga aat gct ttg tgt ctg caa ttc gcg ggc gat ctc 931
Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln Phe Ala Gly Asp Leu
265 270 275

tca gat cgc att ggc cgt aaa ccg atg att att tcc ggg ctg atc gtc 979
Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile Ser Gly Leu Ile Val
280 285 290

aat gca gtg ttc acg gca atg atc gga ttc ggc aca gaa gtg tgg atc 1027
Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly Thr Glu Val Trp Ile
295 300 305

ctg atc acg gta tct gcg ttg gca ggt gct ggt gcg ggc ttg ctt aat 1075
Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly Ala Gly Leu Leu Asn
310 315 320 325

cca agt cag cag gcg gtg ctc gct gat gtt ata gat tcc cgc ccc ggc 1123
Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile Asp Ser Arg Pro Gly
330 335 340

gga aaa gtc tta gcg aat ttc caa atg gcg cag gat ttc ggt gcg att 1171
Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln Asp Phe Gly Ala Ile
345 350 355

gtt ggc ccg att ctc gta ggc atg atc gca gaa cag gca ggc ttc caa 1219
Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu Gln Ala Gly Phe Gln
360 365 370

atc gga ttc atg ctg tgt ggt gtg atc agt ttg ctg gct gcg gtc gca 1267
Ile Gly Phe Met Leu Cys Gly Val Ile Ser Leu Leu Ala Ala Val Ala
375 380 385

tgg atc ttc ggc cgg gag acg ctg cca acg gcg aaa gtc gag cag gta 1315
Trp Ile Phe Gly Arg Glu Thr Leu Pro Thr Ala Lys Val Glu Gln Val
390 395 400 405

taaatgacgc caattgtgga gtc 1338

<210> 262
<211> 405
<212> PRT
<213> Corynebacterium glutamicum

<400> 262
Met Leu Thr Gln Lys Ile Glu Leu Glu Ala Lys Pro Lys Ile Pro Glu
1 5 10 15

Glu Ile Trp Val Leu Val Val Ala Ala Phe Ile Ile Ala Leu Gly Tyr
20 25 30

Gly Leu Ile Ala Pro Ile Leu Pro Gln Phe Val Val Gly Phe Asp Val
35 40 45

Ser Phe Ala Ala Ala Ser Ala Val Val Ser Ile Phe Ala Gly Ala Arg
50 55 60

Leu Leu Phe Ala Pro Met Ser Gly Ser Leu Ile Asp Lys Ile Gly Ser
65 70 75 80

Arg Arg Val Tyr Leu Thr Gly Leu Leu Thr Val Ala Ile Thr Thr Gly
85 90 95

Leu Val Ala Leu Ala Gln Glu Tyr Trp Gln Ile Leu Leu Leu Arg Gly
100 105 110

Ile Ala Gly Ile Gly Ser Thr Met Phe Thr Val Ser Ala Met Gly Leu
115 120 125

Ile Val Lys Met Ala Pro Val Glu Ile Arg Gly Arg Cys Ser Ser Val
130 135 140

Tyr Ala Ser Ser Phe Leu Phe Gly Asn Ile Ile Gly Pro Val Val Gly
145 150 155 160

Ala Ala Met Ser Gly Leu Gly Met Arg Trp Pro Phe Ala Ile Tyr Gly
165 170 175

Ala Ser Val Gly Leu Ala Ala Leu Val Val Trp Trp Arg Met Pro Lys
180 185 190

Thr Asn Asp Ser Leu Arg Lys Ala Asp Ser Asn Ser Val Pro Ala Leu
195 200 205

Arg Phe Ala Glu Ala Ile Lys Asp Ser Ala Tyr Arg Ser Ala Leu Phe
210 215 220

Ser Ala Phe Ala Asn Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val
225 230 235 240

Leu Pro Leu Phe Ala Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala
245 250 255

Gly Phe Ala Met Ala Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln
260 265 270

Phe Ala Gly Asp Leu Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile
275 280 285

Ser Gly Leu Ile Val Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly
290 295 300

Thr Glu Val Trp Ile Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly
305 310 315 320

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Ala Gly Leu Leu Asn Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile
                325                 330                 335

Asp Ser Arg Pro Gly Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln
            340                 345                 350

Asp Phe Gly Ala Ile Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu
        355                 360                 365

Gln Ala Gly Phe Gln Ile Gly Phe Met Leu Cys Gly Val Ile Ser Leu
    370                 375                 380

Leu Ala Ala Val Ala Trp Ile Phe Gly Arg Glu Thr Leu Pro Thr Ala
385                 390                 395                 400

Lys Val Glu Gln Val
                405
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<210> 263
<211> 1239
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1216)
<223> RXA00764

<400> 263

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acctgggacg actggattat taggggtgga attttcgctc atg aca ctc aag act   115
                                           Met Thr Leu Lys Thr
                                           1               5

agc gtt ttg gca cta ctc tta gat aac gtg cat gtt ctt ctg att gcg   163
Ser Val Leu Ala Leu Leu Leu Asp Asn Val His Val Leu Leu Ile Ala
                10                  15                  20

aat cct gag tcg acc acg cag acg cag aaa ctt ttc cgt cgt gtg gtg   211
Asn Pro Glu Ser Thr Thr Gln Thr Gln Lys Leu Phe Arg Arg Val Val
            25                  30                  35

cct gcg ttg atg gcg ctt gat ggt gtg tcg ctt gaa gcg agg ttt acg   259
Pro Ala Leu Met Ala Leu Asp Gly Val Ser Leu Glu Ala Arg Phe Thr
        40                  45                  50

cac tat gga ggc cat gcg gag gaa atg gtt gcg ggt ttg acg gtg gat   307
His Tyr Gly Gly His Ala Glu Glu Met Val Ala Gly Leu Thr Val Asp
    55                  60                  65

gat ttt gat gtg att atc ccc gcg ggt ggg gac ggc acc gtc aac gaa   355
Asp Phe Asp Val Ile Ile Pro Ala Gly Gly Asp Gly Thr Val Asn Glu
70                  75                  80                  85

gtg ata aat ggg tta ctt ggg tcg gcg gaa ggt gat ttt aga aac ctt   403
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Val Ile Asn Gly Leu Leu Gly Ser Ala Glu Gly Asp Phe Arg Asn Leu
90 95 100

gag gat ttg ccg gcg att gcg gtg ttg cca acg ggg tct gcc aat gtg 451
Glu Asp Leu Pro Ala Ile Ala Val Leu Pro Thr Gly Ser Ala Asn Val
105 110 115

ttt gcc cgt gcg ctt ggt tac ccc act gac ccg tat gct gcc gct gat 499
Phe Ala Arg Ala Leu Gly Tyr Pro Thr Asp Pro Tyr Ala Ala Ala Asp
120 125 130

gcc ctg gtg gag ttg att cgg aag aac cac acc aga act atc acc ttg 547
Ala Leu Val Glu Leu Ile Arg Lys Asn His Thr Arg Thr Ile Thr Leu
135 140 145

ggt acg tgg aag ggt gat gat cag ggg act cgt tgg ttc gcg gtt aat 595
Gly Thr Trp Lys Gly Asp Asp Gln Gly Thr Arg Trp Phe Ala Val Asn
150 155 160 165

gct ggg ttt ggt att gat gcg gat gtt att gcc agg gtc gaa cgg gcg 643
Ala Gly Phe Gly Ile Asp Ala Asp Val Ile Ala Arg Val Glu Arg Ala
170 175 180

aga tct ttc ggc ttt gcg gct tca ccg ttg ttg tat ctg cag gtg agt 691
Arg Ser Phe Gly Phe Ala Ala Ser Pro Leu Leu Tyr Leu Gln Val Ser
185 190 195

ctt cgg gcg tgg gtg aaa act cag att aag cca ccg aaa att acc gtg 739
Leu Arg Ala Trp Val Lys Thr Gln Ile Lys Pro Pro Lys Ile Thr Val
200 205 210

gag gcg gtg gac agc aaa ggg cac aaa ttg caa aaa gag gaa gtg cca 787
Glu Ala Val Asp Ser Lys Gly His Lys Leu Gln Lys Glu Glu Val Pro
215 220 225

atg ctg ctt gcc tcg aat acc aat ccg tgg act ttt ttg ggt ccg ctt 835
Met Leu Leu Ala Ser Asn Thr Asn Pro Trp Thr Phe Leu Gly Pro Leu
230 235 240 245

cct gtg gtg aca aat ccg cag aat tct ttt gac aca ggt ctg ggg ctt 883
Pro Val Val Thr Asn Pro Gln Asn Ser Phe Asp Thr Gly Leu Gly Leu
250 255 260

ttt ggc ttg act agt gtg cga gga ttc ggg gga gtg gca gcg atg atg 931
Phe Gly Leu Thr Ser Val Arg Gly Phe Gly Gly Val Ala Ala Met Met
265 270 275

cac ctg att ggc gtg ggg cat ggt cgg aag ttg gag aag ttg atc gct 979
His Leu Ile Gly Val Gly His Gly Arg Lys Leu Glu Lys Leu Ile Ala
280 285 290

aag cgc acc att gct ttt gat gat gcg gag aaa gta acg ctc acg tgc 1027
Lys Arg Thr Ile Ala Phe Asp Asp Ala Glu Lys Val Thr Leu Thr Cys
295 300 305

gac agc gat cag cgt ttc caa gtt gat ggt gag tat gaa ggc aaa cca 1075
Asp Ser Asp Gln Arg Phe Gln Val Asp Gly Glu Tyr Glu Gly Lys Pro

310 315 320 325

aca aag gtg gtg ttg gaa tca atc act gat gcg gtg cga gtg tat gcg 1123
Thr Lys Val Val Leu Glu Ser Ile Thr Asp Ala Val Arg Val Tyr Ala
330 335 340

ccg aag acg cat ccg aca ccg ccg atc atg aat tgg gct gtc cat ttg 1171
Pro Lys Thr His Pro Thr Pro Pro Ile Met Asn Trp Ala Val His Leu
345 350 355

ttt aag cac gtc cgt gat ttc ctc cgg gtg cgc acg ttt ggc atc 1216
Phe Lys His Val Arg Asp Phe Leu Arg Val Arg Thr Phe Gly Ile
360 365 370

taggattcat cggagttttc ttc 1239

<210> 264
<211> 372
<212> PRT
<213> Corynebacterium glutamicum

<400> 264
Met Thr Leu Lys Thr Ser Val Leu Ala Leu Leu Leu Asp Asn Val His
1 5 10 15

Val Leu Leu Ile Ala Asn Pro Glu Ser Thr Thr Gln Thr Gln Lys Leu
20 25 30

Phe Arg Arg Val Val Pro Ala Leu Met Ala Leu Asp Gly Val Ser Leu
35 40 45

Glu Ala Arg Phe Thr His Tyr Gly Gly His Ala Glu Glu Met Val Ala
50 55 60

Gly Leu Thr Val Asp Asp Phe Asp Val Ile Ile Pro Ala Gly Gly Asp
65 70 75 80

Gly Thr Val Asn Glu Val Ile Asn Gly Leu Leu Gly Ser Ala Glu Gly
85 90 95

Asp Phe Arg Asn Leu Glu Asp Leu Pro Ala Ile Ala Val Leu Pro Thr
100 105 110

Gly Ser Ala Asn Val Phe Ala Arg Ala Leu Gly Tyr Pro Thr Asp Pro
115 120 125

Tyr Ala Ala Ala Asp Ala Leu Val Glu Leu Ile Arg Lys Asn His Thr
130 135 140

Arg Thr Ile Thr Leu Gly Thr Trp Lys Gly Asp Asp Gln Gly Thr Arg
145 150 155 160

Trp Phe Ala Val Asn Ala Gly Phe Gly Ile Asp Ala Asp Val Ile Ala
165 170 175

Arg Val Glu Arg Ala Arg Ser Phe Gly Phe Ala Ala Ser Pro Leu Leu

180 185 190

Tyr Leu Gln Val Ser Leu Arg Ala Trp Val Lys Thr Gln Ile Lys Pro
195 200 205

Pro Lys Ile Thr Val Glu Ala Val Asp Ser Lys Gly His Lys Leu Gln
210 215 220

Lys Glu Glu Val Pro Met Leu Leu Ala Ser Asn Thr Asn Pro Trp Thr
225 230 235 240

Phe Leu Gly Pro Leu Pro Val Val Thr Asn Pro Gln Asn Ser Phe Asp
245 250 255

Thr Gly Leu Gly Leu Phe Gly Leu Thr Ser Val Arg Gly Phe Gly Gly
260 265 270

Val Ala Ala Met Met His Leu Ile Gly Val Gly His Gly Arg Lys Leu
275 280 285

Glu Lys Leu Ile Ala Lys Arg Thr Ile Ala Phe Asp Asp Ala Glu Lys
290 295 300

Val Thr Leu Thr Cys Asp Ser Asp Gln Arg Phe Gln Val Asp Gly Glu
305 310 315 320

Tyr Glu Gly Lys Pro Thr Lys Val Val Leu Glu Ser Ile Thr Asp Ala
325 330 335

Val Arg Val Tyr Ala Pro Lys Thr His Pro Thr Pro Pro Ile Met Asn
340 345 350

Trp Ala Val His Leu Phe Lys His Val Arg Asp Phe Leu Arg Val Arg
355 360 365

Thr Phe Gly Ile
370

<210> 265
<211> 271
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(271)
<223> RXN03125

<400> 265
tgacaccggc gcgacgtatg gcattactgg cgtcacccca atttacgatg acatctctgc 60

tcgcctcggc gacgtcctgg ttccttacgt tctgatcgtt ttg gtt cta gcg ttc 115
Leu Val Leu Ala Phe
1 5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163

```
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
                10                  15                  20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg     211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
            25                  30                  35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca     259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
        40                  45                  50

ctg ctg tgc ttc                                                     271
Leu Leu Cys Phe
    55


<210> 266
<211> 57
<212> PRT
<213> Corynebacterium glutamicum

<400> 266
Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp
1               5                   10                  15

Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
            20                  25                  30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
        35                  40                  45

Asp Asp Pro Gln Pro Leu Leu Cys Phe
    50                  55


<210> 267
<211> 1443
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1420)
<223> RXN01553

<400> 267
atgatgatgt cctcagcaag tccaagcgcc aagccatgct ggaaacaatt ctcgagctga 60

taccaagcca gacttaaatt tctaccttaa agtcttgagc atg act gtt cag gaa    115
                                            Met Thr Val Gln Glu
                                            1               5

ttc gac cgc gcg acc aaa ccc aca cca aaa ccc cca att gtt tct tgg     163
Phe Asp Arg Ala Thr Lys Pro Thr Pro Lys Pro Pro Ile Val Ser Trp
                10                  15                  20

gcg ttt tgg gat tgg ggt tcc gcc tct ttc aac gcg gtc ctc gtg acc     211
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Ala Phe Trp Asp Trp Gly Ser Ala Ser Phe Asn Ala Val Leu Val Thr
            25                  30                  35

ttt att ttc tcg gtc tat ctc act gat tca gtc ggc gcc acc ctc ccc     259
Phe Ile Phe Ser Val Tyr Leu Thr Asp Ser Val Gly Ala Thr Leu Pro
        40                  45                  50

gag ggt tcc aac gcc aca tca ctg tat tcg atg gcg gtc gcc atc gct     307
Glu Gly Ser Asn Ala Thr Ser Leu Tyr Ser Met Ala Val Ala Ile Ala
    55                  60                  65

ggc gtc att gtt gcg gtt gtt gcc cca gtc atg ggc agg cga tca gat     355
Gly Val Ile Val Ala Val Val Ala Pro Val Met Gly Arg Arg Ser Asp
70                  75                  80                  85

atc aag ggc act cgc cgc agg tca ctg cgc atg tgg aca ctt gtc acc     403
Ile Lys Gly Thr Arg Arg Arg Ser Leu Arg Met Trp Thr Leu Val Thr
                90                  95                  100

gtg ttc ttg atg ttt tgt ctc ttt aca gta aag aac act gat ccc aca     451
Val Phe Leu Met Phe Cys Leu Phe Thr Val Lys Asn Thr Asp Pro Thr
            105                 110                 115

ttt ttc tgg ttt ggt gta gcc atc atg gcg atc gcc aac atc acc ttt     499
Phe Phe Trp Phe Gly Val Ala Ile Met Ala Ile Ala Asn Ile Thr Phe
        120                 125                 130

gag ttc gct gaa gtt cag tac tat gcg cag ctc tcc caa atc tcg acc     547
Glu Phe Ala Glu Val Gln Tyr Tyr Ala Gln Leu Ser Gln Ile Ser Thr
    135                 140                 145

cgc gaa aac gtg ggc cga gtt tct ggt ttc ggc tgg tcc atg ggt tac     595
Arg Glu Asn Val Gly Arg Val Ser Gly Phe Gly Trp Ser Met Gly Tyr
150                 155                 160                 165

ttc ggt ggc atc gtt cta ctg ctt gtt tgt tac cta ggt ttt gtt gcc     643
Phe Gly Gly Ile Val Leu Leu Leu Val Cys Tyr Leu Gly Phe Val Ala
                170                 175                 180

ggt gat ggc gat acc cgc gga ttc cta aac ctg ccc atc gaa gac ggc     691
Gly Asp Gly Asp Thr Arg Gly Phe Leu Asn Leu Pro Ile Glu Asp Gly
            185                 190                 195

atg aat atc cgc ctc gtc gca gtg ctt gca gcc gtt tgg ttc ttg gtc     739
Met Asn Ile Arg Leu Val Ala Val Leu Ala Ala Val Trp Phe Leu Val
        200                 205                 210

tct gcg att ccg gca ctt ctt cga gtc cca gaa att gag gca cag gta     787
Ser Ala Ile Pro Ala Leu Leu Arg Val Pro Glu Ile Glu Ala Gln Val
    215                 220                 225

gct gcc gaa gac cac ccc aaa ggc ctc ata gct gcc tac aag gat ctc     835
Ala Ala Glu Asp His Pro Lys Gly Leu Ile Ala Ala Tyr Lys Asp Leu
230                 235                 240                 245

ttt ggg cag atc gct gag ctg tgg aaa caa gac cgc aac tcc gtg tat     883
Phe Gly Gln Ile Ala Glu Leu Trp Lys Gln Asp Arg Asn Ser Val Tyr
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                250                 255                 260

ttc ctc atc gca gca act gtt ttc cgt gac gga ctc gcc gga gta ttt      931
Phe Leu Ile Ala Ala Thr Val Phe Arg Asp Gly Leu Ala Gly Val Phe
            265                 270                 275

acc ttc ggt gcc atc ctt gcg gtc tct gtg tac gga cta tct gcc ggt      979
Thr Phe Gly Ala Ile Leu Ala Val Ser Val Tyr Gly Leu Ser Ala Gly
        280                 285                 290

gat gtc ctc ctc ttc ggt gtc gca gcc aac gtg gtc tct gcg ttg gga     1027
Asp Val Leu Leu Phe Gly Val Ala Ala Asn Val Val Ser Ala Leu Gly
    295                 300                 305

gca ctc ctc gga gga ttc cta gac gat cgc gtc ggg cca aaa ccc atc     1075
Ala Leu Leu Gly Gly Phe Leu Asp Asp Arg Val Gly Pro Lys Pro Ile
310                 315                 320                 325

atc ttg att tct ctt gcc atc atg atc gcc gat gct gca att ctc ttc     1123
Ile Leu Ile Ser Leu Ala Ile Met Ile Ala Asp Ala Ala Ile Leu Phe
                330                 335                 340

ttc gtt gaa ggc ccc act aat ttc tgg atc ttc gga tta atc ctc tgt     1171
Phe Val Glu Gly Pro Thr Asn Phe Trp Ile Phe Gly Leu Ile Leu Cys
            345                 350                 355

gcg ttt gtg gga cct gca cag tca gcg tcg aga agc tat tta aca cgt     1219
Ala Phe Val Gly Pro Ala Gln Ser Ala Ser Arg Ser Tyr Leu Thr Arg
        360                 365                 370

ctt tcc cca gat ggc cag gaa ggc cag ctc ttc ggc ctt tat gcc act     1267
Leu Ser Pro Asp Gly Gln Glu Gly Gln Leu Phe Gly Leu Tyr Ala Thr
    375                 380                 385

acc ggc cgt gcc gtg agt tgg atg gtg ccg tcg ctg ttt ggt gta ttt     1315
Thr Gly Arg Ala Val Ser Trp Met Val Pro Ser Leu Phe Gly Val Phe
390                 395                 400                 405

gtg ggg ctc acc ggc gat gac cgc act ggt att ttg gcc atc gcg ctg     1363
Val Gly Leu Thr Gly Asp Asp Arg Thr Gly Ile Leu Ala Ile Ala Leu
                410                 415                 420

att ctg cta ttc ggt att gtg ctg ctg agc atg gtg aag cca ccg cac     1411
Ile Leu Leu Phe Gly Ile Val Leu Leu Ser Met Val Lys Pro Pro His
            425                 430                 435

aag gtg aag tagacaaagc gcccacaagg att                               1443
Lys Val Lys
        440
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<210> 268
<211> 440
<212> PRT
<213> Corynebacterium glutamicum

<400> 268

Met Thr Val Gln Glu Phe Asp Arg Ala Thr Lys Pro Thr Pro Lys Pro
1 5 10 15

Pro Ile Val Ser Trp Ala Phe Trp Asp Trp Gly Ser Ala Ser Phe Asn
20 25 30

Ala Val Leu Val Thr Phe Ile Phe Ser Val Tyr Leu Thr Asp Ser Val
35 40 45

Gly Ala Thr Leu Pro Glu Gly Ser Asn Ala Thr Ser Leu Tyr Ser Met
50 55 60

Ala Val Ala Ile Ala Gly Val Ile Val Ala Val Val Ala Pro Val Met
65 70 75 80

Gly Arg Arg Ser Asp Ile Lys Gly Thr Arg Arg Arg Ser Leu Arg Met
85 90 95

Trp Thr Leu Val Thr Val Phe Leu Met Phe Cys Leu Phe Thr Val Lys
100 105 110

Asn Thr Asp Pro Thr Phe Phe Trp Phe Gly Val Ala Ile Met Ala Ile
115 120 125

Ala Asn Ile Thr Phe Glu Phe Ala Glu Val Gln Tyr Tyr Ala Gln Leu
130 135 140

Ser Gln Ile Ser Thr Arg Glu Asn Val Gly Arg Val Ser Gly Phe Gly
145 150 155 160

Trp Ser Met Gly Tyr Phe Gly Gly Ile Val Leu Leu Leu Val Cys Tyr
165 170 175

Leu Gly Phe Val Ala Gly Asp Gly Asp Thr Arg Gly Phe Leu Asn Leu
180 185 190

Pro Ile Glu Asp Gly Met Asn Ile Arg Leu Val Ala Val Leu Ala Ala
195 200 205

Val Trp Phe Leu Val Ser Ala Ile Pro Ala Leu Leu Arg Val Pro Glu
210 215 220

Ile Glu Ala Gln Val Ala Ala Glu Asp His Pro Lys Gly Leu Ile Ala
225 230 235 240

Ala Tyr Lys Asp Leu Phe Gly Gln Ile Ala Glu Leu Trp Lys Gln Asp
245 250 255

Arg Asn Ser Val Tyr Phe Leu Ile Ala Ala Thr Val Phe Arg Asp Gly
260 265 270

Leu Ala Gly Val Phe Thr Phe Gly Ala Ile Leu Ala Val Ser Val Tyr
275 280 285

Gly Leu Ser Ala Gly Asp Val Leu Leu Phe Gly Val Ala Ala Asn Val
290 295 300

Val Ser Ala Leu Gly Ala Leu Leu Gly Gly Phe Leu Asp Asp Arg Val
305 310 315 320

Gly Pro Lys Pro Ile Ile Leu Ile Ser Leu Ala Ile Met Ile Ala Asp
325 330 335

Ala Ala Ile Leu Phe Phe Val Glu Gly Pro Thr Asn Phe Trp Ile Phe
340 345 350

Gly Leu Ile Leu Cys Ala Phe Val Gly Pro Ala Gln Ser Ala Ser Arg
355 360 365

Ser Tyr Leu Thr Arg Leu Ser Pro Asp Gly Gln Glu Gly Gln Leu Phe
370 375 380

Gly Leu Tyr Ala Thr Thr Gly Arg Ala Val Ser Trp Met Val Pro Ser
385 390 395 400

Leu Phe Gly Val Phe Val Gly Leu Thr Gly Asp Asp Arg Thr Gly Ile
405 410 415

Leu Ala Ile Ala Leu Ile Leu Leu Phe Gly Ile Val Leu Leu Ser Met
420 425 430

Val Lys Pro Pro His Lys Val Lys
435 440

<210> 269
<211> 840
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(817)
<223> RXN00535

<400> 269
aatcgcatgg ggcaccgtgg tcagacaccg gatcgcgctc cgcaccccaa aagatggctc 60

cctaaggagc tcacctttac tcaatgctct gatgacaccg atg tgg tgg gca ggc 115
Met Trp Trp Ala Gly
1 5

atg agt acc gcg atg ctg gca tat ttc tta caa aca gta gca ctt ggt 163
Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln Thr Val Ala Leu Gly
10 15 20

ttc ggc acc ctc ttg gta gtg caa cca gtg ctt gtc ctg tcg ctg atg 211
Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu Val Leu Ser Leu Met
25 30 35

ttc acg ctg ccg ctc tca gca cga ttc aat ggc tac cga cta cgc cga 259
Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly Tyr Arg Leu Arg Arg
40 45 50

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act gaa atc ttc tgg gct acc ctc ctc acc gta gcc gtg ggc atc atg     307
Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val Ala Val Gly Ile Met
     55                  60                  65

atc gtt ttg gga cgc ccc ctt ccc gga aac ccc cac ccc cca ctc gat     355
Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro His Pro Pro Leu Asp
 70                  75                  80                  85

cga tgg att cca gta ctt tta gtc ggc gtt gca gta atg ggt gga atg     403
Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala Val Met Gly Gly Met
                 90                  95                 100

tgg ctg ctt gcg gaa tac gta tta aag aag gac aaa gcc ctc atc ctt     451
Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp Lys Ala Leu Ile Leu
            105                 110                 115

ggt ctt gtg acg ggt gca ttg ttt ggc tac gta gca gtg atg tcc aaa     499
Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val Ala Val Met Ser Lys
        120                 125                 130

gcc gcg gtg gat ctt ttt gtc cat caa ggc ata acg gga ctc atc ttg     547
Ala Ala Val Asp Leu Phe Val His Gln Gly Ile Thr Gly Leu Ile Leu
    135                 140                 145

aac tgg gaa ggc tac ggc cta atc ctc acc gca tta ctt gga aca atc     595
Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala Leu Leu Gly Thr Ile
150                 155                 160                 165

gtg cag cag tat tcc ttt aac gct ggc gaa cta caa aaa tcg cta ccc     643
Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu Gln Lys Ser Leu Pro
                170                 175                 180

gcc atg acc att gcc gaa cca att gtt gcc ttc agt ttg ggc tac ttg     691
Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe Ser Leu Gly Tyr Leu
            185                 190                 195

gtt ctg ggc gaa aaa ttc caa gtc gtg gac tgg gaa tgg atc gcc atg     739
Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp Glu Trp Ile Ala Met
        200                 205                 210

ggc atc gca cta ctg gtg atg att gtt tcc acc att gca ctg tct cgt     787
Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr Ile Ala Leu Ser Arg
    215                 220                 225

aca agc aca atg ccg gcc gga tcg aaa agg taaaactcca aagttccccc      837
Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
230                 235

cga                                                                 840
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<210> 270
<211> 239
<212> PRT
<213> Corynebacterium glutamicum

<400> 270

Met Trp Trp Ala Gly Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln
1   5   10   15

Thr Val Ala Leu Gly Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu
            20   25   30

Val Leu Ser Leu Met Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly
        35   40   45

Tyr Arg Leu Arg Arg Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val
    50   55   60

Ala Val Gly Ile Met Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro
65   70   75   80

His Pro Pro Leu Asp Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala
                85   90   95

Val Met Gly Gly Met Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp
            100   105   110

Lys Ala Leu Ile Leu Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val
        115   120   125

Ala Val Met Ser Lys Ala Ala Val Asp Leu Phe Val His Gln Gly Ile
    130   135   140

Thr Gly Leu Ile Leu Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala
145   150   155   160

Leu Leu Gly Thr Ile Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu
                165   170   175

Gln Lys Ser Leu Pro Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe
            180   185   190

Ser Leu Gly Tyr Leu Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp
        195   200   205

Glu Trp Ile Ala Met Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr
    210   215   220

Ile Ala Leu Ser Arg Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
225   230   235

<210> 271
<211> 2472
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2449)
<223> RXN00453

<400> 271

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tagtggggcg tgaaaaaata gctcatttaa gaggagaagc aaccccgtgg cgaaattgct 60

attcaggttg gggcgatggt cctataatcg caagtggatt gtg att tcg gca tgg   115
                                            Val Ile Ser Ala Trp
                                             1               5

cta ctt att ttg gcc att gtt ggt ggt ctg gcc ctg acg atg cag aag   163
Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys
                10                  15                  20

ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc   211
Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr Pro Ser Ile Asp Ala
            25                  30                  35

act gtt tct ctg gtt gaa aat ttc cct gat cag acg aac ccg gtg acg   259
Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln Thr Asn Pro Val Thr
        40                  45                  50

gcc gcc gga gtt aac gtg gtt ttc caa tcc ccg gaa gga acc acg ctt   307
Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro Glu Gly Thr Thr Leu
    55                  60                  65

gat gat cct cag atg atg act gcg atg gat gca gtc gtt gat tac att   355
Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala Val Val Asp Tyr Ile
70                  75                  80                  85

gag gac aat ttg cct gat ttt ggt ggg gga gag cgc ttc ggc aat cct   403
Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu Arg Phe Gly Asn Pro
                90                  95                  100

gtt gag gtg tct cct gcg ttg gaa gag atg gtc atc gag cag atg acc   451
Val Glu Val Ser Pro Ala Leu Glu Glu Met Val Ile Glu Gln Met Thr
            105                 110                 115

agc atg ggg ctt cct gag gaa acc gct gca aag gat gct gcc aat ctg   499
Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys Asp Ala Ala Asn Leu
        120                 125                 130

gcg gtg ttg agc gaa gac aaa acc att ggc tac acc tct ttc aac att   547
Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr Thr Ser Phe Asn Ile
    135                 140                 145

gat gtt gag gcc gca gaa tat gtg gag caa aaa cac cgc gat gtg atc   595
Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys His Arg Asp Val Ile
150                 155                 160                 165

aac gaa gcg atg caa atc ggt gaa gat tta ggt gtc cgg gtg gaa gcc   643
Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly Val Arg Val Glu Ala
                170                 175                 180

ggt gga cct gct ttc ggt gat cca att cag att gaa acc acc agt gag   691
Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile Glu Thr Thr Ser Glu
            185                 190                 195

atc atc ggt att ggc atc gcg ttc atc gtg ttg att ttc acc ttt ggt   739
Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu Ile Phe Thr Phe Gly
        200                 205                 210
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tct ttg att gct gca ggc ttg cct ttg att acc gcg gtg atc ggc gtg 787
Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr Ala Val Ile Gly Val
215 220 225

ggc att ggt gcg ctg gca att gtg ctg gcc acg gcg ttt act gat ctc 835
Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr Ala Phe Thr Asp Leu
230 235 240 245

aac aat gtg act cca gtg ctc gca gtg atg att ggc ctg gcc gtg ggc 883
Asn Asn Val Thr Pro Val Leu Ala Val Met Ile Gly Leu Ala Val Gly
250 255 260

att gac tac gcg ctg ttt att ttg tct agg tac cgt gcg gag tat aag 931
Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr Arg Ala Glu Tyr Lys
265 270 275

cgc atg cca cgt gcc gat gct gcc gga atg gcg gtg ggc aca gct ggt 979
Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala Val Gly Thr Ala Gly
280 285 290

agt gcg gtg gtg ttt gct ggc gcg acg gtg att atc gcg ctg gta gcc 1027
Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile Ile Ala Leu Val Ala
295 300 305

ctc atc att gcg gat atc gga ttc ctc acg gcc atg ggt att tct gcg 1075
Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala Met Gly Ile Ser Ala
310 315 320 325

gcg ttt acg gtg ttc gtg gct gtg ctc att gcg ttg acg ttt atc ccg 1123
Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala Leu Thr Phe Ile Pro
330 335 340

gcg ctg ttg ggt gtg ttt ggt ggt cat gcg ttc aag ggc aag atc cct 1171
Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe Lys Gly Lys Ile Pro
345 350 355

gga att ggt gga aac cca acg cca aag cag acg tgg gag caa gcg ctt 1219
Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr Trp Glu Gln Ala Leu
360 365 370

aat cgt cgt tcc aag ggt cgc tca tgg gtc aag ctt gta cag aaa gca 1267
Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys Leu Val Gln Lys Ala
375 380 385

ccg ggt ctt gtg gtg gca gtg gtg gtc ttg ggt ctt ggt gcc ttg acc 1315
Pro Gly Leu Val Val Ala Val Val Val Leu Gly Leu Gly Ala Leu Thr
390 395 400 405

att cct gca atg aac ctg cag ttg tca ctg cct tct gac tcc acc tcc 1363
Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro Ser Asp Ser Thr Ser
410 415 420

aat att gat acc act cag cgt cag tcg gct gat ttg atg gca gag ggc 1411
Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp Leu Met Ala Glu Gly
425 430 435

```
ttt ggc gcg ggc gtt aat gcg ccg ttc ttg gtc atc gtc gat acg cat    1459
Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val Ile Val Asp Thr His
        440                 445                 450

gag gtc aat gct gat tcc acc gca ttg cag cca ctg att gag gca cag    1507
Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro Leu Ile Glu Ala Gln
    455                 460                 465

gag cct gaa gag ggc gag ttc gat cgg gag cag gcg gct cgt ttt gct    1555
Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln Ala Ala Arg Phe Ala
470                 475                 480                 485

acc tat atg tat gtc acc cag acc tac aat tcc aac atc gat gtg aag    1603
Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser Asn Ile Asp Val Lys
                490                 495                 500

aat gcg cag atc atc agc gtc aat gat gat ttc act gcg gcg cag att    1651
Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe Thr Ala Ala Gln Ile
            505                 510                 515

ctc gtg act cca tac acc gga cct gcg gat aaa gag acc cct gag ttg    1699
Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys Glu Thr Pro Glu Leu
        520                 525                 530

atg cac gtg ctg cgt gcg cag gaa gct cag att gag gat gtt acg gga    1747
Met His Val Leu Arg Ala Gln Glu Ala Gln Ile Glu Asp Val Thr Gly
    535                 540                 545

act gaa ctg ggt acc act ggg ttt acg gcg gtt cag ttg gac att act    1795
Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val Gln Leu Asp Ile Thr
550                 555                 560                 565

gag cag ctg gaa gac gca atg ccg gtt tac ctc gct gtg gtt gtt ggt    1843
Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu Ala Val Val Val Gly
                570                 575                 580

ttg gct att ttc ctc ctc att ctg gtg ttc cgt tcc ctg ctt gtt ccg    1891
Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg Ser Leu Leu Val Pro
            585                 590                 595

ctg gtt gct ggc ctt ggc ttc ttg ttg tct gtg ggt gcg gcc ttc ggt    1939
Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val Gly Ala Ala Phe Gly
        600                 605                 610

gcg acg gtg ttg gtc tgg cag gag ggc ttc ggt ggc ttt gtg aac acc    1987
Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly Gly Phe Val Asn Thr
    615                 620                 625

cct ggt ccg ctg att tcc ttc atg ccg atc ttc ctc atc ggc gtg acc    2035
Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe Leu Ile Gly Val Thr
630                 635                 640                 645

ttc ggt ttg gcc atg gac tat cag gtg ttc ctt gtg act cgc atg cgc    2083
Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu Val Thr Arg Met Arg
                650                 655                 660

gag cac tac acc cac cac aat ggc aag gga cag cct ggt tcc aag tac    2131
```

```
Glu His Tyr Thr His His Asn Gly Lys Gly Gln Pro Gly Ser Lys Tyr
            665                 670                 675

acc ccg gtt gag cag tca gtg att gaa ggc ttc acg cag ggc tcc cgc    2179
Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe Thr Gln Gly Ser Arg
        680                 685                 690

gtg gtt aca gca gcg gca ctg atc atg att gcc gtg ttc gtg gcg ttt    2227
Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala Val Phe Val Ala Phe
    695                 700                 705

att gat cag ccg ttg cca ttt att aag atc ttc ggt ttc gcg ttg ggt    2275
Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe Gly Phe Ala Leu Gly
710                 715                 720                 725

gcg ggc gtg ttt ttc gat gct ttc ttc att cgc atg ggt ctg gtc ccc    2323
Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg Met Gly Leu Val Pro
                730                 735                 740

gcg tcg atg ttc ctg atg ggc aag gcc acg tgg tgg atg cct aag tgg    2371
Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp Trp Met Pro Lys Trp
            745                 750                 755

ctg gat cga att ctg cca agt ttg gac att gaa ggc acc gca ctg gag    2419
Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu Gly Thr Ala Leu Glu
        760                 765                 770

aag gaa tgg gag gag aag cag gct gca cgt tagacttggc acctatgtca     2469
Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
    775                 780

gat                                                                2472
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<210> 272
<211> 783
<212> PRT
<213> Corynebacterium glutamicum

<400> 272

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Val Ile Ser Ala Trp Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala
1               5                   10                  15

Leu Thr Met Gln Lys Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr
            20                  25                  30

Pro Ser Ile Asp Ala Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln
        35                  40                  45

Thr Asn Pro Val Thr Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro
    50                  55                  60

Glu Gly Thr Thr Leu Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala
65                  70                  75                  80

Val Val Asp Tyr Ile Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu
                85                  90                  95
```

Arg Phe Gly Asn Pro Val Glu Val Ser Pro Ala Leu Glu Glu Met Val
100 105 110

Ile Glu Gln Met Thr Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys
115 120 125

Asp Ala Ala Asn Leu Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr
130 135 140

Thr Ser Phe Asn Ile Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys
145 150 155 160

His Arg Asp Val Ile Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly
165 170 175

Val Arg Val Glu Ala Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile
180 185 190

Glu Thr Thr Ser Glu Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu
195 200 205

Ile Phe Thr Phe Gly Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr
210 215 220

Ala Val Ile Gly Val Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr
225 230 235 240

Ala Phe Thr Asp Leu Asn Asn Val Thr Pro Val Leu Ala Val Met Ile
245 250 255

Gly Leu Ala Val Gly Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr
260 265 270

Arg Ala Glu Tyr Lys Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala
275 280 285

Val Gly Thr Ala Gly Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile
290 295 300

Ile Ala Leu Val Ala Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala
305 310 315 320

Met Gly Ile Ser Ala Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala
325 330 335

Leu Thr Phe Ile Pro Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe
340 345 350

Lys Gly Lys Ile Pro Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr
355 360 365

Trp Glu Gln Ala Leu Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys
370 375 380

Leu Val Gln Lys Ala Pro Gly Leu Val Val Ala Val Val Val Leu Gly
385 390 395 400

```
Leu Gly Ala Leu Thr Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro
                405                 410                 415

Ser Asp Ser Thr Ser Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp
            420                 425                 430

Leu Met Ala Glu Gly Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val
        435                 440                 445

Ile Val Asp Thr His Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro
    450                 455                 460

Leu Ile Glu Ala Gln Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln
465                 470                 475                 480

Ala Ala Arg Phe Ala Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser
                485                 490                 495

Asn Ile Asp Val Lys Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe
            500                 505                 510

Thr Ala Ala Gln Ile Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys
        515                 520                 525

Glu Thr Pro Glu Leu Met His Val Leu Arg Ala Gln Glu Ala Gln Ile
    530                 535                 540

Glu Asp Val Thr Gly Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val
545                 550                 555                 560

Gln Leu Asp Ile Thr Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu
                565                 570                 575

Ala Val Val Val Gly Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg
            580                 585                 590

Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val
        595                 600                 605

Gly Ala Ala Phe Gly Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly
    610                 615                 620

Gly Phe Val Asn Thr Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe
625                 630                 635                 640

Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu
                645                 650                 655

Val Thr Arg Met Arg Glu His Tyr Thr His His Asn Gly Lys Gly Gln
            660                 665                 670

Pro Gly Ser Lys Tyr Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe
        675                 680                 685

Thr Gln Gly Ser Arg Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala
    690                 695                 700
```

```
Val Phe Val Ala Phe Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe
705                 710                 715                 720

Gly Phe Ala Leu Gly Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg
                725                 730                 735

Met Gly Leu Val Pro Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp
            740                 745                 750

Trp Met Pro Lys Trp Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu
        755                 760                 765

Gly Thr Ala Leu Glu Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
    770                 775                 780


<210> 273
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXN00932

<400> 273
cccaattaat ttatgcactt cggtgaggtt actcacaaag agtagcgtgc aaagcccagc 60

aataaggtga tgtttcaacg attaggttac ggtaggggcc atg acg cca cag aaa    115
                                            Met Thr Pro Gln Lys
                                            1               5

ctt cac cgt ttt gca gcc ctt tta gaa atg ggt acc tgg acc ctg ctg    163
Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly Thr Trp Thr Leu Leu
                10                  15                  20

atc atc ggc atg atc tta aaa tac agt gga gtg aca gac gcc gta acc    211
Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val Thr Asp Ala Val Thr
            25                  30                  35

cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc    259
Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe Leu Cys Phe Ala Ala
        40                  45                  50

atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt    307
Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp Thr Phe Pro Gln Gly
    55                  60                  65

atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt    355
Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp Ala Ala Leu Pro Phe
70                  75                  80                  85

gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt    403
Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala Gly Gly Trp Arg Phe
                90                  95                  100
```

tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct 451
Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe Asp Lys Ile Leu Ala
105 110 115

caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att 499
Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu Ile Leu Leu Val Ile
120 125 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat 547
Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
135 140 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac 594
Pro Asp Ala Ile Ala Asn Thr Val Asp
150 155

atg 597

<210> 274
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 274
Met Thr Pro Gln Lys Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly
1 5 10 15

Thr Trp Thr Leu Leu Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val
20 25 30

Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
35 40 45

Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
50 55 60

Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
65 70 75 80

Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
85 90 95

Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
100 105 110

Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
115 120 125

Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
130 135 140

Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
145 150 155

<210> 275
<211> 534
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (65)..(511)
<223> RXN03022

<400> 275
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acgcctgtgt catccttttc attagagtgg agaaaagccc atacagaaag ttggcgcccg 60

agcagtg atc atc acc gct ggc atc ttg gta gcg acc gcg acc gcc ctc    109
        Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu
          1               5                  10                  15

cta atg atc acc gcg gtc agc gag tca acg tac atc gtc atc tcc ctc    157
Leu Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu
                20                  25                  30

gcc ggc ttc tcc ctt tat ggc ctt ggc ctc gga ctc ttc gcc acc cca    205
Ala Gly Phe Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro
            35                  40                  45

gtc acc gat act gcg ctt gga aca ctt ccc aaa gac cgt acc ggc gct    253
Val Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala
        50                  55                  60

ggt gca ggt gta ttc aag atg tcc tct tcc ctc ggc gca gca ctc ggc    301
Gly Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly
    65                  70                  75

atc gca atc tcc act tca gtg ttc ctc gca ctt cgc gac ggc acc tcc    349
Ile Ala Ile Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser
80                  85                  90                  95

atc aac tcc gac gtc gca ctc gcc gga aca gtt tca ctt ggc atc aac    397
Ile Asn Ser Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn
                100                 105                 110

gtt gta ttc gca gca aca gcc acc atc acc gca gca gtc ctt att cca    445
Val Val Phe Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro
            115                 120                 125

aaa gcc gct ggc aaa gtc tca caa acc agc atc acc ctt cct gag cca    493
Lys Ala Ala Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro
        130                 135                 140

gct atc gct gta aaa atc taaaacttca ccaggacaga taa                  534
Ala Ile Ala Val Lys Ile
    145
```

<210> 276
<211> 149
<212> PRT

<213> Corynebacterium glutamicum

<400> 276
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Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu Leu
 1               5                  10                  15

Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu Ala
            20                  25                  30

Gly Phe Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro Val
        35                  40                  45

Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala Gly
    50                  55                  60

Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly Ile
65                  70                  75                  80

Ala Ile Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser Ile
                85                  90                  95

Asn Ser Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn Val
            100                 105                 110

Val Phe Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro Lys
        115                 120                 125

Ala Ala Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro Ala
    130                 135                 140

Ile Ala Val Lys Ile
145
```

<210> 277
<211> 586
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXN03151

<400> 277
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ccgaacttgg agctttgctg ttggaggcag ccaaatagtc ccaatgtaaa cgcactgggt 60

agtatttgtt taaccatcca cctcaaggag taaaacgcac gtg ctt tcc cac atc   115
                                          Val Leu Ser His Ile
                                           1               5

att gat gtc ctc gcc gac ccg atc gat ggc acc cca ctt gta ggc gcc   163
Ile Asp Val Leu Ala Asp Pro Ile Asp Gly Thr Pro Leu Val Gly Ala
                10                  15                  20

gaa gat ttc tca cgg ttg gtg tct gaa tct ggg cat tcc tac gat gtt   211
Glu Asp Phe Ser Arg Leu Val Ser Glu Ser Gly His Ser Tyr Asp Val
```

```
                25                  30                  35

gct cgt caa ggg tat gtc acc ctg gct ggt ggc gca ggt ctg cgc tat      259
Ala Arg Gln Gly Tyr Val Thr Leu Ala Gly Gly Ala Gly Leu Arg Tyr
        40                  45                  50

tca ggc gat gat gca cag atg atc gcg gat cgg gaa acc ttc ctt tct      307
Ser Gly Asp Asp Ala Gln Met Ile Ala Asp Arg Glu Thr Phe Leu Ser
    55                  60                  65

ggc ggt cac ttc gcg ccc ttc gtg gaa gct gtc acc gag cat gtt caa      355
Gly Gly His Phe Ala Pro Phe Val Glu Ala Val Thr Glu His Val Gln
70                  75                  80                  85

gat gtc gtt gac cag gca ggc ctt agc gat gac gca cag cca gtg gtc      403
Asp Val Val Asp Gln Ala Gly Leu Ser Asp Asp Ala Gln Pro Val Val
                90                  95                  100

tgc gaa atc ggc gcg gga acc ggc tac tac ttg tcc cat acc ctt gat      451
Cys Glu Ile Gly Ala Gly Thr Gly Tyr Tyr Leu Ser His Thr Leu Asp
            105                 110                 115

tct gtt gca gga tct cgc gga att ggc att gac gtt tcc gtg cac gcc      499
Ser Val Ala Gly Ser Arg Gly Ile Gly Ile Asp Val Ser Val His Ala
        120                 125                 130

gca aag cgt ttg gca aag tgt cac cct cgc gtc ggc gca gtc atc gcg      547
Ala Lys Arg Leu Ala Lys Cys His Pro Arg Val Gly Ala Val Ile Ala
    135                 140                 145

aac gca tgg gca cgc ctg ccg att gca gat aac tcc tcg                  586
Asn Ala Trp Ala Arg Leu Pro Ile Ala Asp Asn Ser Ser
150                 155                 160


<210> 278
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 278
Val Leu Ser His Ile Ile Asp Val Leu Ala Asp Pro Ile Asp Gly Thr
  1               5                  10                  15

Pro Leu Val Gly Ala Glu Asp Phe Ser Arg Leu Val Ser Glu Ser Gly
            20                  25                  30

His Ser Tyr Asp Val Ala Arg Gln Gly Tyr Val Thr Leu Ala Gly Gly
        35                  40                  45

Ala Gly Leu Arg Tyr Ser Gly Asp Asp Ala Gln Met Ile Ala Asp Arg
    50                  55                  60

Glu Thr Phe Leu Ser Gly Gly His Phe Ala Pro Phe Val Glu Ala Val
65                  70                  75                  80

Thr Glu His Val Gln Asp Val Val Asp Gln Ala Gly Leu Ser Asp Asp
```

85 90 95

Ala Gln Pro Val Val Cys Glu Ile Gly Ala Gly Thr Gly Tyr Tyr Leu
100 105 110

Ser His Thr Leu Asp Ser Val Ala Gly Ser Arg Gly Ile Gly Ile Asp
115 120 125

Val Ser Val His Ala Ala Lys Arg Leu Ala Lys Cys His Pro Arg Val
130 135 140

Gly Ala Val Ile Ala Asn Ala Trp Ala Arg Leu Pro Ile Ala Asp Asn
145 150 155 160

Ser Ser

<210> 279
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(543)
<223> RXN02832

<400> 279
cgc ggg cca gtg atg gat tat aca aat caa tca tta gta gca ttt ttc 48
Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe
1 5 10 15

ttt aaa gca tta acg tca tat tta aag aaa cac aat tgt tta tat gtc 96
Phe Lys Ala Leu Thr Ser Tyr Leu Lys Lys His Asn Cys Leu Tyr Val
20 25 30

ctt gta gat cca tat tta att gaa aat tta cgc aat gca gac ggt gaa 144
Leu Val Asp Pro Tyr Leu Ile Glu Asn Leu Arg Asn Ala Asp Gly Glu
35 40 45

att gtt aaa tct tat gat aac cga gca ttt gtt aga aca atg gat aaa 192
Ile Val Lys Ser Tyr Asp Asn Arg Ala Phe Val Arg Thr Met Asp Lys
50 55 60

tta ggt tat aaa cac caa ggt ttc cct gta ggt tat gat tca atg agc 240
Leu Gly Tyr Lys His Gln Gly Phe Pro Val Gly Tyr Asp Ser Met Ser
65 70 75 80

caa atc cgt tgg ctg tca gtg tta gat tta aaa gat aag act gaa gac 288
Gln Ile Arg Trp Leu Ser Val Leu Asp Leu Lys Asp Lys Thr Glu Asp
85 90 95

caa ctt tta aaa gaa atg gat tat caa acg aga cgt aat att aaa aaa 336
Gln Leu Leu Lys Glu Met Asp Tyr Gln Thr Arg Arg Asn Ile Lys Lys
100 105 110

```
aca tat gat att ggt gtc aaa act aaa acg tta acg att gat gaa acg     384
Thr Tyr Asp Ile Gly Val Lys Thr Lys Thr Leu Thr Ile Asp Glu Thr
        115                 120                 125

caa act ttt ttc gac tta ttc cat atg gct gag gaa aag cac ggt ttc     432
Gln Thr Phe Phe Asp Leu Phe His Met Ala Glu Glu Lys His Gly Phe
    130                 135                 140

aaa ttc cgt gag tta cca tac ttt gaa gaa atg caa aag tta tac gat     480
Lys Phe Arg Glu Leu Pro Tyr Phe Glu Glu Met Gln Lys Leu Tyr Asp
145                 150                 155                 160

gac cac gcc atg tta aag ttg gcg tat att gat tta aac gag tat tta     528
Asp His Ala Met Leu Lys Leu Ala Tyr Ile Asp Leu Asn Glu Tyr Leu
                165                 170                 175

aaa acg ttg caa tta                                                 543
Lys Thr Leu Gln Leu
            180


<210> 280
<211> 181
<212> PRT
<213> Corynebacterium glutamicum

<400> 280
Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe
 1               5                  10                  15

Phe Lys Ala Leu Thr Ser Tyr Leu Lys Lys His Asn Cys Leu Tyr Val
            20                  25                  30

Leu Val Asp Pro Tyr Leu Ile Glu Asn Leu Arg Asn Ala Asp Gly Glu
        35                  40                  45

Ile Val Lys Ser Tyr Asp Asn Arg Ala Phe Val Arg Thr Met Asp Lys
    50                  55                  60

Leu Gly Tyr Lys His Gln Gly Phe Pro Val Gly Tyr Asp Ser Met Ser
65                  70                  75                  80

Gln Ile Arg Trp Leu Ser Val Leu Asp Leu Lys Asp Lys Thr Glu Asp
                85                  90                  95

Gln Leu Leu Lys Glu Met Asp Tyr Gln Thr Arg Arg Asn Ile Lys Lys
            100                 105                 110

Thr Tyr Asp Ile Gly Val Lys Thr Lys Thr Leu Thr Ile Asp Glu Thr
        115                 120                 125

Gln Thr Phe Phe Asp Leu Phe His Met Ala Glu Glu Lys His Gly Phe
    130                 135                 140

Lys Phe Arg Glu Leu Pro Tyr Phe Glu Glu Met Gln Lys Leu Tyr Asp
145                 150                 155                 160
```

```
Asp His Ala Met Leu Lys Leu Ala Tyr Ile Asp Leu Asn Glu Tyr Leu
                165                 170                 175

Lys Thr Leu Gln Leu
            180


<210> 281
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1516)
<223> RXN00165

<400> 281
aaacctcccc gggcccggcg cgcgaccgtc caagatgccg gcgttggatg ccaaattatg 60

gactctcaaa gtggcgttgt cgcagcggcc gtggagcttt gtg gcg tct gct ggc   115
                                           Val Ala Ser Ala Gly
                                           1               5

atg gcg gcg tct ttt atc tgc aat ggg tta acg cct gtg att gtg ggt   163
Met Ala Ala Ser Phe Ile Cys Asn Gly Leu Thr Pro Val Ile Val Gly
                10                  15                  20

aag gcg gtg gat gag gct att ggc acg agc gat ctg cag cga ttg tgg   211
Lys Ala Val Asp Glu Ala Ile Gly Thr Ser Asp Leu Gln Arg Leu Trp
            25                  30                  35

ttc tgg att gcc atg ttg gcg gtt ctt ttc tta acg gcg atg acg gtg   259
Phe Trp Ile Ala Met Leu Ala Val Leu Phe Leu Thr Ala Met Thr Val
        40                  45                  50

aac tgg att gct cgg tac atg ttg gtg cgg agc cag cag ttg gtc agc   307
Asn Trp Ile Ala Arg Tyr Met Leu Val Arg Ser Gln Gln Leu Val Ser
    55                  60                  65

cat gat ttg cgc atg ttg gtg act gat cgg att caa gat ccg cgt ggt   355
His Asp Leu Arg Met Leu Val Thr Asp Arg Ile Gln Asp Pro Arg Gly
70                  75                  80                  85

ttt gct gga aaa gag cgc act gcg ggt gga ttg ttg tcg att gcg tca   403
Phe Ala Gly Lys Glu Arg Thr Ala Gly Gly Leu Leu Ser Ile Ala Ser
                90                  95                  100

tcg gat acg cag cgg gtg ggc gat atc gtc atg atg acg gtg ttc ccg   451
Ser Asp Thr Gln Arg Val Gly Asp Ile Val Met Met Thr Val Phe Pro
            105                 110                 115

gtg gcg gaa ttg gcg tcg att att tat ggc gcc gtg gtg atg tac agc   499
Val Ala Glu Leu Ala Ser Ile Ile Tyr Gly Ala Val Val Met Tyr Ser
        120                 125                 130

att aat ccg tgg ttg agt gtg gct gtg ctg att ggt gga ccg ctg ctg   547
```

```
Ile Asn Pro Trp Leu Ser Val Ala Val Leu Ile Gly Gly Pro Leu Leu
    135                 140                 145

gtt gtg gtg gct att cag gtc tca aag ccg ttg cag aag cgt tcg ggt     595
Val Val Val Ala Ile Gln Val Ser Lys Pro Leu Gln Lys Arg Ser Gly
150                 155                 160                 165

gct cgt cag cag gcg gtg gca cag gct gcg gct act gca act gat gtg     643
Ala Arg Gln Gln Ala Val Ala Gln Ala Ala Ala Thr Ala Thr Asp Val
                170  -              175                 180

gtg cag ggc ttg aga att ttg aag ggt ttg ggc gcg att gtc acg gtg     691
Val Gln Gly Leu Arg Ile Leu Lys Gly Leu Gly Ala Ile Val Thr Val
            185                 190                 195

cgc cgt cgg tac gag gcg att tct ggt gag gct tat cgg aag acg gtt     739
Arg Arg Arg Tyr Glu Ala Ile Ser Gly Glu Ala Tyr Arg Lys Thr Val
        200                 205                 210

cat gcg gat gct gcg gaa gct cgc ttg aat ggt gtc acc gat gcg gcg     787
His Ala Asp Ala Ala Glu Ala Arg Leu Asn Gly Val Thr Asp Ala Ala
    215                 220                 225

ggc gcc atc ttt gtg tcc gcg ttg ggt att gga gca gga ttt ttg gcg     835
Gly Ala Ile Phe Val Ser Ala Leu Gly Ile Gly Ala Gly Phe Leu Ala
230                 235                 240                 245

ctg caa ggt cag atg agt att ggt gat ttg atc acg gtt gtg gga ctc     883
Leu Gln Gly Gln Met Ser Ile Gly Asp Leu Ile Thr Val Val Gly Leu
                250                 255                 260

aca cag ttt ttg atc atg ccg atg acc atg ctt ggt cga aat gtg gca     931
Thr Gln Phe Leu Ile Met Pro Met Thr Met Leu Gly Arg Asn Val Ala
            265                 270                 275

tcg cgc tgg gca tcg gcg gag gcg tcg gca aag cgt att agg gga gtg     979
Ser Arg Trp Ala Ser Ala Glu Ala Ser Ala Lys Arg Ile Arg Gly Val
        280                 285                 290

ctc ggt gct gat ttt gag aga gtg tct gcg cat gat gcg gac aag gct     1027
Leu Gly Ala Asp Phe Glu Arg Val Ser Ala His Asp Ala Asp Lys Ala
    295                 300                 305

gag gag att atc caa caa ctt gcc aaa ggt ttg acg gtt att cga ggc     1075
Glu Glu Ile Ile Gln Gln Leu Ala Lys Gly Leu Thr Val Ile Arg Gly
310                 315                 320                 325

act gat gag cag ctc gtt gag gta tta gag cag ttg cca cgt act cgg     1123
Thr Asp Glu Gln Leu Val Glu Val Leu Glu Gln Leu Pro Arg Thr Arg
                330                 335                 340

gtg att gtg gct cct cat gcg gcg gat ctt ttt gat caa agt gtc agg     1171
Val Ile Val Ala Pro His Ala Ala Asp Leu Phe Asp Gln Ser Val Arg
            345                 350                 355

gac aat gtg cat ccc gtg gca gag gtc gcg gag aaa gcc att gaa gtt     1219
Asp Asn Val His Pro Val Ala Glu Val Ala Glu Lys Ala Ile Glu Val
```

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        360                 365                 370

gcc tcc tgt gac gat att cca ggt ggt agt tcc aag att gtg ggc gag     1267
Ala Ser Cys Asp Asp Ile Pro Gly Gly Ser Ser Lys Ile Val Gly Glu
    375                 380                 385

ggt gga cgg ttg ctc tcg ggt ggt cag cgt cag cgc gtt gca ctg gct     1315
Gly Gly Arg Leu Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Leu Ala
390                 395                 400                 405

cgg gcg att gct ttt gat cca gag gtg ttg gtg ctt caa gat ccc aca     1363
Arg Ala Ile Ala Phe Asp Pro Glu Val Leu Val Leu Gln Asp Pro Thr
                410                 415                 420

acg gca gtg gat tct gtg acg gag caa aac att gct cag caa gtg gca     1411
Thr Ala Val Asp Ser Val Thr Glu Gln Asn Ile Ala Gln Gln Val Ala
            425                 430                 435

gca cac cgt gca gga aaa gtg acc att gtg ttt agt gag gca ccc gcg     1459
Ala His Arg Ala Gly Lys Val Thr Ile Val Phe Ser Glu Ala Pro Ala
        440                 445                 450

tgg agt gcg gtg gct gat caa cac gtt gag gca gct gct ttg cgg gag     1507
Trp Ser Ala Val Ala Asp Gln His Val Glu Ala Ala Ala Leu Arg Glu
    455                 460                 465

gtt atg aaa tgagtgggga gacgtcgaaa agc                               1539
Val Met Lys
470
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<210> 282
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 282

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Val Ala Ser Ala Gly Met Ala Ala Ser Phe Ile Cys Asn Gly Leu Thr
 1               5                  10                  15

Pro Val Ile Val Gly Lys Ala Val Asp Glu Ala Ile Gly Thr Ser Asp
            20                  25                  30

Leu Gln Arg Leu Trp Phe Trp Ile Ala Met Leu Ala Val Leu Phe Leu
        35                  40                  45

Thr Ala Met Thr Val Asn Trp Ile Ala Arg Tyr Met Leu Val Arg Ser
    50                  55                  60

Gln Gln Leu Val Ser His Asp Leu Arg Met Leu Val Thr Asp Arg Ile
65                  70                  75                  80

Gln Asp Pro Arg Gly Phe Ala Gly Lys Glu Arg Thr Ala Gly Gly Leu
                85                  90                  95

Leu Ser Ile Ala Ser Ser Asp Thr Gln Arg Val Gly Asp Ile Val Met
            100                 105                 110
```

```
Met Thr Val Phe Pro Val Ala Glu Leu Ala Ser Ile Ile Tyr Gly Ala
        115                 120                 125

Val Val Met Tyr Ser Ile Asn Pro Trp Leu Ser Val Ala Val Leu Ile
    130                 135                 140

Gly Gly Pro Leu Leu Val Val Val Ala Ile Gln Val Ser Lys Pro Leu
145                 150                 155                 160

Gln Lys Arg Ser Gly Ala Arg Gln Gln Ala Val Ala Gln Ala Ala Ala
                165                 170                 175

Thr Ala Thr Asp Val Val Gln Gly Leu Arg Ile Leu Lys Gly Leu Gly
            180                 185                 190

Ala Ile Val Thr Val Arg Arg Arg Tyr Glu Ala Ile Ser Gly Glu Ala
        195                 200                 205

Tyr Arg Lys Thr Val His Ala Asp Ala Ala Glu Ala Arg Leu Asn Gly
    210                 215                 220

Val Thr Asp Ala Ala Gly Ala Ile Phe Val Ser Ala Leu Gly Ile Gly
225                 230                 235                 240

Ala Gly Phe Leu Ala Leu Gln Gly Gln Met Ser Ile Gly Asp Leu Ile
                245                 250                 255

Thr Val Val Gly Leu Thr Gln Phe Leu Ile Met Pro Met Thr Met Leu
            260                 265                 270

Gly Arg Asn Val Ala Ser Arg Trp Ala Ser Ala Glu Ala Ser Ala Lys
        275                 280                 285

Arg Ile Arg Gly Val Leu Gly Ala Asp Phe Glu Arg Val Ser Ala His
    290                 295                 300

Asp Ala Asp Lys Ala Glu Glu Ile Ile Gln Gln Leu Ala Lys Gly Leu
305                 310                 315                 320

Thr Val Ile Arg Gly Thr Asp Glu Gln Leu Val Glu Val Leu Glu Gln
                325                 330                 335

Leu Pro Arg Thr Arg Val Ile Val Ala Pro His Ala Ala Asp Leu Phe
            340                 345                 350

Asp Gln Ser Val Arg Asp Asn Val His Pro Val Ala Glu Val Ala Glu
        355                 360                 365

Lys Ala Ile Glu Val Ala Ser Cys Asp Asp Ile Pro Gly Gly Ser Ser
    370                 375                 380

Lys Ile Val Gly Glu Gly Gly Arg Leu Leu Ser Gly Gly Gln Arg Gln
385                 390                 395                 400

Arg Val Ala Leu Ala Arg Ala Ile Ala Phe Asp Pro Glu Val Leu Val
                405                 410                 415
```

```
Leu Gln Asp Pro Thr Thr Ala Val Asp Ser Val Thr Glu Gln Asn Ile
            420                 425                 430

Ala Gln Gln Val Ala Ala His Arg Ala Gly Lys Val Thr Ile Val Phe
        435                 440                 445

Ser Glu Ala Pro Ala Trp Ser Ala Val Ala Asp Gln His Val Glu Ala
    450                 455                 460

Ala Ala Leu Arg Glu Val Met Lys
465                 470


<210> 283
<211> 1470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1447)
<223> RXN01190

<400> 283
cagggttttg atgagaacaa cacacaccgc ttcaagcatt ctgcgaagaa tgatcaggcg 60

gcagcggggc aaggttgcgt ttggcgcatt ctttttgggg atg tgg cag ctg tcg    115
                                           Met Trp Gln Leu Ser
                                             1               5

gaa gca ttg gtg ccg att gcg att ggt ttg atc gtt gat cat gcg gtt    163
Glu Ala Leu Val Pro Ile Ala Ile Gly Leu Ile Val Asp His Ala Val
                 10                  15                  20

ctc aca aaa gat ctc cgc cga tta gtg gtc ggg ctt gtc gct ttt gtt    211
Leu Thr Lys Asp Leu Arg Arg Leu Val Val Gly Leu Val Ala Phe Val
             25                  30                  35

gtg ctg ttt gtg gtg ttg agt ttt tct aat cgt ttc ggt tcg cgc gcg    259
Val Leu Phe Val Val Leu Ser Phe Ser Asn Arg Phe Gly Ser Arg Ala
         40                  45                  50

ttg aat agg gcc gtg aac ttt gaa tcc cat gcg ctc cgc gta gag gta    307
Leu Asn Arg Ala Val Asn Phe Glu Ser His Ala Leu Arg Val Glu Val
     55                  60                  65

gcc gat cat gcg ttg aag aat ctg gat ccg cgc aat ttg gtg cct ggc    355
Ala Asp His Ala Leu Lys Asn Leu Asp Pro Arg Asn Leu Val Pro Gly
 70                  75                  80                  85

gag gtg atg tcg cgg tcc acc gca gat gcg gat tct tcg acg cgt att    403
Glu Val Met Ser Arg Ser Thr Ala Asp Ala Asp Ser Ser Thr Arg Ile
                 90                  95                 100

ttc ggg cag atc gga acc ggt gtt tcg gct gcg acg gga ttt ctt ggt    451
Phe Gly Gln Ile Gly Thr Gly Val Ser Ala Ala Thr Gly Phe Leu Gly
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            105                     110                     115

gca gcg acc tac ctg ttg atc agt gac tgg ctg gtc ggg ttg ttg gtg      499
Ala Ala Thr Tyr Leu Leu Ile Ser Asp Trp Leu Val Gly Leu Leu Val
        120                     125                     130

ctt gtg ctg gta ccg atc att tcg gga gtg gtt gca ctg gct agc aag      547
Leu Val Leu Val Pro Ile Ile Ser Gly Val Val Ala Leu Ala Ser Lys
    135                     140                     145

ggc att tct aaa agg agt gtc acc cag cag gag aag ttg gcg gag tct      595
Gly Ile Ser Lys Arg Ser Val Thr Gln Gln Glu Lys Leu Ala Glu Ser
150                 155                     160                 165

ggt gcg cag gca agt gac atc atg atg ggg ctg cgc gtg atc aag gcg      643
Gly Ala Gln Ala Ser Asp Ile Met Met Gly Leu Arg Val Ile Lys Ala
                170                     175                 180

atc ggt ggc gag cgt tgg gcc gtg aag act ttt gaa aag gcg tcg cag      691
Ile Gly Gly Glu Arg Trp Ala Val Lys Thr Phe Glu Lys Ala Ser Gln
            185                     190                     195

gca tca gcg aga gcg gcg gtt gat act gca gtt gct tcg ggc aaa gtc      739
Ala Ser Ala Arg Ala Ala Val Asp Thr Ala Val Ala Ser Gly Lys Val
        200                     205                     210

gct ggt att ggt gag ttg tcc att gcg gtg aat ttg gct gcg gtg ttg      787
Ala Gly Ile Gly Glu Leu Ser Ile Ala Val Asn Leu Ala Ala Val Leu
    215                     220                     225

ttg ctt gct ggt tgg cgg gtc acc acg ggg gag ttg ggg cct ggc cag      835
Leu Leu Ala Gly Trp Arg Val Thr Thr Gly Glu Leu Gly Pro Gly Gln
230                 235                     240                 245

ttg atc gca att gtg ggt gtg gcg gtg tat ttg tca gag ccg att cgc      883
Leu Ile Ala Ile Val Gly Val Ala Val Tyr Leu Ser Glu Pro Ile Arg
                250                     255                 260

ttg ctg agc aac tcg att aat gcc tca gct att gcg cac ggt gca gcg      931
Leu Leu Ser Asn Ser Ile Asn Ala Ser Ala Ile Ala His Gly Ala Ala
            265                     270                     275

gag cgg gtg gct aat ttc tta aac ctc gac gaa tct cag gca cag tac      979
Glu Arg Val Ala Asn Phe Leu Asn Leu Asp Glu Ser Gln Ala Gln Tyr
        280                     285                     290

gaa agc agc gaa aca atc aat gac ggc gaa ttc ctc gtc atc gtg ccc     1027
Glu Ser Ser Glu Thr Ile Asn Asp Gly Glu Phe Leu Val Ile Val Pro
    295                     300                     305

cca gcc agc acg ctt cca cac ggc gac aat atc ttg gct aca cct cat     1075
Pro Ala Ser Thr Leu Pro His Gly Asp Asn Ile Leu Ala Thr Pro His
310                 315                     320                 325

gct gcc gac att ttc gaa ggt acc ttg cgg tca aat att tcc atg aat     1123
Ala Ala Asp Ile Phe Glu Gly Thr Leu Arg Ser Asn Ile Ser Met Asn
                330                     335                 340
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cat gag gac aac gtg cca att gat ccg cag gta att cgc gct tct ggt 1171
His Glu Asp Asn Val Pro Ile Asp Pro Gln Val Ile Arg Ala Ser Gly
345 350 355

ctg act gac atc att gag gtg gac gga ctt gat gcg ccg gtg cgc gat 1219
Leu Thr Asp Ile Ile Glu Val Asp Gly Leu Asp Ala Pro Val Arg Asp
360 365 370

acg gga agc aat tta tcg ggt ggg cag cgt cag cga gtg gct ttg gcc 1267
Thr Gly Ser Asn Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Leu Ala
375 380 385

agg gcg ttg cat gca gac gcg gaa gta ctg gtg ctg atg gat cca acc 1315
Arg Ala Leu His Ala Asp Ala Glu Val Leu Val Leu Met Asp Pro Thr
390 395 400 405

agc gcg gtg gat tca gtg acg gag gtg tct atc gcg cag ggg att aag 1363
Ser Ala Val Asp Ser Val Thr Glu Val Ser Ile Ala Gln Gly Ile Lys
410 415 420

cag ctg cga gca ggc aaa acc acc att gtg gtg agt tct tcg ccc gcg 1411
Gln Leu Arg Ala Gly Lys Thr Thr Ile Val Val Ser Ser Ser Pro Ala
425 430 435

ttt tac aac ttg gcg gat cgg gtg att tca cat gtc taatttgatg 1457
Phe Tyr Asn Leu Ala Asp Arg Val Ile Ser His Val
440 445

gcatcatcga cac 1470

<210> 284
<211> 449
<212> PRT
<213> Corynebacterium glutamicum

<400> 284
Met Trp Gln Leu Ser Glu Ala Leu Val Pro Ile Ala Ile Gly Leu Ile
1 5 10 15

Val Asp His Ala Val Leu Thr Lys Asp Leu Arg Arg Leu Val Val Gly
20 25 30

Leu Val Ala Phe Val Val Leu Phe Val Val Leu Ser Phe Ser Asn Arg
35 40 45

Phe Gly Ser Arg Ala Leu Asn Arg Ala Val Asn Phe Glu Ser His Ala
50 55 60

Leu Arg Val Glu Val Ala Asp His Ala Leu Lys Asn Leu Asp Pro Arg
65 70 75 80

Asn Leu Val Pro Gly Glu Val Met Ser Arg Ser Thr Ala Asp Ala Asp
85 90 95

Ser Ser Thr Arg Ile Phe Gly Gln Ile Gly Thr Gly Val Ser Ala Ala

100 105 110

Thr Gly Phe Leu Gly Ala Ala Thr Tyr Leu Leu Ile Ser Asp Trp Leu
115 120 125

Val Gly Leu Leu Val Leu Val Leu Val Pro Ile Ile Ser Gly Val Val
130 135 140

Ala Leu Ala Ser Lys Gly Ile Ser Lys Arg Ser Val Thr Gln Gln Glu
145 150 155 160

Lys Leu Ala Glu Ser Gly Ala Gln Ala Ser Asp Ile Met Met Gly Leu
165 170 175

Arg Val Ile Lys Ala Ile Gly Gly Glu Arg Trp Ala Val Lys Thr Phe
180 185 190

Glu Lys Ala Ser Gln Ala Ser Ala Arg Ala Ala Val Asp Thr Ala Val
195 200 205

Ala Ser Gly Lys Val Ala Gly Ile Gly Glu Leu Ser Ile Ala Val Asn
210 215 220

Leu Ala Ala Val Leu Leu Leu Ala Gly Trp Arg Val Thr Thr Gly Glu
225 230 235 240

Leu Gly Pro Gly Gln Leu Ile Ala Ile Val Gly Val Ala Val Tyr Leu
245 250 255

Ser Glu Pro Ile Arg Leu Leu Ser Asn Ser Ile Asn Ala Ser Ala Ile
260 265 270

Ala His Gly Ala Ala Glu Arg Val Ala Asn Phe Leu Asn Leu Asp Glu
275 280 285

Ser Gln Ala Gln Tyr Glu Ser Ser Glu Thr Ile Asn Asp Gly Glu Phe
290 295 300

Leu Val Ile Val Pro Pro Ala Ser Thr Leu Pro His Gly Asp Asn Ile
305 310 315 320

Leu Ala Thr Pro His Ala Ala Asp Ile Phe Glu Gly Thr Leu Arg Ser
325 330 335

Asn Ile Ser Met Asn His Glu Asp Asn Val Pro Ile Asp Pro Gln Val
340 345 350

Ile Arg Ala Ser Gly Leu Thr Asp Ile Ile Glu Val Asp Gly Leu Asp
355 360 365

Ala Pro Val Arg Asp Thr Gly Ser Asn Leu Ser Gly Gly Gln Arg Gln
370 375 380

Arg Val Ala Leu Ala Arg Ala Leu His Ala Asp Ala Glu Val Leu Val
385 390 395 400

Leu Met Asp Pro Thr Ser Ala Val Asp Ser Val Thr Glu Val Ser Ile

405 410 415

Ala Gln Gly Ile Lys Gln Leu Arg Ala Gly Lys Thr Thr Ile Val Val
420 425 430

Ser Ser Ser Pro Ala Phe Tyr Asn Leu Ala Asp Arg Val Ile Ser His
435 440 445

Val

<210> 285
<211> 1368
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1345)
<223> RXN01102

<400> 285
attctatggt tgttgggaga gatgacttaa tttggaatca cgggctttaa cacgcgctga 60

cattgagcaa cttcccagca tgtggaaaag cccaggtttc gtg gct gtc ctc gtg 115
Val Ala Val Leu Val
1 5

gcg gtt gca gca gcg ttc ggc agt tgg tca ctc ctt ctt ccc gtc gta 163
Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu Leu Leu Pro Val Val
10 15 20

ccg cta gcg gtc ctc aac aac ggc gga tca agc gct gtc gcc ggt gcc 211
Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser Ala Val Ala Gly Ala
25 30 35

acc act ggc atc ttc atg gca gct aca gtg atc act cag att ttc act 259
Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile Thr Gln Ile Phe Thr
40 45 50

ccc gct gcg ctg cgg aaa att ggc tac acc cca gtg atg gct ttc gcc 307
Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro Val Met Ala Phe Ala
55 60 65

gca ttc atg ctg ggt gtg cca gcc atc ggg tac atc ttc agc gtc gag 355
Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr Ile Phe Ser Val Glu
70 75 80 85

cca att cca gtg ctg gta gtg tcc gca ctt cga gga att ggg ttc ggt 403
Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg Gly Ile Gly Phe Gly
90 95 100

gcg ctc acc gtc gca gaa tct gcg ttg gtg gct gaa ctc gtt ccc gta 451
Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala Glu Leu Val Pro Val
105 110 115

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cgc ttc ttg ggc aaa gct tct gga atg ttg ggc gta ttt att ggc ctt    499
Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly Val Phe Ile Gly Leu
        120                 125                 130

tcc caa atg ctt ttc ctg cct gcc ggg ttg gcg tta ggt gac caa ttt    547
Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala Leu Gly Asp Gln Phe
    135                 140                 145

ggc tac aac gtg gtc tat gtt tta ggt gcc gtt atc gca cta gtt gca    595
Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val Ile Ala Leu Val Ala
150                 155                 160                 165

gcg gtg atg tgt ctg cgt att ccg cag gtt aag gca gcg gca aag cag    643
Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys Ala Ala Ala Lys Gln
                170                 175                 180

caa cca cag gtg agc gaa cag gag cgt tct gtt tcc acc tgg aag ttg    691
Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val Ser Thr Trp Lys Leu
            185                 190                 195

gtg ctg gtt ccc tcc ttg gct gtt acc agt ttg tca atg act ttt ggc    739
Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu Ser Met Thr Phe Gly
        200                 205                 210

gca gtg tct tca ttc ctt cca gct gca gtc att gag tta gat cca gga    787
Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile Glu Leu Asp Pro Gly
    215                 220                 225

tta ggt gct gca tta gcg ggt att att tta tcc att acc ggt ggt tct    835
Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser Ile Thr Gly Gly Ser
230                 235                 240                 245

tca atg gtg ttc cgc tac ctg tcc ggc gtt atc gct gac cgc cgc ggt    883
Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile Ala Asp Arg Arg Gly
                250                 255                 260

gtg cct ggt acc acg atg att cct gct cag atc att ggg ttc tta ggt    931
Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile Ile Gly Phe Leu Gly
            265                 270                 275

gtc gtt tta atc acc gtc aca atc ttc caa ggc tgg tcc gtg tgg ctt    979
Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly Trp Ser Val Trp Leu
        280                 285                 290

ttg att ata ggt gca gtg atg ttt ggt ggt gct ttt ggc atg gtg caa    1027
Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala Phe Gly Met Val Gln
    295                 300                 305

aac gaa gcg ttg ctt tca atg ttt ttc cgg ctt cct cgc act aga gtc    1075
Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu Pro Arg Thr Arg Val
310                 315                 320                 325

tcc gaa gcc tcc gcc atc tgg aat atc gcc ttt gat tcg gga aca gga    1123
Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe Asp Ser Gly Thr Gly
                330                 335                 340

atc gga agc ttc ctc ctt ggc ata gtt gcc gca tcg ctt gct tac agt    1171
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Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala Ser Leu Ala Tyr Ser
345 350 355

ggt gct ttt ggt tcc gga gcc gtg gtg att ttg ttt gga atc gtt ttg 1219
Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu Phe Gly Ile Val Leu
360 365 370

acc acc gcc gat cga atc att ggg cgg cac cgc att act gaa tac aac 1267
Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg Ile Thr Glu Tyr Asn
375 380 385

aac acc cgc gcg cgt ttg cgc cag gtg cca gtc gct cgg cgt gca gtg 1315
Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val Ala Arg Arg Ala Val
390 395 400 405

caa ggg ctg cgc aac agg cgc aaa gat cgc taaaacgctt ttcgacgcca 1365
Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
410 415

ccc 1368

<210> 286
<211> 415
<212> PRT
<213> Corynebacterium glutamicum

<400> 286
Val Ala Val Leu Val Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu
1 5 10 15

Leu Leu Pro Val Val Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser
20 25 30

Ala Val Ala Gly Ala Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile
35 40 45

Thr Gln Ile Phe Thr Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro
50 55 60

Val Met Ala Phe Ala Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr
65 70 75 80

Ile Phe Ser Val Glu Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg
85 90 95

Gly Ile Gly Phe Gly Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala
100 105 110

Glu Leu Val Pro Val Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly
115 120 125

Val Phe Ile Gly Leu Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala
130 135 140

Leu Gly Asp Gln Phe Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val
145 150 155 160

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Ile Ala Leu Val Ala Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys
                165                 170                 175

Ala Ala Ala Lys Gln Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val
            180                 185                 190

Ser Thr Trp Lys Leu Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu
        195                 200                 205

Ser Met Thr Phe Gly Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile
    210                 215                 220

Glu Leu Asp Pro Gly Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser
225                 230                 235                 240

Ile Thr Gly Gly Ser Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile
                245                 250                 255

Ala Asp Arg Arg Gly Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile
            260                 265                 270

Ile Gly Phe Leu Gly Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly
        275                 280                 285

Trp Ser Val Trp Leu Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala
    290                 295                 300

Phe Gly Met Val Gln Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu
305                 310                 315                 320

Pro Arg Thr Arg Val Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe
                325                 330                 335

Asp Ser Gly Thr Gly Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala
            340                 345                 350

Ser Leu Ala Tyr Ser Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu
        355                 360                 365

Phe Gly Ile Val Leu Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg
    370                 375                 380

Ile Thr Glu Tyr Asn Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val
385                 390                 395                 400

Ala Arg Arg Ala Val Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
                405                 410                 415
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<210> 287
<211> 348
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(325)
<223> RXN00788

<400> 287
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ttgatccagc actgcttgca gtgaggcctc attagttggc atg gcc tcc tcc atc 115
Met Ala Ser Ser Ile
1 5

aac atc gga gtg ttc aac ctt gga aat gct gtt gct gcc tgg ctt gct 163
Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val Ala Ala Trp Leu Ala
10 15 20

ggt gca acc atc acc act tcc ctt gga ctc aca tca gcc gga tta gtt 211
Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr Ser Ala Gly Leu Val
25 30 35

ggc ggt ttg atg acg tcc ctc gga cta gtg ttg gcc atc gtg gct gtg 259
Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu Ala Ile Val Ala Val
40 45 50

gtt ttg cgt cga aaa gcg caa ggc acc caa gcg acc atc agc gtt gtg 307
Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala Thr Ile Ser Val Val
55 60 65

gag cac cag ccc gcc caa taaataattt ctctcttcta att 348
Glu His Gln Pro Ala Gln
70 75

<210> 288
<211> 75
<212> PRT
<213> Corynebacterium glutamicum

<400> 288
Met Ala Ser Ser Ile Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val
1 5 10 15

Ala Ala Trp Leu Ala Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr
20 25 30

Ser Ala Gly Leu Val Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu
35 40 45

Ala Ile Val Ala Val Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala
50 55 60

Thr Ile Ser Val Val Glu His Gln Pro Ala Gln
65 70 75

<210> 289
<211> 1764
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(1741)
<223> RXN02119

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gcttaaattg cttgtcgacg cctagtgcca caatggagac atg acc gaa aca ctt   115
                                           Met Thr Glu Thr Leu
                                           1               5

gtg gtg aat ggc ctt gca ggc ggc tat ggg cac cgc aca tta ttt aac   163
Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His Arg Thr Leu Phe Asn
                10                  15                  20

gat gtg aat ctc acc gta gct gcc ggc gat gtc gtg ggc gtt gtc ggc   211
Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val Val Gly Val Val Gly
            25                  30                  35

gtc aat ggc gct ggt aaa tcc aca ttt cta aaa att ctg gcg ggc gtg   259
Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys Ile Leu Ala Gly Val
        40                  45                  50

gaa aag cca ctg gct gga act atc gcg ctt tcg cca gcc gat gct ttt   307
Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser Pro Ala Asp Ala Phe
    55                  60                  65

gtg ggc tac ttg cca cag gaa cac acc cgc acg tct gga gag acg atc   355
Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr Ser Gly Glu Thr Ile
70                  75                  80                  85

gca gtt tac att gct cgt cga acc ggc tgc caa gct gca aca act gcc   403
Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln Ala Ala Thr Thr Ala
                90                  95                  100

atg gat gac acc gcc gaa gcg ttt ggt gcg gat cca gac aac gct gcc   451
Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp Pro Asp Asn Ala Ala
            105                 110                 115

ttg gcc gat gca tac gcc gag gcg ctg gat cgg tgg atg gcc agt ggc   499
Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg Trp Met Ala Ser Gly
        120                 125                 130

gca gcc gat ttg gat gaa cgc atc ccc atc gtg ctc gct gat ttg ggc   547
Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val Leu Ala Asp Leu Gly
    135                 140                 145

ttt gag ctt ccc acc tcg acg ctg atg gaa gga ctt tca ggc ggg cag   595
Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly Leu Ser Gly Gly Gln
150                 155                 160                 165

gca gcc cgg gtc ggg ctg gcg gcg tta ctg ttg tca cgt ttt gac att   643
Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu Ser Arg Phe Asp Ile
                170                 175                 180
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gtg ctt ctc gac gag ccc acc aac gat ttg gat ctc gac ggt ctt gag     691
Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Leu Asp Gly Leu Glu
            185                 190                 195

caa ctg gag aat ttt gtt cag ggg ctt cgc ggg gga gtc gta ctg gtc     739
Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly Gly Val Val Leu Val
        200                 205                 210

agc cat gat cgt gag ttt ctt tcc agg tgt gtg acc act gtg ctg gaa     787
Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val Thr Thr Val Leu Glu
    215                 220                 225

ctc gat ctg cac caa aat tcc cac cat gtt tat ggc ggt gga tat gat     835
Leu Asp Leu His Gln Asn Ser His His Val Tyr Gly Gly Gly Tyr Asp
230                 235                 240                 245

tcc tac ctt gag gaa cgc gca gtg cta cgc cag cac gcc cgt gac caa     883
Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln
                250                 255                 260

tat gag gaa ttt gcg gaa aag aag aag gac ctt gtg gca cgt gct cga     931
Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg
            265                 270                 275

acg cag cgt gaa tgg tct agt cac ggt gtc cgc aat gct att aaa cgt     979
Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg Asn Ala Ile Lys Arg
        280                 285                 290

gca cct gac aac gac aaa ctt cgg aag aaa gcc gct gcg gaa tcc agt     1027
Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala Ala Ala Glu Ser Ser
    295                 300                 305

gaa aag cag gct caa aaa gtc cgc cag atg gaa agc cgc atc gct cgg     1075
Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu Ser Arg Ile Ala Arg
310                 315                 320                 325

tta gaa gaa gtt gaa gag cca cgt aaa gaa tgg aaa ctg cag ttc agc     1123
Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp Lys Leu Gln Phe Ser
                330                 335                 340

gtc ggt aag gcg tcg cgg tca agt tct gtt gtt tcc acg ttg aat gat     1171
Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val Ser Thr Leu Asn Asp
            345                 350                 355

gca agc ttc acc caa ggc gat ttc acc ttg gga cca gta tcc atc caa     1219
Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly Pro Val Ser Ile Gln
        360                 365                 370

gta aat gct ggc gat cgc att ggc atc aca gga ccc aac ggt gct ggt     1267
Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly Pro Asn Gly Ala Gly
    375                 380                 385

aaa tcc aca ttg ctg cgc gga cta ttg gga aac caa gaa ccc acc agc     1315
Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn Gln Glu Pro Thr Ser
390                 395                 400                 405

ggt act gcc acg atg ggc acg agc gtg gcg atc gga gaa atc gat cag     1363
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Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile Gly Glu Ile Asp Gln
410 415 420

gca cga gcg tta ctt gat cca cag ttg cca ctg att tct gcg ttt gaa 1411
Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu Ile Ser Ala Phe Glu
425 430 435

aag cat gtt cca gac tta ccg atc agt gag gtg cgc aca ctg ctc gcg 1459
Lys His Val Pro Asp Leu Pro Ile Ser Glu Val Arg Thr Leu Leu Ala
440 445 450

aaa ttt ggg ctg aat gat aat cat gtg gaa cgg gac gtc gaa aag cta 1507
Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg Asp Val Glu Lys Leu
455 460 465

tct cct ggc gag cgc acg cgc gcc gga ctt gcg ctg cta cag gtg cgg 1555
Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala Leu Leu Gln Val Arg
470 475 480 485

ggc gtc aac gtg ctt gtt ctt gat gag ccc acc aac cac ctt gac ctg 1603
Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr Asn His Leu Asp Leu
490 495 500

gag gcc atc gag caa ttg gag caa gcg ttg gcc tcg tat gat ggt gtg 1651
Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala Ser Tyr Asp Gly Val
505 510 515

ttg ctg ctg gtc acg cac gat cgt cgc atg ttg gac gct gtg cag acc 1699
Leu Leu Leu Val Thr His Asp Arg Arg Met Leu Asp Ala Val Gln Thr
520 525 530

aat cgt cgt tgg cat gtc gag gct ggc gaa gtt agg gag cta 1741
Asn Arg Arg Trp His Val Glu Ala Gly Glu Val Arg Glu Leu
535 540 545

taaccgtttc cgtattgatg cca 1764

<210> 290
<211> 547
<212> PRT
<213> Corynebacterium glutamicum

<400> 290
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Arg Thr Leu Phe Asn Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val
20 25 30

Val Gly Val Val Gly Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys
35 40 45

Ile Leu Ala Gly Val Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser
50 55 60

Pro Ala Asp Ala Phe Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr

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65                  70                  75                  80

Ser Gly Glu Thr Ile Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln
                85                  90                  95

Ala Ala Thr Thr Ala Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp
            100                 105                 110

Pro Asp Asn Ala Ala Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg
        115                 120                 125

Trp Met Ala Ser Gly Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val
    130                 135                 140

Leu Ala Asp Leu Gly Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly
145                 150                 155                 160

Leu Ser Gly Gly Gln Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu
                165                 170                 175

Ser Arg Phe Asp Ile Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp
            180                 185                 190

Leu Asp Gly Leu Glu Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly
        195                 200                 205

Gly Val Val Leu Val Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val
    210                 215                 220

Thr Thr Val Leu Glu Leu Asp Leu His Gln Asn Ser His His Val Tyr
225                 230                 235                 240

Gly Gly Gly Tyr Asp Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln
                245                 250                 255

His Ala Arg Asp Gln Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu
            260                 265                 270

Val Ala Arg Ala Arg Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg
        275                 280                 285

Asn Ala Ile Lys Arg Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala
    290                 295                 300

Ala Ala Glu Ser Ser Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu
305                 310                 315                 320

Ser Arg Ile Ala Arg Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp
                325                 330                 335

Lys Leu Gln Phe Ser Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val
            340                 345                 350

Ser Thr Leu Asn Asp Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly
        355                 360                 365

Pro Val Ser Ile Gln Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly
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370 375 380

Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn
385 390 395 400

Gln Glu Pro Thr Ser Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile
405 410 415

Gly Glu Ile Asp Gln Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu
420 425 430

Ile Ser Ala Phe Glu Lys His Val Pro Asp Leu Pro Ile Ser Glu Val
435 440 445

Arg Thr Leu Leu Ala Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg
450 455 460

Asp Val Glu Lys Leu Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala
465 470 475 480

Leu Leu Gln Val Arg Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr
485 490 495

Asn His Leu Asp Leu Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala
500 505 510

Ser Tyr Asp Gly Val Leu Leu Leu Val Thr His Asp Arg Arg Met Leu
515 520 525

Asp Ala Val Gln Thr Asn Arg Arg Trp His Val Glu Ala Gly Glu Val
530 535 540

Arg Glu Leu
545

<210> 291
<211> 1638
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1615)
<223> RXN01605

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attgaagtca gcgccgagga agccgcgagg gaatcagacg acgggcacct actacttcgg 60

cattgaaatt ccgaagaact tcagcgattc tattgccagc gtg acc agc gat tca 115
Val Thr Ser Asp Ser
1 5

ccc gcg cca gca acc gtc aac gcg gta ttc aac aac agc aac ggc ttc 163
Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn Asn Ser Asn Gly Phe
10 15 20

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att gcc tcc atg ctg ggc aac cag gtg gtc aac act gtt gtg gag acc    211
Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn Thr Val Val Glu Thr
            25                  30                  35

atg gac acg gaa ttc ggc gtc cgc att gtg gat aac atg ctc gtc ggt    259
Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp Asn Met Leu Val Gly
        40                  45                  50

ttc tcc acc ttg ggc gac ggc atg aac caa gcc gcc gaa ggt gcc act    307
Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala Ala Glu Gly Ala Thr
    55                  60                  65

acg ctc agc gat ggc gtc ggt tcc gcc aac gac ggt gca gtt cag ctt    355
Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp Gly Ala Val Gln Leu
70                  75                  80                  85

gcc gac ggc gcg gtc acc ctg cgc gac ggc atc gca agt gcc aat gag    403
Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile Ala Ser Ala Asn Glu
                90                  95                  100

ggt gcg caa tcg ctt gcc gac ggc gcc agc cag ctc gac acc ggc ctc    451
Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln Leu Asp Thr Gly Leu
            105                 110                 115

ggc tcc gcg gct aca ggc agc caa acg ctc gcc gac ggt cta tcc agc    499
Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala Asp Gly Leu Ser Ser
        120                 125                 130

ctg tct gcg ggc acc gcc caa cta ggc caa ggc gca acc cag gtt tca    547
Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly Ala Thr Gln Val Ser
    135                 140                 145

gat ggc gtg ggc caa ctt gtc gac caa gta gca cca ctg acc gcc tat    595
Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala Pro Leu Thr Ala Tyr
150                 155                 160                 165

gtt cca gac atc aac tct cag ttg atc acc ctg cgc gac ggc gca gcc    643
Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu Arg Asp Gly Ala Ala
                170                 175                 180

acc att gcc tct gaa cta tct gat ccc tcc agc acc tac cgc tcc ggc    691
Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser Thr Tyr Arg Ser Gly
            185                 190                 195

gtg gac tcc gct gtg agc gca tcc cag caa cta gca gcc ggc ctg caa    739
Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu Ala Ala Gly Leu Gln
        200                 205                 210

acc ctg aaa gac gga tcc agc caa ctc agc atc ggt gca cgc acc ctc    787
Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile Gly Ala Arg Thr Leu
    215                 220                 225

gct gat ggc acc agc caa ttg gcc gca ggt tcc gaa cag cta gtt gtt    835
Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser Glu Gln Leu Val Val
230                 235                 240                 245

ggc gca caa gca ctg cgc gac ggc acc gtc cag ctt gat gaa ggc tcc    883
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Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln Leu Asp Glu Gly Ser
                250                 255                 260

agc gaa ctc gcc ctc aaa ctc acc gac ggc gca agc caa gta cca acc      931
Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala Ser Gln Val Pro Thr
            265                 270                 275

ttc gct gac ggc gca gac acc acc atc gca acc cca gtt gaa aca gaa      979
Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr Pro Val Glu Thr Glu
        280                 285                 290

caa gca gga gac acc aca ccg ctc ttc ggt att ggt ctc gca cca ttc     1027
Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile Gly Leu Ala Pro Phe
    295                 300                 305

ttc atg gct gtc ggc ctg ttc atg gga gca acc gtt gcc tgg atg atc     1075
Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr Val Ala Trp Met Ile
310                 315                 320                 325

ctg cac cca atc agt cgc cgc gca ctc gac tcc cgc atg gga ggc ttc     1123
Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser Arg Met Gly Gly Phe
                330                 335                 340

cga ggc acc ctg gca agc tac ctt cca tca aca gtc tta ggc ctt ggc     1171
Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr Val Leu Gly Leu Gly
            345                 350                 355

caa gca acc atc atg tgg gca gta ctg tac ttc ctg ctc gac ctc aat     1219
Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe Leu Leu Asp Leu Asn
        360                 365                 370

cca gct cac cca gct gga ctg tgg atg gcg atg gtc gcc atc tca tgg     1267
Pro Ala His Pro Ala Gly Leu Trp Met Ala Met Val Ala Ile Ser Trp
    375                 380                 385

gta ttc atc tcc att acc cat atg ttc aac aac gtg gca gga ccc tcc     1315
Val Phe Ile Ser Ile Thr His Met Phe Asn Asn Val Ala Gly Pro Ser
390                 395                 400                 405

gca ggc cgt gtg ctg tcc atc gtg atg atg tcc ttc cag cta gtc tcc     1363
Ala Gly Arg Val Leu Ser Ile Val Met Met Ser Phe Gln Leu Val Ser
                410                 415                 420

tcc ggt ggc cta tac cca cca gaa acc cag cca gca ttc ttc cac tgg     1411
Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro Ala Phe Phe His Trp
            425                 430                 435

ttc cac acc tac gac ccg atc acc tac gca gtc aac ctc gtg cgc caa     1459
Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val Asn Leu Val Arg Gln
        440                 445                 450

atg atc ttc aac gaa acc cca tcc aac gac cca cgc ttc ata caa gca     1507
Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro Arg Phe Ile Gln Ala
    455                 460                 465

atc tgg gta ctg ctc ttc atc tgg gca ctg atg ctc gcc atc tcc acc     1555
Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met Leu Ala Ile Ser Thr
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470                 475                 480                 485

ctg gcg aat aga aca aac aag gtt ctt cgc atg aag gac tac cac cca     1603
Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met Lys Asp Tyr His Pro
                490                 495                 500

gaa ctg aag gtc taaaagcttt tcccgcccgg ttc                           1638
Glu Leu Lys Val
            505


<210> 292
<211> 505
<212> PRT
<213> Corynebacterium glutamicum

<400> 292
Val Thr Ser Asp Ser Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn
 1               5                  10                  15

Asn Ser Asn Gly Phe Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn
            20                  25                  30

Thr Val Val Glu Thr Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp
        35                  40                  45

Asn Met Leu Val Gly Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala
    50                  55                  60

Ala Glu Gly Ala Thr Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp
65                  70                  75                  80

Gly Ala Val Gln Leu Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile
                85                  90                  95

Ala Ser Ala Asn Glu Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln
            100                 105                 110

Leu Asp Thr Gly Leu Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala
        115                 120                 125

Asp Gly Leu Ser Ser Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly
    130                 135                 140

Ala Thr Gln Val Ser Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala
145                 150                 155                 160

Pro Leu Thr Ala Tyr Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu
                165                 170                 175

Arg Asp Gly Ala Ala Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser
            180                 185                 190

Thr Tyr Arg Ser Gly Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu
        195                 200                 205

Ala Ala Gly Leu Gln Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile
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210 215 220

Gly Ala Arg Thr Leu Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser
225 230 235 240

Glu Gln Leu Val Val Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln
245 250 255

Leu Asp Glu Gly Ser Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala
260 265 270

Ser Gln Val Pro Thr Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr
275 280 285

Pro Val Glu Thr Glu Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile
290 295 300

Gly Leu Ala Pro Phe Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr
305 310 315 320

Val Ala Trp Met Ile Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser
325 330 335

Arg Met Gly Gly Phe Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr
340 345 350

Val Leu Gly Leu Gly Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe
355 360 365

Leu Leu Asp Leu Asn Pro Ala His Pro Ala Gly Leu Trp Met Ala Met
370 375 380

Val Ala Ile Ser Trp Val Phe Ile Ser Ile Thr His Met Phe Asn Asn
385 390 395 400

Val Ala Gly Pro Ser Ala Gly Arg Val Leu Ser Ile Val Met Met Ser
405 410 415

Phe Gln Leu Val Ser Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro
420 425 430

Ala Phe Phe His Trp Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val
435 440 445

Asn Leu Val Arg Gln Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro
450 455 460

Arg Phe Ile Gln Ala Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met
465 470 475 480

Leu Ala Ile Ser Thr Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met
485 490 495

Lys Asp Tyr His Pro Glu Leu Lys Val
500 505

<210> 293
<211> 664
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXN01091

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ggtctatgct ggactatcgc cttttgacac gagtatcgca atg gtc ccg aac aca 115
Met Val Pro Asn Thr
1 5

gtc ctt atc cat gac gaa acc gcc gat ctg gcg acg cag atc cag cgg 163
Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala Thr Gln Ile Gln Arg
10 15 20

ctg gaa cat atc atg gcg tgc ctg cgc gat ccg gtc agc gga tgc ccg 211
Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro Val Ser Gly Cys Pro
25 30 35

tgg gat att gaa cag acc ttt gcc agc atc gcg ccc cac acg att gag 259
Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala Pro His Thr Ile Glu
40 45 50

gaa ggc tac gag gtt gcc gac gcc atc gcg cag gaa gac tgg ccc gag 307
Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln Glu Asp Trp Pro Glu
55 60 65

cta cgc ggc gag ttg ggc gat ttg ctg ttt cag acc gtg ttt cac gcc 355
Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln Thr Val Phe His Ala
70 75 80 85

caa atg gcg cgc gag gca ggc cat ttc gct ttg gtt gac gtg gtg aag 403
Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu Val Asp Val Val Lys
90 95 100

gca att tcg gac aag atg gtt ttg cgc cat ccg cac gtg ttc ggc gcg 451
Ala Ile Ser Asp Lys Met Val Leu Arg His Pro His Val Phe Gly Ala
105 110 115

cag tcg aac gcg aaa tcc gcc gac cag cag gtg gaa gat tgg gaa gtc 499
Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val Glu Asp Trp Glu Val
120 125 130

atc aag gcg ccc gag cgc gcg ggc aaa gcg caa aag ggc gtt ttg gat 547
Ile Lys Ala Pro Glu Arg Ala Gly Lys Ala Gln Lys Gly Val Leu Asp
135 140 145

ggc gtc gcg ctg gga ctg cct gcc ctg atg cgc gcg acg aag ctg caa 595
Gly Val Ala Leu Gly Leu Pro Ala Leu Met Arg Ala Thr Lys Leu Gln
150 155 160 165

aac aac gcc gcg cgc gtt ggg ttt gat tgg ccc gac att ggg cag gta 643
Asn Asn Ala Ala Arg Val Gly Phe Asp Trp Pro Asp Ile Gly Gln Val
170 175 180

ctt gga aag gtg acc gag gaa 664
Leu Gly Lys Val Thr Glu Glu
185

<210> 294
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 294
Met Val Pro Asn Thr Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala
1 5 10 15

Thr Gln Ile Gln Arg Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro
20 25 30

Val Ser Gly Cys Pro Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala
35 40 45

Pro His Thr Ile Glu Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln
50 55 60

Glu Asp Trp Pro Glu Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln
65 70 75 80

Thr Val Phe His Ala Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu
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act ctc aag caa aca act ctt cgc tct gat gag ttc tct tgc cca tcc 163
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Cys Val Ser Lys Ile Glu Asn Lys Leu Asn Gly Leu Asp Gly Val Asp
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Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile Leu Val Asp His Asp
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Pro Ser Lys Val Ser Ile Lys Asp Leu Val Ala Ala Val Ala Glu Val
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acg ctg aag aac acc acc ttg cgc tct gat gag ttc acc tgt ccg agc   163
Thr Leu Lys Asn Thr Thr Leu Arg Ser Asp Glu Phe Thr Cys Pro Ser
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tgt gtc gcc aag atc gaa aac aag ctg aat ggt ttg gac ggc gtg gag   211
Cys Val Ala Lys Ile Glu Asn Lys Leu Asn Gly Leu Asp Gly Val Glu
            25                  30                  35

aat gcg gag gtg aag ttc tcc tcc gga cgc atc ctg atc acc cac gac   259
Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile Leu Ile Thr His Asp
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cca cag aag gtc tcc gta cgt gac ctg gtc acc gcg gta gcc gag gtc   307
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                                             1               5

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             25                  30                  35

gca ctt cga aac agt ggt gaa ctt tcc gta aac cac ctc gcg gac atc   259
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gtc gat aaa tcc ccc gca gca gtt tcc caa cac ctc gcc cgg ctg cgc   307
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     55                  60                  65

atg gcc cga atc gtg tcc acc cgt caa gaa ggt caa cga gtt ttc tac   355
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 70                  75                  80                  85

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35 40 45

His Leu Ala Asp Ile Val Asp Lys Ser Pro Ala Ala Val Ser Gln His
50 55 60

Leu Ala Arg Leu Arg Met Ala Arg Ile Val Ser Thr Arg Gln Glu Gly
65 70 75 80

Gln Arg Val Phe Tyr Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val
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BGI-124CPPC - 97 -

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199 31 457.8	8 July 1999 (08.07.1999)	DE
199 32 230.9	9 July 1999 (09.07.1999)	DE
199 32 209.0	9 July 1999 (09.07.1999)	DE
199 32 914.1	14 July 1999 (14.07.1999)	DE
60/151,214	27 August 1999 (27.08.1999)	US
199 40 764.9	27 August 1999 (27.08.1999)	DE
199 41 382.7	31 August 1999 (31.08.1999)	DE

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(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:
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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 01/00804 A3

(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING STRESS, RESISTANCE AND TOLERANCE PROTEINS

(57) Abstract: Isolated nucleic acid molecules, designated SRT nucleic acid molecules, which encode novel SRT proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SRT nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SRT proteins, mutated SRT proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SRT genes in this organism.

INTERNATIONAL SEARCH REPORT

Inte nal Application No
PCT/IB 00/00922

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/31 C12N1/21 C12Q1/68 C07K14/34

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EBI [Online] AC X13385, 19 March 1999 (1999-03-19) BARASH S. ET AL.: "Enterococcus faecalis genome contig" XP002152527 abstract ---	6,8
X	JAEGER WOLFGANG ET AL: "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli." JOURNAL OF BACTERIOLOGY, vol. 179, no. 7, 1997, pages 2449-2451, XP002152524 ISSN: 0021-9193 the whole document ---	1,2, 8-19,22

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 November 2000	13. 02. 01

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Kania, T

INTERNATIONAL SEARCH REPORT

Inte: nal Application No
PCT/IB 00/00922

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WEHRMANN AXEL ET AL: "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum." JOURNAL OF BACTERIOLOGY, vol. 180, no. 12, June 1998 (1998-06), pages 3159-3165, XP002152525 ISSN: 0021-9193 cited in the application the whole document ---	1,2,8, 19,22
X	PETER H ET AL: "CORYNEBACTERIUM GLUTAMICUM IS EQUIPPED WITH FOUR SECONDARY CARRIERSFOR COMPATIBLE SOLUTES: IDENTIFICATION, SEQUENCING, AND CHARACTERIZATION OF THE PROLINE/ECTOINE UPTAKE SYSTEM, PROP, AND THE ECTOINE/PROLINE/GLYCINE BETAINE CARRIER, ECTP" JOURNAL OF BACTERIOLOGY,WASHINGTON, DC,US, vol. 180, no. 22, 1998, pages 6005-6012, XP000917352 ISSN: 0021-9193 the whole document ---	1,2, 8-19,22
X	CHAN MING-SHUN ET AL: "Cloning of m-fluorophenylalanine-resistant gene and mutational analysis of feedback-resistant prephenate dehydratase from Corynebacterium glutamicum." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 219, no. 2, 1996, pages 537-542, XP002152526 ISSN: 0006-291X the whole document ---	1,2, 8-19,22
X	EP 0 752 472 A (AJINOMOTO KK) 8 January 1997 (1997-01-08) the whole document ---	1,2, 8-19,22, 25-34
X	WO 99 02692 A (YAGOSHI CHIZU ;AJINOMOTO KK JP); KIMURA EIICHIRO (JP); NAKAMURA J) 21 January 1999 (1999-01-21) the whole document & EP 1 002 866 A (AJINOMOTO KK) 24 May 2000 (2000-05-24) ---	1,2, 8-19,22, 25-34
X	WO 88 09819 A (MASSACHUSETTS INST TECHNOLOGY) 15 December 1988 (1988-12-15) the whole document ---	1,2, 8-19,22, 25-34

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INTERNATIONAL SEARCH REPORT

Inte.   nal Application No
PCT/IB 00/00922

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	FR 2 607 827 A (PASTEUR INSTITUT) 10 June 1988 (1988-06-10) the whole document ---	1-38
A	EP 0 252 558 A (SCLAVO SPA) 13 January 1988 (1988-01-13) the whole document ---	35
P,X	DATABASE EBI [Online] AC AF237667, 14 March 2000 (2000-03-14) KIM H. AND LEE H.: "Nucleotide sequence of the lmrB gene in Corynebacterium glutamicum" XP002152528 abstract -----	1-24

INTERNATIONAL SEARCH REPORT

ıational application No.
PCT/IB 00/00922

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-38 partially

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: invention 1: claims 1-38 partially

   An isolated nucleic acid molecule from Corynebacterium glutamicum encoding a stress, resistance, or tolerance gene disclaiming the F-designated genes in table 1. Said gene having the SEQ ID NO:1, homologs (at least 50% homology), variants, and DNA sequences hybridizing thereto, as well as vectors and host cells comprising said sequences. An isolated stress, resistance, or tolerance polypeptide from C. glutamicum. Said protein having the SEQ ID NO:2, homologs (at least 50% homology), and variants thereof. The use of said sequences to modify the production of or produce a fine chemical from said host cell, the fine chemical especially being an amino acid.A method for diagnosing the presence or activity of Corynebacterium diphtheriae in a subject employing said sequences.A host cell comprising said nucleic acid sequences wherein said sequences are disrupted modified, or under the control of a heterologous regulatory region.

2. Claims: inventions 2-122: claims 1-38 partially

   as invention 1 but relating to the pairs of sequences as listed in Table 1 (apart from the ones disclaimed)

INTERNATIONAL SEARCH REPORT

..formation on patent family members

Inte. 'nal Application No
PCT/IB 00/00922

Patent document cited in search report		Publication date	Patent family member(s)			Publication date
EP 0752472	A	08-01-1997	BR	9506883	A	19-08-1997
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			DE	69514914	T	15-06-2000
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